

GenCore version 5.1.6
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 in search, using sw model
 rch 30, 2004, 15:00:47 ; Search time 22 Seconds
 (without alignments)
 1262.490 Million cell updates/sec

1:09-976-740-43

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IGO

pop 60.0 , Gapext 60.0

9414 seqs, 51625971 residues

ts satisfying chosen parameters: 389414

gth: 0

gth: 2000000000

isting first 150 summaries

ssued Patents AA.*

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/cgn2_6/ptodata/2/iaa/backfiles.pep.*

the number of results predicted by chance to have a
 r than or equal to the score of the result being printed,
 ed by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

Publication US/09616289

ION:

es, Ann M.

W, Simon W.

ona, Anibal A.

ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ION: ATHEROSCLEROSIS

ION: ATHEROSCLEROSIS

ION NUMBER: US/09/616,289

DATE: 2000-07-14

ION NUMBER: US 09/517,849

ATE: 2000-03-02

ION NUMBER: US 08/979,608

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RESULT 2

US-08-979-608A-7
; Sequence 7, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGN
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA

02110-2804
 EADABLE FORM:
 M TYPE: Diskette
 TER: IBM Compatible
 TING SYSTEM: DOS
 ARE: FastSeq for Windows Version 2.0
 PLICATION DATA:
 G DATE: 03-JUN-1997
 G DATE: 26-NOV-1997
 G DATE: 27-NOV-1996
 GENT INFORMATION:
 Myers, Louis
 TRATION NUMBER: 35,965
 ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
 ICATION INFORMATION:
 HONE: 617/542-5070
 AX: 617/542-8906
 SEQ ID NO: 7:
 CHARACTERISTICS:
 H: 217 amino acids
 amino acid
 OGY: linear
 YPE: protein
 ESRIPTION: SEQ ID NO: 7:

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 nservative 0; Mismatches 0; Indels 0; Gaps 0;
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 RLGLPALKIYEHKIVLQGHFEDDDPDGFLG 217

cation US/09517849

ATION:
 Lees, Ann M.
 Lees, Robert S.
 Law, Simon W.
 Arjona, Anibal A.
 INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
 BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
 TREATING ATHEROSCLEROSIS
 SEQUENCES: 42
 DENCE ADDRESS:
 ESSEE: Fish & Richardson P.C.
 IT: 225 Franklin Street
 : Boston
 3: MA
 TRY: USA
 02110-2804
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COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
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 APPLICATION NUMBER: US/09/517,849
 FILING DATE: 02-Mar-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/979,608
 FILING DATE: 26-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Louis
 REGISTRATION NUMBER: 35,965
 REFERENCE/DOCKET NUMBER: 10797-003001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
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 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-517-849-7

Query Match 40.3%; Score 217; DB 4; Length 217;
 Best Local Similarity 100.0%; Pred. No. 1.3e-180;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; G

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 QY 382 PCGPHQQDEGRGAPGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVPLPPGKPA.
 Db 61 PCGPHQQDEGRGAPGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVPLPPGKPA.
 QY 442 DGPFGCPGRKEKPSDPVWTVMDVVEYFTAGFPEQATAFOEQEIDGKSLLMQ
 Db 121 DGPFGCPGRKEKPSDPVWTVMDVVEYFTAGFPEQATAFOEQEIDGKSLLMQ
 QY 502 LTGLSRLGPALKIYEHKIVLQGHFEDDDPDGFLG 538
 Db 181 LTGLSRLGPALKIYEHKIVLQGHFEDDDPDGFLG 217

RESULT 4
 US-09-616-289-7
 ; Sequence 7, Application US/09616289
 ; Patent No. 6632923
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/09/616,289
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 217

sapiens

40.3%; Score 217; DB 4; Length 217;
arity 100.0%; Pred. No. 1.3e-180; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

LEKEEEEDDEDEDDVSGSEVPESDRPAQHQLNGERGPQSAKERVKEWT 381
LEKEEEEDDEDEDDVSGSEVPESDRPAQHQLNGERGPQSAKERVKEWT 60
HQQDEGRGPAGSGTRQVFSMAANKEGGTASVATGPDSPSPVPLPGKPALPCA 441
HQQDEGRGPAGSGTRQVFSMAANKEGGTASVATGPDSPSPVPLPGKPALPCA 120
PGCPGRKEKESDPVWNTVMDVVEYFTAGPEQATAFQOEIDGKSLLMQRTDV 501
PGCPGRKEKESDPVWNTVMDVVEYFTAGPEQATAFQOEIDGKSLLMQRTDV 180
SIRLGPALKIYEHHIKVLQOQHFEEDDDPDGFLG 538
SIRLGPALKIYEHHIKVLQOQHFEEDDDPDGFLG 217

lication US/09616289

23
TON:
, Ann M.
, Robert S.
, Simon W.
ona, Anibal A.
TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TON: ATHEROSCLEROSIS
10797-004001
TION NUMBER: US/09/616,289
DATE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/379,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

18.4%; Score 99; DB 4; Length 550;
arity 100.0%; Pred. No. 9.6e-78;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ASSAASPHYQEWILTIDSLRSRKARPDLERICRMVRRRHGPEPERTRAELEKLIQ 78
ASSAASPHYQEWILTIDSLRSRKARPDLERICRMVRRRHGPEPERTRAELEKLIQ 79
JLRVSYKGSISYRNAARVQPPRGATPPAPPRARG 117
JLRVSYKGSISYRNAARVQPPRGATPPAPPRARG 118

lication US/08979608A

151

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGN
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-979-608A-3
Query Match 14.1%; Score 76; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.1e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; (

QY 458 DPVWNTVMDVVEYFTAGPEQATAFQOEIDGKSLLMQRTDVLTLGLRGPAL
Db 152 DPVWNTVMDVVEYFTAGPEQATAFQOEIDGKSLLMQRTDVLTLGLRGPAL
QY 518 HHKVLQOQHFEEDDDP 533
Db 212 HHKVLQOQHFEEDDDP 227

RESULT 7
US-09-517-849-3
; Sequence 3, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGN
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.

225 Franklin Street
Boston
MA

NY: USA

02110-2804

ADABLE FORM:

4 TYPE: Diskette

TER: IBM Compatible

ING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

CATION NUMBER: US/09/517,849

3 DATE: 02-Mar-2000

ICATION DATA:

CATION NUMBER: 08/979,608

3 DATE: 26-NOV-1997

SENT INFORMATION:

Myers, Louis

REGISTRATION NUMBER: 35,965

ENCE/DOCKET NUMBER: 10797-003001

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 3

CHARACTERISTICS:

3: 232 amino acids

amino acid

OGY: linear

YPE: protein

SCRIPTION: SEQ ID NO: 3

14.1%; Score 76; DB 4; Length 232;

100.0%; Pred. No. 4.1e-58; Indels 0; Gaps 0;
aservative 0; Mismatches 0;

I VMDVVEYFTFAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517

I VMDVVEYFTFAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 211

LQGHFEDDDP 533

LQGHFEDDDP 227

cation US/09616289

3

ON:

Ann M.

Robert S.

Simon W.

na, Anibal A.

ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ON: ATHEROSCLEROSIS

10797-004001

ION NUMBER: US/09/616,289

ATE: 2000-07-14

N NUMBER: US 09/517,849

E: 2000-03-02

N NUMBER: US 08/979,608

E: 1997-11-26

N NUMBER: US 60/031,930

E: 1996-11-27

N NUMBER: US 60/048,547

E: 1997-06-03

NOS: 53

Q for Windows Version 4.0

ORGANISM: Oryctolagus cuniculus
US-09-616-289-3

Query Match 14.1%; Score 76; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.1e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVETVMDVVEYFTFAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK
DB 152 DPVETVMDVVEYFTFAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK

QY 518 HHKVLQGHFEDDDP 533

DB 212 HHKVLQGHFEDDDP 227

RESULT 9

US-08-979-608A-4

; Sequence 4, Application US/08979608A

; Patent No. 6355451

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; Lees, Robert S.

; Law, Simon W.

; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSIS
TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/979,608A

; FILING DATE: 26-NOV-1997

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 60/048,547

; FILING DATE: 03-JUN-1997

; APPLICATION NUMBER: US 60/031,930

; FILING DATE: 27-NOV-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5981)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-08-979-608A-4

Query Match 14.1%; Score 76; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 4.5e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVETVMDVVEYFTFAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK
DB 172 DPVETVMDVVEYFTFAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK

VLOQGHFDDDP 533
|||||
VLOQGHFDDDP 247

ication US/09517849
88
ACTION:
: Lees, Ann M.
: Lees, Robert S.
: Law, Simon W.
: Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
DENCE ADDRESS:
ESSEE: Fish & Richardson P.C.
ET: 225 Franklin Street
: Boston
E: MA
TRY: USA
02110-2804
READABLE FORM:
UM TYPE: Diskette
UTER: IBM Compatible
ATING SYSTEM: DOS
WARE: FastSEQ for Windows Version 2.0
PLICATION DATA:
ICATION NUMBER: US/09/517,849
NG DATE: 02-Mar-2000
LICATION DATA:
ICATION NUMBER: 08/979,608
NG DATE: 26-NOV-1997
AGENT INFORMATION:
: Myers, Louis
STRATION NUMBER: 35,965
RENCE/DOCKET NUMBER: 10797-003001
NICATION INFORMATION:
PHONE: 617/542-5070
FAX: 617/542-8906
R SEQ ID NO: 4:
CHARACTERISTICS:
TH: 252 amino acids
LOGY: linear
TYPE: protein
DESCRIPTION: SEQ ID NO: 4:

14.1%; Score 76; DB 4; Length 252;
arity 100.0%; Pred. No. 4.5e-58;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TWVMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGSLRGLPKIYE 517
TWVMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGSLRGLPKIYE 231

VLOQGHFDDDP 533
|||||
VLOQGHFDDDP 247

ication US/09616289
123
ION:
: Ann M.
: Robert S.
: Simon W.

APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 252
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-616-289-4

Query Match 14.1%; Score 76; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 4.5e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; C

QY 458 DPVETWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGSLRGLPAI
Db 172 DPVETWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGSLRGLPAI

QY 518 HHKVLQGHFDDDP 533
Db 232 HHKVLQGHFDDDP 247

RESULT 12
US-08-979-608A-2
; Sequence 2, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGN
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/596

ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 2:
HARACTERISTICS:
H: 317 amino acids
amino acid
OGY: linear
YPE: protein
SCRIPTION: SEQ ID NO: 2:

14.1%; Score 76; DB 4; Length 317;
rity 100.0%; Pred. No. 5.5e-58;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
TVMDVVEYFTAGPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
TVMDVVEYFTAGPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 296
LQGHFEDDDP 533
LQGHFEDDDP 312

cation US/09517849
8

TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA

RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
TING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
PLICATION DATA:
CATION NUMBER: US/09/517,849
G DATE: 02-Mar-2000
ICATION DATA:
CATION NUMBER: 08/979,608
G DATE: 26-NOV-1997
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-003001
ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 2:
HARACTERISTICS:
H: 317 amino acids
amino acid
OGY: linear
YPE: protein
SCRIPTION: SEQ ID NO: 2:

14.1%; Score 76; DB 4; Length 317;

Best Local Similarity 100.0%; Pred. No. 5.5e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; G:
QY 458 DPVEVTVMVVEYFTAGPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
Db 237 DPVEVTVMVVEYFTAGPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQGHFEDDDP 533
Db 297 HHKVLQGHFEDDDP 312

RESULT 14
US-09-616-289-2
; Sequence 2, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT:
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(317)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-616-289-2

Query Match 14.1%; Score 76; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 5.5e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; G:
QY 458 DPVEVTVMVVEYFTAGPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
Db 237 DPVEVTVMVVEYFTAGPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQGHFEDDDP 533
Db 297 HHKVLQGHFEDDDP 312

RESULT 15
US-08-979-608A-20
; Sequence 20, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNOSE
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-517-289-20

Query Match 4.8%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEDDEDEEDDYSEGSEVPESD 354
      |||||||
Db 1 EEEEDDEDEEDDYSEGSEVPESD 26

RESULT 17
US-09-616-289-20
; Sequence 20, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-616-289-20

Query Match 4.8%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEDDEDEEDDYSEGSEVPESD 354
      |||||||
Db 1 EEEEDDEDEEDDYSEGSEVPESD 26

RESULT 18
US-08-973-608A-19
; Sequence 19, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:

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Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA
RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
ING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
PLICATION DATA:
CATION NUMBER: US/08/979,608A
3 DATE: 26-NOV-1997
ICATION DATA:
CATION NUMBER: US 60/048,547
3 DATE: 03-JUN-1997
CATION NUMBER: US 60/031,930
G DATE: 27-NOV-1996
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 19:
HARACTERISTICS:
H: 15 amino acids
amino acid
OGY: linear
YPE: protein
ESCRPTION: SEQ ID NO: 19:
2.8%; Score 15; DB 4; Length 15;
rity 100.0%; Pred. No. 3.3e-06;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDEDEDD 343
| | | | | | | | | |
DDEDEDD 15
ication US/09517849
8
TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA
RY: USA
02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-517-849-19
Query Match 2.8%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 329 EEEEDDEDEDD 343
| | | | | | | | | |
DB 1 EEEEDDEDEDD 15
RESULT 20
US-09-616-289-19
; Sequence 19, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-616-289-19
Query Match 2.8%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 329 EEEEDDEDEDD 343
| | | | | | | | | |

DDEDEDEDD 15

Location US/08979608A

31

ATION:

: Lees, Ann M.

Lees, Robert S.

Law, Simon W.

Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

DENCE ADDRESS:

SSEE: Fish & Richardson P.C.

ET: 225 Franklin Street

: Boston

3: MA

CRY: USA

02110-2804

READABLE FORM:

IM TYPE: Diskette

ITER: IBM Compatible

ATING SYSTEM: DOS

ARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/08/979,608A

IG DATE: 26-Nov. 6355451-1997

ICATION DATA:

ICATION NUMBER: US 60/048,547

IG DATE: 03-JUN-1997

ICATION NUMBER: US 60/031,930

IG DATE: 27-NOV-1996

AGENT INFORMATION:

Myers, Louis

ISTRATION NUMBER: 35,965

ERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 21:

CHARACTERISTICS:

H: 11 amino acids

amino acid

OGY: linear

YPE: protein

DESCRIPTION: SEQ ID NO: 21:

2.0%; Score 11; DB 4; Length 11;

urity 100.0%; Pred. No. 0.0074;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354

|||||

EVPSD 11

ication US/09517849

38

ATION:

: Lees, Ann M.

Lees, Robert S.

Law, Simon W.

Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

2.0%; Score 11; DB 4; Length 11;
city 100.0%; Pred. No. 0.0074;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354
|||||
EVPSD 11

ication US/08979608A

1

TION:

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

VENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

SSEE: Fish & Richardson P.C.
R: 225 Franklin Street
Boston

: MA

RY: USA

02110-2804

ADABLE FORM:

4 TYPE: Diskette
TER: IBM Compatible

ING SYSTEM: DOS

ARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

CATION NUMBER: US/08/979,608A

3 DATE: 26-NOV-1997

ICATION DATA:

CATION NUMBER: US 60/048,547

3 DATE: 03-JUN-1997

CATION NUMBER: US 60/031,930

3 DATE: 27-NOV-1996

SENT INFORMATION:

Myers, Louis

ISTRATION NUMBER: 35,965

ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 27:

CHARACTERISTICS:

d: 12 amino acids

amino acid

OGY: linear

YPE: protein

SCRIPTION: SEQ ID NO: 27:

2.0%; Score 11; DB 4; Length 12;
city 100.0%; Pred. No. 0.008;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354

|||||

EVPSD 12

ication US/09517849

8

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSE
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/517,849

FILING DATE: 02-Mar-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,608

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-517-849-27

Query Match 2.0%; Score 11; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 VSEGSSEVPESD 354

|||||

Db 2 VSEGSSEVPESD 12

RESULT 26

US-09-616-289-27

Sequence 27, Application US/09616289

Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

ON NUMBER: US 60/048,547
IE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

2.0%; Score 11; DB 4; Length 12;
arity 100.0%; Pred.No. 0.008;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||
SEVPESD 12

lication US/08979608A
51

ACTION:

: Lees, Ann M.
: Lees, Robert S.
: Law, Simon W.
: Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

DENCE ADDRESS:

ESSEE: Fish & Richardson P.C.
ST: 225 Franklin Street
: Boston

E: MA

TRY: USA

02110-2804

READABLE FORM:

UM TYPE: Diskette

UTER: IBM Compatible

ATING SYSTEM: DOS

WARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/08/979,608A

NG DATE: 26-NO. 6355451-1997

LICATION DATA:

ICATION NUMBER: US 60/048,547

NG DATE: 03-JUN-1997

ICATION NUMBER: US 60/031,930

NG DATE: 27-NOV-1996

AGENT INFORMATION:

: Myers, Louis

STRATION NUMBER: 35,965

RENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

FAX: 617/542-8906

R SEQ ID NO: 26:

CHARACTERISTICS:

TH: 28 amino acids

: amino acid

LOGY: linear

TYPE: protein

DESCRIPTION: SEQ ID NO: 26:

2.0%; Score 11; DB 4; Length 28;

arity 100.0%; Pred.No. 0.017;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354

Db 18 VSEGEVPSD 28
|||||

RESULT 28

US-09-517-849-26

; Sequence 26, Application US/09517849

; Patent No. 6605588

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; Lees, Robert S.

; Law, Simon W.

; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGN
TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/517,849

; FILING DATE: 02-Mar-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/979,608

; FILING DATE: 26-NOV-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10797-003001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-517-849-26

Query Match 2.0%; Score 11; DB 4; Length 28;
Best Local Similarity 100.0%; Pred.No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

Qy 344 VSEGEVPSD 354

|||||

Db 18 VSEGEVPSD 28

RESULT 29

US-09-616-289-26

; Sequence 26, Application US/09616289

; Patent No. 6632923

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

ION NUMBER: US/09/616,289
ATE: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
E: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

olagus cuniculus

2.0%; Score 11; DB 4; Length 28;
rity 100.0%; Pred. No. 0.017; 0; Indels 0;
nservative 0; Mismatches 0; Gaps 0;
3VPESD 354
|||||
3VPESD 28

ication US/09135994A

3
DN:
et al.
DN: SCA7 GENE AND METHODS OF USE
University of Minnesota
ION NUMBER: US/09/135,994A
ATE: 1998-08-18
ION NUMBER: 60/056,170
ATE: 1997-08-19
NOS: 14
In Ver. 2.0

apiens

2.0%; Score 11; DB 3; Length 129;
city 100.0%; Pred. No. 0.07; 0; Indels 0;
nservative 0; Mismatches 0; Gaps 0;
PPQPQ 232
|||||
PPQPQ 44

.cation US/09684843A

3
DN:
et al.
DN: SCA7 GENE AND METHODS OF USE
regence of the University of Minnesota
ION NUMBER: US/09/684,843A
ATE: 2000-10-06
N NUMBER: 60/056,170
E: 1997-08-19
N NUMBER: 09/135,994
E: 1998-08-18
NOS: 14
In Ver. 2.0

LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-09-684-843A-12

Query Match 2.0%; Score 11; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 222 QQQPPPPPPQ 232
|||||
DB 34 QQQPPPPPPQ 44
|||||

RESULT 32

US-08-979-608A-22
Sequence 22, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSIS
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-Nov-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5981)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-979-608A-22

Query Match 1.9%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 529 EDDPDGFLG 538
|||||
DB 1 EDDPDGFLG 10
|||||

RESULT 33

lication US/08979608A
31
ATION:
: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
DENCE ADDRESS:
ESSEE: Fish & Richardson P.C.
ET: 225 Franklin Street
: Boston
E: MA
TRY: USA
02110-2804
READABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
ATING SYSTEM: DOS
WARE: FastSEQ for Windows Version 2.0
PLICATION DATA:
ICATION NUMBER: US/08/979,608A
NG DATE: 26-NOV-1997
ICATION DATA:
ICATION NUMBER: US 60/048,547
NG DATE: 03-JUN-1997
ICATION NUMBER: US 60/031,930
NG DATE: 27-NOV-1996
AGENT INFORMATION:
: Myers, Louis
STRATION NUMBER: 35,965
RENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
PHONE: 617/542-5070
R SEQ ID NO: 28
CHARACTERISTICS:
TH: 10 amino acids
: amino acid
LOGR: linear
TYPE: protein
DESCRIPTION: SEQ ID NO: 28:

1.9%; Score 10; DB 4; Length 10;
arity 100.0%; Pred. No. 0.05;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

PALPGA 441
|||||
PALPGA 10

lication US/09517849
38
ATION:
: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
DENCE ADDRESS:
ESSEE: Fish & Richardson P.C.
ET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-517-849-22

Query Match 1.9%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 529 EDDDPDGFGLG 538
Db 1 EDDDPDGFGLG 10

RESULT 35
US-09-517-849-28
; Sequence 28, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNO
; TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis

ATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-003001

ICATION INFORMATION:

HONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 28:

CHARACTERISTICS:

H: 10 amino acids

amino acid

OGY: linear

YPE: protein

SCRIPTION: SEQ ID NO: 28:

1.9%; Score 10; DB 4; Length 10;

100.0%; Pred. No. 0.05;

nservative 0; Mismatches 0; Indels 0;

nservative 0; Gaps 0;

ALPGA 441

|||||

ALPGA 10

ication US/09616289

3

ON:

Ann M.

Robert S.

Simon W.

na, Anibal A.

ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ON: ATHEROSCLEROSIS

10797-004001

ION NUMBER: US/09/616,289

ATE: 2000-07-14

N NUMBER: US 09/517,849

E: 2000-03-02

N NUMBER: US 08/979,608

E: 1997-11-26

N NUMBER: US 60/031,930

E: 1996-11-27

N NUMBER: US 60/048,547

E: 1997-06-03

NOS: 53

Q for Windows Version 4.0

sapiens

1.9%; Score 10; DB 4; Length 10;

100.0%; Pred. No. 0.05;

nservative 0; Mismatches 0; Indels 0;

nservative 0; Gaps 0;

DGFLG 538

|||||

DGFLG 10

ication US/09616289

3

ON:

Ann M.

Robert S.

Simon W.

na, Anibal A.

ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/616,289

; CURRENT FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-616-289-28

Query Match

Best Local Similarity 1.9%; Score 10; DB 4; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 432 PPGKPAALPGA 441

|||||

Db 1 PPGKPAALPGA 10

RESULT 38

US-09-489-039A-8583

; Sequence 8583, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8583

; LENGTH: 126

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8583

Query Match

Best Local Similarity 1.9%; Score 10; DB 4; Length 126;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 118 APAAAAAAP 127

|||||

Db 92 APAAAAAAP 101

RESULT 39

US-09-328-352-7651

; Sequence 7651, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING T

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 7651

; LENGTH: 254

stobacter baumannii

1.9%; Score 10; DB 4; Length 254;
arity 100.0%; Pred. No. 0.96;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 146
|||||
AAAAA 157

3
Application US/09489039A

36

ON:
Breton et. al
ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
ON: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

2709.2004001

ION NUMBER: US/09/489.039A

DATE: 2000-01-27

ON NUMBER: US 60/117,747

CE: 1999-01-29

NOS: 14342

siella pneumoniae

1.9%; Score 10; DB 4; Length 324;
arity 100.0%; Pred. No. 1.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 127
|||||
AAAAA 266

cation US/09056226B

4

ON:
anti, Joseph J.
resan, Venkatesan
ON: Control of Floral Induction in Plants
ON: and Uses Therefor

CSHL94-04A4

ION NUMBER: US/09/056,226B

ATE: 1998-04-07

ION NUMBER: US 09/000,640

ATE: 1997-12-30

ION NUMBER: US 08/804,104

ATE: 1997-02-20

ION NUMBER: PCT/US96/03466

ATE: 1996-03-15

ION NUMBER: US 08/406,186

ATE: 1995-03-16

NOS: 20

QX for Windows Version 3.0

ays

1.9%; Score 10; DB 3; Length 436;
arity 100.0%; Pred. No. 1.6;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 210 PLPPPPPPA 219
Db 45 PLPPPPPPA 54

RESULT 42

US-08-938-291A-9
; Sequence 9, Application US/08938291A

; Patent No. 6117673

; GENERAL INFORMATION:

; APPLICANT: Lev, Sima

; APPLICANT: Plowman, Gregory D.

; APPLICANT: Schlessinger, Joseph

; TITLE OF INVENTION: RDGB PROTEINS AND RELATED

; TITLE OF INVENTION: PRODUCTS AND METHODS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: 60/027,337

; FILING DATE: October 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 228/172

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1250 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-938-291A-9

Query Match 1.9%; Score 10; DB 3; Length 1250;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 329 EEEEDDEDE 338

Db 324 EEEEDDEDE 333

RESULT 43

US-09-589-619-9

; Sequence 9, Application US/09589619

; Patent No. 6576442

; GENERAL INFORMATION:

; APPLICANT: Lev, Sima

; APPLICANT: Plowman, Gregory D.

; APPLICANT: Schlessinger, Joseph

; TITLE OF INVENTION: RDGB PROTEINS AND RELATED

PRODUCTS AND METHODS

SEQUENCES: 11
SOURCE ADDRESS:
SEE: Lyon & Lyon
633 West Fifth Street
Suite 4700
Los Angeles
California
RY: U.S.A.
0071-2066
READABLE FORM:
1 TYPE: 3.5" Diskette, 1.44 Mb
TER: IBM Compatible
TING SYSTEM: IBM P.C. DOS 5.0
ARE: FastSeq
PLICATION DATA:
ATION NUMBER: US/09/589,619
DATE: 07-Jun-2000
ICATION: <Unknown>
ICATION DATA:
ATION NUMBER: US/08/938,291
DATE: September 26, 1997
ATION NUMBER: 60/027,337
DATE: October 11, 1996
ENT INFORMATION:
Warburg, Richard J.
ATION NUMBER: 32,327
ENCE/DOCKET NUMBER: 228/172
ICATION INFORMATION:
ONE: (213) 489-1600
X: (213) 955-0440
67-3510
SEQ ID NO: 9:
HARACTERISTICS:
I: 1250 amino acids
amino acid
EDNESS: single
XY: linear
PE: peptide
SCRIPTION: SEQ ID NO: 9:
1.9%; Score 10; DB 4; Length 1250;
city 100.0%; Pred.No. 4.1;
servative 0; Mismatches 0; Indels 0; Gaps 0;
DEDE 338
DEDE 333
BSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
RON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
A C.; DANFORTH, HARRY D.
ION: GENETICALLY ENGINEERED COCCIDIOSIS
ANTIGEN, AC-6B
NCES: 11
ATION DATA:
NUMBER: US/07/581,693
12-SEP-1990
ON DATA:
NUMBER: 215,162
05-JUL-1988
NUMBER: 746,520
19-JUN-1985
NUMBER: 627,811
05-JUL-1984

5273901-11

Query Match 1.7%; Score 9; DB 6; Length 76;
Best Local Similarity 100.0%; Pred.No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 118 AAAAAAAAAA 126
Db 23 AAAAAAAAAA 31
RESULT 45
5482709-10
; Patent No. 5482709
; APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
; SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
; TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
; ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,432
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 581,693
; FILING DATE: 12-SEP-1990
; APPLICATION NUMBER: 215,162
; FILING DATE: 05-JUL-1989
; APPLICATION NUMBER: 746,520
; FILING DATE: 19-JUN-1985
; APPLICATION NUMBER: 627,811
; FILING DATE: 05-JUL-1984
; SEQ ID NO: 10:
; LENGTH: 76
5482709-10
Query Match 1.7%; Score 9; DB 6; Length 76;
Best Local Similarity 100.0%; Pred.No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 118 AAAAAAAAAA 126
Db 23 AAAAAAAAAA 31
RESULT 46
US-09-314-268-133
; Sequence 133, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAP
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/314,268
; EARLIER FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Human papillomavirus type 20
US-09-314-268-133
Query Match 1.7%; Score 9; DB 4; Length 99;
Best Local Similarity 100.0%; Pred.No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 210 FLPPPPQPP 218
Db 69 FLPPPPQPP 77

```

43 Application US/09252991A
95
ION:
C J. Rubenfield et al.
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
TION NUMBER: US/09/252,991A
DATE: 1999-02-18
ON NUMBER: US 60/074,788
TE: 1998-02-18
ON NUMBER: US 60/094,190
TE: 1998-07-27
D NOS: 33142

domonas aeruginosa
43
1.7%; Score 9; DB 4; Length 145;
arity 100.0%; Pred. No. 4.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

PARAP 149
|||||
PARAP 10

30 Application US/09252991A
95
ION:
C J. Rubenfield et al.
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
TION NUMBER: US/09/252,991A
DATE: 1999-02-18
ON NUMBER: US 60/074,788
TE: 1998-02-18
ON NUMBER: US 60/094,190
TE: 1998-07-27
D NOS: 33142

domonas aeruginosa
30
1.7%; Score 9; DB 4; Length 180;
arity 100.0%; Pred. No. 5.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

PARAP 149
|||||
PARAP 116

1 CORSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
ARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
IA C.; DANFORTH, HARRY D.
TION: GENETICALLY ENGINEERED COCCIDIOSIS
3 ANTIGEN, AC-6B
JENCES: 11

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/581,693
; FILING DATE: 12-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 215,162
; FILING DATE: 05-JUL-1988
; APPLICATION NUMBER: 746,520
; FILING DATE: 19-JUN-1985
; APPLICATION NUMBER: 627,811
; FILING DATE: 05-JUL-1984
; SEQ ID NO: 7:
; LENGTH: 180
5273901-7

Query Match 1.7%; Score 9; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 118 AAAAAAAAAA 126
Db 73 AAAAAAAAAA 81

RESULT 50
5482709-6
; Patent No. 5482709
; APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
; SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
; TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
; ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,432
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 581,693
; FILING DATE: 12-SEP-1990
; APPLICATION NUMBER: 215,162
; FILING DATE: 05-JUL-1989
; APPLICATION NUMBER: 746,520
; FILING DATE: 19-JUN-1985
; APPLICATION NUMBER: 627,811
; FILING DATE: 05-JUL-1984
; SEQ ID NO: 6:
; LENGTH: 180
5482709-6

Query Match 1.7%; Score 9; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 118 AAAAAAAAAA 126
Db 73 AAAAAAAAAA 81

RESULT 51
US-09-702-705-1816
; Sequence 1816, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

```


210121.478C14
ION NUMBER: US/09/702,705
ATE: 2000-10-30
NOS: 1833
EQ for Windows Version 3.0

sapiens

1.7%; Score 9; DB 4; Length 325;
city 100.0%; Pred. No. 8.9;
iservative 0; Mismatches 0; Indels 0; Gaps 0;

APPP 129
|||||
APPP 72

Application US/09736457

3

DN:

Mr. Tongtong
Mr. Chaitanya S.

Mr. Michael A.

Mr. Gary

Mr. Tom

Mr. Darrick

Mr. Marc

Mr. Jane

Mr. Liqun

Mr. Aijun

DN: COMPOSITIONS AND METHODS FOR THE THERAPY AND

DN: DIAGNOSIS OF LUNG CANCER

210121.478C15

ION NUMBER: US/09/736,457

ATE: 2000-12-13

NOS: 1864

EQ for Windows Version 3.0

sapiens

1.7%; Score 9; DB 4; Length 325;
city 100.0%; Pred. No. 8.9;
iservative 0; Mismatches 0; Indels 0; Gaps 0;

APPP 129
|||||
APPP 72

Application US/09671325

3

DN:

Mr. Tongtong

Mr. Chaitanya S.

Mr. Michael A.

Mr. Gary

Mr. Tom

Mr. Darrick

Mr. Marc

Mr. Jane

Mr. Liqun

Mr. Aijun

DN: COMPOSITIONS AND METHODS FOR THE THERAPY AND

DN: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens
US-09-671-325-1816

Query Match 1.7%; Score 9; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AAAAAAAPP 129

|||||

DB 64 AAAAAAAPP 72

RESULT 54

US-09-252-991A-28443

Sequence 28443; Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TO THE THERAPY AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28443

LENGTH: 333

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28443

Query Match 1.7%; Score 9; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 PPAGPRRAP 200

|||||

DB 103 PPAGPRRAP 111

RESULT 55

US-08-710-249-4

Sequence 4; Application US/08710249

Patent No. 5858777

GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant

APPLICANT: Feng, Junli

APPLICANT: Andrews, William H.

APPLICANT: Adams, Robert R.

TITLE OF INVENTION: Methods and Reagents for Regulating

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:
  NUMBER: US/08/710,249
  : 13-SEP-1996
ION: 536
ION DATA:
  NUMBER: US 08/583,808
  : 05-JAN-1996
ION DATA:
  NUMBER: US 60/003,492
  : 08-SEP-1995
T INFORMATION:
  ella, John R.
N NUMBER: 32,944
CKET NUMBER: 015389-001220US
TION INFORMATION:
  (415) 576-0200
  415) 576-0300
SEQ ID NO: 4:
ACTERISTICS:
  4 amino acids
  c acid
  linear
  : protein

      1.7%; Score 9; DB 2; Length 434;
arity 100.0%; Pred.No.12;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 352

ication US/09220157A
10
ION:
illeponteau, Bryant
eng, Junli
adrews, William H.
ams, Robert R.
TION: Methods and Reagents for Regulating
TION: Telomere Length and Telomerase Activity
UENCES: 26
E ADDRESS:
Townsend and Townsend and Crew LLP
c Embarcadero Center, Eighth Floor
francisco
ifornia
SA
-3834
ABLE FORM:
: Floppy disk
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:
  NUMBER: US/09/220,157A
  :
ION:
TION DATA:
  NUMBER: US/08/710,249
  : 13-SEP-1996
  NUMBER: US 08/583,808
  : 05-JAN-1996
ION DATA:
  NUMBER: US 60/003,492
  : 08-SEP-1995
T INFORMATION:

```

```

; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-220-157A-4

Query Match      1.7%; Score 9; DB 4; Length 434;
Best Local Similarity 100.0%; Pred.No.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY      118 AAAAAAAAA 126
      |||||
Db      344 AAAAAAAAA 352

RESULT 57
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match      1.7%; Score 9; DB 4; Length 440;
Best Local Similarity 100.0%; Pred.No.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY      120 AAAAAAAPP 128
      |||||
Db      14 AAAAAAAPP 22

RESULT 58
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1

```

2844-US
ION NUMBER: US/09/778,510
ATE: 2001-02-07
N NUMBER: PCT/US99/17906
E: 1999-08-05
N NUMBER: 60/095,663
E: 1998-08-07
NOS: 22
tentIn Ver. 2.0

sapien

1.7%; Score 9; DB 4; Length 442;
rity 100.0%; Pred. No. 12;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAPP 128
|||||
AAPP 22

cation US/09930803

3
OHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
ES, Roger
INOKI, Muramaki
ON: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
JHUI770-1
ION NUMBER: US/09/930,803
ATE: 2001-08-15
NOS: 22
In version 3.0

sapiens

1.7%; Score 9; DB 4; Length 442;
rity 100.0%; Pred. No. 12;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAPP 128
|||||
AAPP 22

4
Application US/09252991A

5
J. Rubenfield et al.
ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
ION NUMBER: US/09/252,991A
ATE: 1999-02-18
N NUMBER: US 60/074,788
E: 1998-02-18
N NUMBER: US 60/094,190
E: 1998-07-27
NOS: 33142

omonas aeruginosa

US-09-252-991A-22614

Query Match 1.7%; Score 9; DB 4; Length 458;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 PLAAPPAP 184
|||||
Db 73 PLAAPPAP 81

RESULT 61

US-09-023-905A-10
; Sequence 10, Application US/09023905A
; Patent No. 6475778
; GENERAL INFORMATION:
; APPLICANT: Roberts, Thomas M.
; APPLICANT: King, Frederick J.
; APPLICANT: Harris, David F.
; APPLICANT: Hu, Erding
; APPLICANT: Spiegelman, Bruce
; APPLICANT: Chan, Joanne
; TITLE OF INVENTION: Differentiation Enhancing Factors and Uses
; FILE REFERENCE: DFN-021
; CURRENT APPLICATION NUMBER: US/09/023,905A
; CURRENT FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/038,191
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 903
; TYPE: PRT
; ORGANISM: Danio rerio
US-09-023-905A-10

Query Match 1.7%; Score 9; DB 4; Length 903;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 PAPPPPPAP 139
|||||
Db 824 PAPPPPPAP 832

RESULT 62

US-09-252-991A-18882
; Sequence 1882, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18882
; LENGTH: 955
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18882

Query Match 1.7%; Score 9; DB 4; Length 955;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAPP 128

|||||
AAPP 70

ication US/08764870

16

ION:
Scanlan, Thomas S.
Baxter, John D.
Fletcher, Robert J.
Wagner, Richard L.
Kushner, Peter J.
Apriletti, James W.
West, Brian L.
Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOM
FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER FILING DATE: 1995-12-14
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 984
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (695)...(969)
OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-15

3A

ABLE FORM:
Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
ACTION DATA:
NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
SEQ ID NO: 530
ACTION DATA:
NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
ACTION DATA:
NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
ACTION DATA:
NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
OTHER INFORMATION:
APPLICANT: Buchbinder, Michael
Jenny
Furness, Michael
Docket Number: UCAL-246/01US
ACTION INFORMATION:
(650)843-5000
SEQ ID NO: 15:
amino acids
acid
3:
linear
protein

1.7%; Score 9; DB 3; Length 984;
arity 100.0%; Pred. No. 24;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QPPPP 229
QPPPP 697

ication US/08980115
22
ION:

APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Fletcher, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Apriletti, James W.
APPLICANT: West, Brian L.
APPLICANT: Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOM
FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER FILING DATE: 1995-12-14
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 984
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (695)...(969)
OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-15

Query Match 1.7%; Score 9; DB 3; Length 984;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 221 PQQQPPPP 229

Db 689 PQQQPPPP 697

RESULT 65

US-09-976-594-127
Sequence 127, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Buchbinder, Michael
Jenny
Furness, Michael
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREA
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 127
LENGTH: 984
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 3230770CD1
US-09-976-594-127

Query Match 1.7%; Score 9; DB 4; Length 984;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 221 PQQQPPPP 229

Db 689 PQQQPPPP 697

RESULT 73
US-08-159-339A-163
; Sequence 163, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.

by, Howard M.
 te, Alessandro
 lis, Esteban
 ION: HLA Binding peptides and Their
 ION: Uses
 ENCES: 1254
 ADDRESS:
 Townsend and Townsend and Crew LLP
 Embarcadero Center, Eighth Floor
 San Francisco

A
 3834
 3LE FORM:
 Diskette
 3M Compatible
 STEM: DOS
 astSEQ for Windows Version 2.0
 ACTION DATA:
 NUMBER: US/08/159,339A
 29-NOV-1993
 ON: 424
 ION DATA:
 NUMBER: US 07/926,666
 07-AUG-1992
 NUMBER: US 08/027,746
 05-MAR-1993
 NUMBER: US 08/103,396
 06-AUG-1993
 INFORMATION:
 , Ellen Lauver
 , NUMBER: 32,762
 TRET NUMBER: 018623-005030US
 ION INFORMATION:
 (415) 576-0200
 15) 576-0300

SEQ ID NO: 163:
 CTERISTICS:
 nino acids
 acid
 : single
 inear
 peptide
 1.5%; Score 8; DB 3; Length 9;
 city 100.0%; Pred. No. 3e+05;
 aservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 125
 ||||
 AAA 8

ication US/08199776

ION:
 inner, Michael B.
 cker, Christina M.
 TION: No. 5594120el integrin alpha subunit
 ENCES: 25
 ADDRESS:
 Wolf, Greenfield and Sacks, P.C.
 Atlantic Avenue
 3

A

3LE FORM:
 Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/199,776
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-199-776-17
 Query Match 1.5%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 326 LEKEEED 333
 Db 2 LEKEEED 9
 RESULT 75
 US-08-663-731-17
 Sequence 17, Application US/08663731
 Patent No. 6057423
 GENERAL INFORMATION:
 APPLICANT: Brenner, Michael B.
 APPLICANT: Parker, Christina M.
 TITLE OF INVENTION: No. 6057423el integrin alpha subunit
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/663,731
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/199,776
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 INFORMATION FOR SEQ ID NO: 17:

CHARACTERISTICS:
amino acids
acid
single
linear
peptide
YES
internal
homo sapiens

1.5%; Score 8; DB 3; Length 10;
arity 100.0%; Pred. No. 2.7;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
|||||
SEED 9

Location US/08879338A

16
[ON:
er, Michael B.
er, Christina M.
[ON: Antibodies to No. 6063906el Integrin Alpha
[ON: Subunit

B080L/708C/ERP
[ION NUMBER: US/08/879,338A
DATE: 1997-06-20
[ION NUMBER: US 08/663,731
DATE: 1996-06-14
[ION NUMBER: US 08/199,776
DATE: 1994-02-18
[NOS: 31
EQ for Windows Version 3.0

Sapiens

1.5%; Score 8; DB 3; Length 10;
arity 100.0%; Pred. No. 2.7;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
|||||
SEED 9

Location US/09293238B

42
[ON:
er, Michael B.
er, Christina M.

[ION: A Method of Treating Ulcerative Colitis
[ION: or Crohn's Disease by Administering an Antibody to Alpha B
[ION: Beta 7 Integrin
L0560/7005/ERP
[TION NUMBER: US/09/293,238B
DATE: 1999-04-16
[ON NUMBER: US 08/879,338
TE: 1997-06-20
[ON NUMBER: US 08/663,731
TE: 1996-06-14
[ON NUMBER: US 08/199,776

; PRIOR FILING DATE: 1994-02-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-293-238B-17

Query Match 1.5%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 326 LEKEEED 333
Db 2 LEKEEED 9

RESULT 78

PCT-US95-02044-17
; Sequence 17, Application PC/TUS9502044
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel integrin alpha subunit
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02044
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,776
; FILING DATE: 18 February 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
PCT-US95-02044-17

Query Match 1.5%; Score 8; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 326 LEKEEED 333
Db 2 LEKEEED 9

ation US/07814220
ON:
eci, Thomas E.
h, Thomas E.
manski, Maria B.W.
ION: SYNTHETIC ANTIFREEZE PEPTIDE AND
ION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NCES: 43
ADDRESS:
WHITHAM, CURTIS & WHITHAM
on Intl. Center, 11800 Sunrise Valley Dr.,
e 900
1
1
FILE FORM:
Floppy disk
M PC compatible
ITEM: PC-DOS/MS-DOS
tentIn Release #1.0, Version #1.30
TION DATA:
NUMBER: US/07/814,220
23-DEC-1991
N: 435
ION DATA:
NUMBER: US 07/588,437
25-SEP-1990
INFORMATION:
um, Michael E.
NUMBER: 32,635
KET NUMBER: CIT.016
ON INFORMATION:
03-391-2510
-391-9035
EQ ID NO: 11:
TERISTICS:
mino acids
acid
near
peptide
1.5%; Score 8; DB 2; Length 11;
ity 100.0%; Pred. No. 3;
servative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
||
ATA 9
ation US/07812421
ON:
eci, Thomas
h, Thomas E.
manski, Maria B.W.
ION: SYNTHETIC ANTIFREEZE PEPTIDE AND
ION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NCES: 43
ADDRESS:
WHITHAM, CURTIS & WHITHAM
on Intl. Center, 11800 Sunrise Valley Dr.,
e 900
1

STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-11
Query Match 1.5%; Score 8; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 151 AAAAAATA 158
Db 2 AAAAAATA 9
RESULT 81
US-08-199-776-19
Sequence 19, Application US/08199776
Patent No. 5594120
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: No. 5594120el integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 19:

CHARACTERISTICS:
amino acids
acid
single
linear
peptide
YES
NO internal
CE:
Homo sapiens

1.5%; Score 8; DB 1; Length 14;
arity 100.0%; Pred.No. 3.7;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
|||||
SEED 9

location US/07814220

ION:
acaci, Thomas
oth, Thomas E.
zumanski, Maria B.W.
TION: SYNTHETIC ANTIPREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
ENCES: 43

E ADDRESS:
WHITHAM, CURTIS & WHITHAM
ston Intl. Center, 11800 Sunrise Valley Dr.,
ite 900
on

SA

ABLE FORM:
Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:
NUMBER: US/07/814,220
: 23-DEC-1991

ION DATA:
NUMBER: US 07/588,437
: 25-SEP-1990
F INFORMATION:
am, Michael E.
X NUMBER: 32,635
CKET NUMBER: CIT.016
ION INFORMATION:
703-391-2510
03-391-9035
SEQ ID NO: 30:

ACTERISTICS:
amino acids
acid
S:
linear
peptide

1.5%; Score 8; DB 2; Length 14;
arity 100.0%; Pred.No. 3.7;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 AAAAAATA 158
Db 4 AAAAAATA 11

RESULT 83

US-07-812-421-30
; Sequence 30, Application US/07812421
; Patent No. 5932697
; GENERAL INFORMATION:
; APPLICANT: Cacaci, Thomas
; APPLICANT: Toth, Thomas E.
; APPLICANT: Szumanski, Maria B.W.
; TITLE OF INVENTION: SYNTHETIC ANTIPREEZE PEPTIDE AND
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
; CITY: Reston
; STATE: VA
; COUNTRY: USA
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/812,421
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/588,437
; FILING DATE: 25-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitham, Michael E.
; REGISTRATION NUMBER: 32,635
; REFERENCE/DOCKET NUMBER: CIT.016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-391-2510
; TELEFAX: 703-391-9035
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-812-421-30

Query Match 1.5%; Score 8; DB 2; Length 14;
Best Local Similarity 100.0%; Pred.No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 151 AAAAAATA 158
Db 4 AAAAAATA 11

RESULT 84

US-08-663-731-19
; Sequence 19, Application US/08663731
; Patent No. 6057423
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: No. 6057423el integrin alpha subunit
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
; STREET: 600 Atlantic Avenue

617-720-3500
17-720-2441 19:
SEQ ID NO:
ACTERISTICS:
amino acids
c acid
s: single
linear
: peptide
: YES
NO
: internal
DE:
Homo sapiens
1.5%; Score 8; DB 5; Length 14;
arity 100.0%; Pred.No.3.7;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
3EED 333
|||||
3EED 9
Application US/08602999A
15
TION:
PARKS, Andrew B.
AY, Brian K.
JOHN, Judith M.
JILLIAM, Lawrence A.
ER, Channing J.
JWLKES, Dana M.
IDER, James E.
TION: SH3 BINDING PEPTIDES AND METHODS OF
CTION: ISOLATING AND USING SAME
ENCES: 467
3 ADDRESS:
Pennie & Edmonds
5 Avenue of the Americas
ork
York
S.A.
-2711
ABLE FORM:
: Floppy disk
IBM PC compatible
STEM: PC-DOS/MS-DOS
atenIn Release #1.0, Version #1.30
ATION DATA:
NUMBER: US/08/602,999A
: 16-FEB-1996
ON: 435
N INFORMATION:
ck, S. Leslie
Y NUMBER: 18,872
CKET NUMBER: 1101-202
TION INFORMATION:
(212) 790-9090
212) 869-9741/8864
11 PENNIE
SEQ ID NO: 439:
ACTERISTICS:
amino acids
c acid
unknown
: peptide
1.5%; Score 8; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 212 PPPQPPA 219
Db 6 PPPQPPA 13
|||||
|||||
RESULT 89
US-09-500-124-439
; Sequence 439, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 439:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-439
Query Match 1.5%; Score 8; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 212 PPPQPPA 219
Db 6 PPPQPPA 13
|||||
|||||
RESULT 90
US-08-630-916A-99
; Sequence 99, Application US/08630916A
; Patent No. 601137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio

Y. Brian K.
wikes, Dana M.
TION: IDENTIFICATION AND ISOLATION OF NOVEL
TION: POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME
ENCES: 124
ADDRESS:
Pennie & Edmonds
5 Avenue of the Americas
York
ited States
2711
BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
atentIn Release #1.0, Version #1.30
ACTION DATA:
NUMBER: US/08/630,916A
03-APR-1996
ON: 435
INFORMATION:
CK. S. LESLIE
NUMBER: 18,872
CKET NUMBER: 1101-203
ION INFORMATION:
(212) 790-9090
12) 896-8864/9741
SEQ ID NO: 99:
TERISTICS:
amino acids
acid
:
nknown
peptide
1.5%; Score 8; DB 3; Length 16;
rity 100.0%; Pred.No.4.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PPA 138
{
PPA 12
lication US/08630915A
0
ION:
ARKS, Andrew B.
FFMAN, No. 6309820h
Y, Brian K.
WIKES, Dana M.
CONNELL, Stephen J.
TION: POLYPEPTIDES HAVING A FUNCTIONAL
TION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
ENCES: 227
ADDRESS:
Pennie & Edmonds LLP
5 Avenue of the Americas
ork
York
A
2711
BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
atentIn Release #1.0, Version #1.30
ACTION DATA:

1.5%; Score 8; DB 1; Length 20;
 arity 100.0%; Pred. No. 5.1;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
 [|||||]
 SEED 9

lication US/07814220

40
 ION:
 acaci, Thomas E.
 th, Thomas E.
 zsumanski, Maria B.W.
 NTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
 NTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
 JENCES: 43
 ADDRESS:
 WHITHAM, CURTIS & WHITHAM
 ston Intl. Center, 11800 Sunrise Valley Dr.,
 ite 900
 on

3A

ABLE FORM:
 : Floppy disk
 IBM PC compatible
 STEM: PC-DOS/MS-DOS
 PatentIn Release #1.0, Version #1.30
 CATION DATA:
 NUMBER: US/07/814,220
 : 23-DEC-1991
 ION: 435
 ION DATA:
 NUMBER: US 07/588,437
 : 25-SEP-1990
 T INFORMATION:
 am, Michael E.
 V NUMBER: 32,635
 CCKET NUMBER: CIT.016
 ION INFORMATION:
 703-391-2510
 03-391-9035
 SEQ ID NO: 27:
 CTERISTICS:
 amino acids
 acid
 3:
 linear
 : Peptide

1.5%; Score 8; DB 2; Length 20;
 arity 100.0%; Pred. No. 5.1;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158
 [|||||]
 ATA 9

lication US/07814221
 97
 ION:
 acaci, Thomas

APPLICANT: Toth, Thomas E.
 APPLICANT: Szumanski, Maria B.W.
 TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
 TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WHITHAM, CURTIS & WHITHAM
 STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
 STREET: Suite 900
 CITY: Reston
 STATE: VA
 COUNTRY: USA
 ZIP: 20191
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/812,421
 FILING DATE: 23-DEC-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/588,437
 FILING DATE: 25-SEP-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Whitham, Michael E.
 REGISTRATION NUMBER: 32,635
 REFERENCE/DOCKET NUMBER: CIT.016
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-391-2510
 TELEFAX: 703-391-9035
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-812-421-27

Query Match 1.5%; Score 8; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 151 AAAAAATA 158
 [|||||]
 Db 2 AAAAAATA 9

RESULT 95

US-08-663-731-21
 : Sequence 21, Application US/08663731
 : Patent No. 6057423
 : GENERAL INFORMATION:
 : APPLICANT: Brenner, Michael B.
 : APPLICANT: Parker, Christina M.
 : TITLE OF INVENTION: No. 6057423el integrin alpha subunit
 : NUMBER OF SEQUENCES: 25
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
 : STREET: 600 Atlantic Avenue
 : CITY: Boston
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02210
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/663,731

CN:
 ION DATA:
 NUMBER: 08/199,776
 INFORMATION:
 r, Elizabeth R.
 NUMBER: 36,637
 CKET NUMBER: B0801/7020
 ION INFORMATION:
 617-720-3500
 7-720-2441
 SEQ ID NO: 21:
 CTERISTICS:
 amino acids
 acid
 : single
 inear
 peptide
 YES
 O internal
 E:
 omo sapiens

1.5%; Score 8; DB 3; Length 20;
 rity 100.0%; Pred. No. 5.1;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

SED 333
 ||||
 EED 9

ication US/08879338A

CN:
 r, Michael B.
 r, Christina M.
 CN: Antibodies to No. 6063906el Integrin Alpha
 CN: Subunit
 B0801/7080/ERP
 ION NUMBER: US/08/879,338A
 ATE: 1997-06-20
 ION NUMBER: US 08/663,731
 ATE: 1996-06-14
 ION NUMBER: US 08/199,776
 ATE: 1994-02-18
 NOS: 31
 Q for Windows Version 3.0

Sapiens

1.5%; Score 8; DB 3; Length 20;
 rity 100.0%; Pred. No. 5.1;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

EED 333
 ||||
 EED 9

ication US/09293238B
 2
 CN:

; APPLICANT: Brenner, Michael B.
 ; APPLICANT: Parker, Christina M.
 ; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis
 ; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody
 ; TITLE OF INVENTION: Beta 7 Integrin
 ; FILE REFERENCE: L0560/7005/ERP
 ; CURRENT APPLICATION NUMBER: US/09/293,238B
 ; CURRENT FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: US 08/879,338
 ; PRIOR FILING DATE: 1997-06-20
 ; PRIOR APPLICATION NUMBER: US 08/663,731
 ; PRIOR FILING DATE: 1996-06-14
 ; PRIOR APPLICATION NUMBER: US 08/199,776
 ; PRIOR FILING DATE: 1994-02-18
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-293-238B-21

Query Match 1.5%; Score 8; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 LEKEEED 333
 |||||
 Db 2 LEKEEED 9

RESULT 98
 PCT-US95-02044-21
 ; Sequence 21, Application PC/TUS9502044
 ; GENERAL INFORMATION:

; APPLICANT:
 ; TITLE OF INVENTION: Novel integrin alpha subunit
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02210

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02044
 ; FILING DATE: herewith
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/199,776
 ; FILING DATE: 18 February 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7020
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO

11:33:39 2004

us-09-976-740-43.olig.ra1

1

```

: internal
CE:
Homo sapiens

1.5%; Score 8; DB 5; Length 20;
arity 100.0%; Pred.No. 5.1; 0; Indels 0; Gaps 0;
Conservative 0; Mismatches 0;

SEED 333
|||||
SEED 9

ication US/08199776
20
TION:
renner, Michael B.
arker, Christina M.
ATION: No. 5594120e1 integrin alpha subunit
ENCES: 25
ADDRESS:
Wolf, Greenfield and Sacks, P.C.
Atlantic Avenue
on

3A
ABLE FORM:
: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
CATION DATA:
NUMBER: US/08/199,776

ION: 514
I INFORMATION:
ar, Elizabeth R.
NUMBER: 35,637
CKET NUMBER: B0801/7020
TION INFORMATION:
617-720-3500
17-720-2441
SEQ ID NO: 5:
ACTERISTICS:
amino acids
acid
3: single
linear
: peptide
YES
NO
: internal
E:
Homo sapiens

1.5%; Score 8; DB 1; Length 21;
arity 100.0%; Pred.No. 5.4; 0; Indels 0; Gaps 0;
Conservative 0; Mismatches 0;

SEED 333
|||||
SEED 9

lication US/07814220
40

: GENERAL INFORMATION:
: APPLICANT: Caceci, Thomas
: APPLICANT: Toth, Thomas E.
: APPLICANT: Szumanski, Maria B.W.
: TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
: TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WHITHAM, CURTIS & WHITHAM
: STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
: STREET: Suite 900
: CITY: Reston
: STATE: VA
: COUNTRY: USA
: ZIP: 20191
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/814,220
: FILING DATE: 23-DEC-1991
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/588,437
: FILING DATE: 25-SEP-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Whitham, Michael E.
: REGISTRATION NUMBER: 32,635
: REFERENCE/DOCKET NUMBER: CIT.016
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-391-2510
: TELEFAX: 703-391-9035
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-07-814-220-24

Query Match 1.5%; Score 8; DB 2; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158
Db 1 AAAAAATA 8

RESULT 101
US-07-812-421-24
: Sequence 24, Application US/07812421
: Patent No. 5932697
: GENERAL INFORMATION:
: APPLICANT: Caceci, Thomas
: APPLICANT: Toth, Thomas E.
: APPLICANT: Szumanski, Maria B.W.
: TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
: TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WHITHAM, CURTIS & WHITHAM
: STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
: STREET: Suite 900
: CITY: Reston
: STATE: VA
: COUNTRY: USA
: ZIP: 20191
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
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3M PC compatible
ITEM: PC-DOS/MS-DOS
ItemIn Release #1.0, Version #1.30
ACTION DATA:
NUMBER: US/07/812,421
23-DEC-1991
DN: 435
ON DATA:
NUMBER: US 07/598,437
25-SEP-1990
INFORMATION:
NAME: Michael E.
NUMBER: 32,635
CKET NUMBER: CIT.016
ON INFORMATION:
703-391-2510
391-9035
SEQ ID NO: 24:
TERISTICS:
amino acids
acid
linear
peptide
1.5%; Score 8; DB 2; Length 21;
city 100.0%; Pred.No. 5.4;
ervative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||
ATA 8
ation US/08663731
ON:
anner, Michael B.
cker, Christina M.
TION: No. 6057423el integrin alpha subunit
NCES: 25
ADDRESS:
Wolf, Greenfield and Sacks, P.C.
Atlantic Avenue
1
1
3LE FORM:
Floppy disk
3M PC compatible
ITEM: PC-DOS/MS-DOS
ItemIn Release #1.0, Version #1.25
ACTION DATA:
NUMBER: US/08/663,731
DN:
ON DATA:
NUMBER: 08/199,776
INFORMATION:
c. Elizabeth R.
NUMBER: 36,637
CKET NUMBER: B0801/7020
ON INFORMATION:
517-720-3500
7-720-2441
SEQ ID NO: 5:
TERISTICS:
amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-663-731-5
Query Match 1.5%; Score 8; DB 3; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Ga
QY 326 LEKEEED 333
|||
Db 2 LEKEEED 9
RESULT 103
US-08-879-338-5
Sequence 5, Application US/08879338A
Patent No. 6063906
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha
TITLE OF INVENTION: Subunit
FILE REFERENCE: B0801/7080/ERP
CURRENT APPLICATION NUMBER: US/08/879,338A
CURRENT FILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: US 08/663,731
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: US 08/199,776
EARLIER FILING DATE: 1994-02-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 21
TYPE: PRT
ORGANISM: Homo Sapiens
US-08-879-338-5
Query Match 1.5%; Score 8; DB 3; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Ga
QY 326 LEKEEED 333
|||
Db 2 LEKEEED 9
RESULT 104
US-08-879-338-26
Sequence 26, Application US/08879338A
Patent No. 6063906
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha
TITLE OF INVENTION: Subunit
FILE REFERENCE: B0801/7080/ERP
CURRENT APPLICATION NUMBER: US/08/879,338A
CURRENT FILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: US 08/663,731
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: US 08/199,776
EARLIER FILING DATE: 1994-02-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 21

ficial Sequence

ION: Synthetic Peptide

1.5%; Score 8; DB 3; Length 21;
arity 100.0%; Pred.No. 5.4;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

EED 333

|||||
EED 9

ication US/09293238B

42

ner, Michael B.

ker, Christina M.

ION: A Method of Treating Ulcerative Colitis

ION: or Crohn's Disease by Administering an Antibody to Alpha E

ION: Beta 7 Integrin

L0560/7005/ERP

TION NUMBER: US/09/293,238B

DATE: 1999-04-16

ON NUMBER: US 08/879,338

TE: 1997-06-20

ON NUMBER: US 08/663,731

TE: 1996-06-14

ON NUMBER: US 08/199,776

TE: 1994-02-18

D NOS: 31

EQ for Windows Version 3.0

sapien

1.5%; Score 8; DB 4; Length 21;
arity 100.0%; Pred.No. 5.4;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

EED 333

|||||
EED 9

lication US/09293238B

42

ION:

ner, Michael B.

ker, Christina M.

ION: A Method of Treating Ulcerative Colitis

ION: or Crohn's Disease by Administering an Antibody to Alpha E

ION: Beta 7 Integrin

L0560/7005/ERP

TION NUMBER: US/09/293,238B

DATE: 1999-04-16

ON NUMBER: US 08/879,338

TE: 1997-06-20

ON NUMBER: US 08/663,731

TE: 1996-06-14

ON NUMBER: US 08/199,776

TE: 1994-02-18

D NOS: 31

EQ for Windows Version 3.0

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Peptide

US-09-293-238B-26

Query Match 1.5%; Score 8; DB 4; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 326 LEKEEED 333

|||||

Db 2 LEKEEED 9

RESULT 107

PCT-US95-02044-5

; Sequence 5, Application PC/TUS9502044

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Novel integrin alpha subunit

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.

; STREET: 600 Atlantic Avenue

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/02044

; FILING DATE: herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/199,776

; FILING DATE: 18 February 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Plumer, Elizabeth R.

; REGISTRATION NUMBER: 36,637

; REFERENCE/DOCKET NUMBER: B0801/7020

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-720-3500

; TELEFAX: 617-720-2441

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: YES

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

PCT-US95-02044-5

Query Match 1.5%; Score 8; DB 5; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 326 LEKEEED 333

|||||

Db 2 LEKEEED 9

RESULT 108

ication US/07814220
ION:
ceci, Thomas
th, Thomas E.
amanski, Maria B.W.
TION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
ENCES: 43

ADDRESS:
WHITHAM, CURTIS & WHITHAM
ton Intl. Center, 11800 Sunrise Valley Dr.,
te 900
n

A
BLE FORM:
FLOPPY disk
BM PC compatible
STEM: PC-DOS/MS-DOS
atentIn Release #1.0, Version #1.30
ATION DATA:
NUMBER: US/07/814,220
23-DEC-1991
ON: 435
ION DATA:
NUMBER: US 07/588,437
25-SEP-1990
INFORMATION:
am, Michael E.
NUMBER: 32,635
CKET NUMBER: CIT.016
ION INFORMATION:
703-391-2510
3-391-9035
SEQ ID NO: 33:
TERISTICS:
amino acids
acid
inear
peptide

city 1.5%; Score 8; DB 2; Length 25;
100.0%; Pred. No. 6.3;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158
|||
ATA 19

ication US/07814241
ION:
ceci, Thomas
th, Thomas E.
amanski, Maria B.W.
TION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
ENCES: 43
ADDRESS:
WHITHAM, CURTIS & WHITHAM
ton Intl. Center, 11800 Sunrise Valley Dr.,
ce 900
n

A
BLE FORM:
FLOPPY disk
BM PC compatible
STEM: PC-DOS/MS-DOS
atentIn Release #1.0, Version #1.30
ATION DATA:
NUMBER: US/07/814,220
23-DEC-1991
ON: 435
ION DATA:
NUMBER: US 07/588,437
25-SEP-1990
INFORMATION:
am, Michael E.
NUMBER: 32,635
CKET NUMBER: CIT.016
ION INFORMATION:
703-391-2510
3-391-9035
SEQ ID NO: 33:
TERISTICS:
amino acids
acid
inear
peptide

ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-33

Query Match 1.5%; Score 8; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 AAAAAATA 158
|||
Db 12 AAAAAATA 19

RESULT 110
US-07-814-220-36
Sequence 36, Application US/07814220
Patent No. 5925540
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016

ION INFORMATION:
703-391-2510
3-391-9035
SEQ ID NO: 36:
ACTERISTICS:
amino acids
acid
linear
peptide

1.5%; Score 8; DB 2; Length 28;
arity 100.0%; Pred.No. 7;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158
|||||
ATA 19

Location US/07812421

ION:
ceci, Thomas E.
th, Thomas E.
umanski, Maria B.W.
TION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
ENCES: 43
ADDRESS:
WHITHAM, CURTIS & WHITHAM
ston Intl. Center, 11800 Sunrise Valley Dr.,
ite 900
n
IA

ABLE FORM:
Floppy disk
IBM PC compatible
STEM: PC-DOS/MS-DOS
ationIn Release #1.0, Version #1.30
ATION DATA:
NUMBER: US/07/812,421
23-DEC-1991
ION: 435
ION DATA:
NUMBER: US 07/588,437
25-SEP-1990
INFORMATION:
am, Michael E.
f NUMBER: 32,635
CKET NUMBER: CIT.016
ION INFORMATION:
703-391-2510
3-391-9035
SEQ ID NO: 36:
ACTERISTICS:
amino acids
acid
linear
peptide

1.5%; Score 8; DB 2; Length 28;
arity 100.0%; Pred.No. 7;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158

Db 12 AAAAAATA 19
|||||

RESULT 112
US-08-180-524-1
Sequence 1, Application US/08180524
Patent No. 5849537
GENERAL INFORMATION:
APPLICANT: Tripp, Matthew
APPLICANT: Lusk, Lance
APPLICANT: Rhodes, Thomas
APPLICANT: Huige, Nick
APPLICANT: Kot, Edward
APPLICANT: Chicove, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.

TITLE OF INVENTION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,524
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/917,216
FILING DATE:
APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-9234-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudopleuronectus americanus
US-08-180-524-1

Query Match 1.5%; Score 8; DB 2; Length 37;
Best Local Similarity 100.0%; Pred.No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 AAAAAATA 158
|||||

Db 29 AAAAAATA 36
|||||

```

culation US/08180524
7
ION: Matthew
ipp, Matthew
sk, Lance
odes, Thomas
ige, Nick
t, Edward
icoye, Etzer
rney, Michael C.
onan, Charles L.
TION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
TION: IN YEAST
ENCES: 10
ADDRESS:
Thad Kryshak, Quarles & Brady
East Wisconsin Avenue
ukee
onsin
A
BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
SWORD Version 5.0
ACTION DATA:
NUMBER: US/08/180,524
ON: 435
ION DATA:
NUMBER: US/07/917,216
NUMBER: US 07/486,333
28-FEB-1990
ION DATA:
NUMBER: US 07/409,217
19-SEP-1989
INFORMATION:
ak, Thad
NUMBER: 35,433
CKET NUMBER: 66-005-9234-1
ION INFORMATION:
(414) 277-5707
14) 277-5591
SEQ ID NO: 8:
TERISTICS:
amino acids
acid
: single
inear
protein
NO
)
1.5%; Score 8; DB 2; Length 37;
city 100.0%; Pred. No. 9;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||
ATA 36
ication US/08180524
7
GENERAL INFORMATION:
APPLICANT: Tripp, Matthew
APPLICANT: Lusk, Lance
APPLICANT: Rhodes, Thomas
APPLICANT: Huige, Nick
APPLICANT: Kot, Edward
APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
NUMBER OF SEQUENCES: 10
NUMBER OF INVENTIONS: IN YEAST
CORRESPONDENCE ADDRESS:
ADDRESSER: Thad Kryshak, Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,524
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/917,216
FILING DATE:
APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-9234-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-180-524-10
Query Match 1.5%; Score 8; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 151 AAAAAATA 158
DB 29 AAAAAATA 36
RESULT 115
US-08-975-166-1
; Sequence 1, Application US/08975166
; Patent No. 5928877
; GENERAL INFORMATION:
; APPLICANT: Tripp, Matthew
; APPLICANT: Lusk, Lance
; APPLICANT: Rhodes, Thomas
; APPLICANT: Huige, Nick

```

Edward, Edward
 Etzer, Etzer
 Michael C.
 Patricia A.
 Charles L.
 Thomas L.
 METHOD OF EXPRESSING ANTIFREEZE PROTEINS
 IN YEAST
 IN YEAST
 ADDRESS:
 Thad Kryshak, Quarles & Brady
 1 East Wisconsin Avenue
 Milwaukee
 Wisconsin
 USA

ABLE FORM:
 : Floppy disk
 : IBM PC compatible
 : SYSTEM: PC-DOS/MS-DOS
 : MSWORD Version 5.0
 : CATION DATA:
 : NUMBER: US/08/975,166

ION: 435
 TION DATA:
 : NUMBER: US/08/180,524
 : NUMBER: US/07/917,216
 : NUMBER: US 07/486,333
 : 28-FEB-1990
 TION DATA:
 : NUMBER: US 07/409,217
 : 19-SEP-1989
 F INFORMATION:
 : NAME: Thad
 : NAME: Kryshak, Thad

REGISTRATION NUMBER: 35,433
 DOCKET NUMBER: 66-005-9234-1
 TION INFORMATION:
 : (414) 277-5707
 : (414) 277-5591
 : SEQ ID NO: 1:
 : amino acids
 : amino acids
 : single
 : linear
 : protein
 : NO
 : 40

?pseudopleuronectus americanus

1.5%; Score 8; DB 2; Length 37;
 irity 100.0%; Pred. No. 9;
 nservative 0; Mismatches 0; Indels 0;

ATA 158
 |||||
 ATA 36

ication US/08975166

77
 TION:
 : Tripp, Matthew
 : Lusk, Lance
 : Rhodes, Thomas
 : Huige, Nick
 : Kot, Edward
 : Chicoye, Etzer
 : Barney, Michael C.
 : Bower, Patricia A.

GENERAL INFORMATION:
 : APPLICANT: Tripp, Matthew
 : APPLICANT: Lusk, Lance
 : APPLICANT: Rhodes, Thomas
 : APPLICANT: Huige, Nick
 : APPLICANT: Kot, Edward
 : APPLICANT: Chicoye, Etzer
 : APPLICANT: Barney, Michael C.
 : APPLICANT: Bower, Patricia A.

US-08-975-166-10

Sequence 10, Application US/08975166

Patent No. 5928877

GENERAL INFORMATION:
 : APPLICANT: Tripp, Matthew
 : APPLICANT: Lusk, Lance
 : APPLICANT: Rhodes, Thomas
 : APPLICANT: Huige, Nick
 : APPLICANT: Kot, Edward
 : APPLICANT: Chicoye, Etzer
 : APPLICANT: Barney, Michael C.
 : APPLICANT: Bower, Patricia A.

US-08-975-166-8

Query Match 1.5%; Score 8; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 AAAAAATA 158
 Db 29 AAAAAATA 36

RESULT 117

US-08-975-166-10

Sequence 10, Application US/08975166

Patent No. 5928877

GENERAL INFORMATION:
 : APPLICANT: Tripp, Matthew
 : APPLICANT: Lusk, Lance
 : APPLICANT: Rhodes, Thomas
 : APPLICANT: Huige, Nick
 : APPLICANT: Kot, Edward
 : APPLICANT: Chicoye, Etzer
 : APPLICANT: Barney, Michael C.
 : APPLICANT: Bower, Patricia A.

US-08-975-166-8

Query Match 1.5%; Score 8; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 AAAAAATA 158
 Db 29 AAAAAATA 36

RESULT 117

US-08-975-166-10

Sequence 10, Application US/08975166

Patent No. 5928877

GENERAL INFORMATION:
 : APPLICANT: Tripp, Matthew
 : APPLICANT: Lusk, Lance
 : APPLICANT: Rhodes, Thomas
 : APPLICANT: Huige, Nick
 : APPLICANT: Kot, Edward
 : APPLICANT: Chicoye, Etzer
 : APPLICANT: Barney, Michael C.
 : APPLICANT: Bower, Patricia A.

onan, Charles L.
TION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
TION: IN YEAST
ENCES: 10

ADDRESS:
Thad Kryshak, Quarles & Brady
East Wisconsin Avenue
ukee
onsin
A

BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
SWORD Version 5.0
TION DATA:
NUMBER: US/08/975,166

DN: 435
ION DATA:
NUMBER: US/08/180,524

NUMBER: US/07/917,216

NUMBER: US 07/486,333
28-FEB-1990

ION DATA:
NUMBER: US 07/409,217
19-SEP-1989
INFORMATION:

ak, Thad
NUMBER: 35,433
CKET NUMBER: 66-005-9234-1
ION INFORMATION:
(414) 277-5707

(4) 277-5591

SEQ ID NO: 10:

TERISTICS:
amino acids
acid

: single

linear

protein

NO

)

1.5%; Score 8; DB 2; Length 37;
city 100.0%; Pred.No. 9;
servative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158

||

ATA 36

cation US/09117121

ION:

g, Zhiyuan

TION: Intracellular Antifreeze Polypeptides
TION: and Nucleic Acids

ENCES: 46

ADDRESS:

ownsend and Townsend and Crew LLP
Embarcadero Center, Eighth Floor
ancisco
ornia

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00062

FILING DATE: 30-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 016252-001610US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: -

LOCATION: 1..37

OTHER INFORMATION: /note= "HPLC-6"

US-09-117-121-39

Query Match

Best Local Similarity 1.5%; Score 8; DB 4; Length 37;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 AAAAAATA 158

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Db 29 AAAAAATA 36

RESULT 119

US-09-117-121-42

; Sequence 42; Application US/09117121

; Patent No. 6307020

; GENERAL INFORMATION:

; APPLICANT: Hew, Choy

; APPLICANT: Gong, Zhiyuan

; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides

; TITLE OF INVENTION: and Nucleic Acids

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/117,121

; FILING DATE: 20-NOV-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/CA97/00062

; FILING DATE: 30-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Kenneth A.

1 NUMBER: 31,677
 DOCKET NUMBER: 016252-001610US
 ION INFORMATION:
 (415) 576-0200
 (415) 576-0300
 SEQ ID NO: 42:
 ACTERISTICS:
 amino acids
 acid
 linear
 : protein
 1.5%; Score 8; DB 4; Length 37;
 arity 100.0%; Pred. No. 9;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 AATA 158
 |||||
 AATA 36
 igation US/09344529
 93
 ION:
 Choy L.
 Research and Development Limited Partnership
 ION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
 016252-002620US
 ION NUMBER: US/09/344,529
 DATE: 1999-06-24
 ION NUMBER: US 60/090,794
 DATE: 1998-06-26
 ION NUMBER: US 60/095,713
 DATE: 1998-08-07
 NOS: 19
 in Ver. 2.0
 conectes americanus
 ION: Winter flounder liver-type antifreeze polypeptide
 ION: (wflAFP-6)
 1.5%; Score 8; DB 4; Length 37;
 arity 100.0%; Pred. No. 9;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 AATA 158
 |||||
 AATA 36
 .cation US/07814220
 to
 ION:
 cecci, Thomas
 th, Thomas E.
 zumanski, Maria B.W.
 ATION: SYNTHETIC ANTIFREEZE PEPTIDE AND
 TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
 JENCES: 43
 3 ADDRESS:
 WHITHAM, CURTIS & WHITHAM
 ston Intl. Center, 11800 Sunrise Valley Dr.,
 ite 900
 on

STATE: VA
 COUNTRY: USA
 ZIP: 20191
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/814,220
 FILING DATE: 23-DEC-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/588,437
 FILING DATE: 25-SEP-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Whitham, Michael E.
 REGISTRATION NUMBER: 32,635
 REFERENCE/DOCKET NUMBER: CIT.016
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-391-2510
 TELEFAX: 703-391-9035
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-814-220-1
 Query Match 1.5%; Score 8; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 151 AAAAAATA 158
 Db 29 AAAAAATA 36
 RESULT 122
 US-07-812-421-1
 ; Sequence 1, Application US/07812421
 ; Patent No. 5932697
 ; GENERAL INFORMATION:
 ; APPLICANT: Caceci, Thomas
 ; APPLICANT: Toth, Thomas E.
 ; APPLICANT: Szumanski, Maria B.W.
 ; TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
 ; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
 ; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
 ; STREET: Suite 900
 ; CITY: Reston
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 20191
 ; COMPUTER READABLE FORM: disk
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/812,421
 ; FILING DATE: 23-DEC-1991
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/588,437
 ; FILING DATE: 25-SEP-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Whitham, Michael E.

NUMBER: 22,635
 CKET NUMBER: CIT.016
 ION INFORMATION:
 703-391-2510
 13-391-9035
 SEQ ID NO: 1:
 CHARACTERISTICS:
 amino acids
 , acid
 ;
 ;
 linear
 peptide

1.5%; Score 8; DB 2; Length 38;
 rity 100.0%; Pred. No. 9.2;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158
 ||||
 ATA 36

ication US/09117121
 0

ION:
 w, Choy
 ng, Zhiyuan
 TION: Intracellular Antifreeze Polypeptides
 TION: and Nucleic Acids
 ENCS: 46

ADDRESS:
 Townsend and Townsend and Crew LLP
 Embarcadero Center, Eighth Floor
 rancisco
 ornia

A 3834
 BLE FORM:
 Floppy disk
 BM PC compatible
 STEM: PC-DOS/MS-DOS
 atentin Release #1.0, Version #1.30
 ATION DATA:
 NUMBER: US/09/117,121
 20-NOV-1998
 ON: 435

ION DATA:
 NUMBER: WO PCT/CA97/00062
 INFORMATION:
 30-JAN-1997
 , Kenneth A.

NUMBER: 31,677
 CKET NUMBER: 016252-001610US
 ION INFORMATION:
 (415) 576-0200
 15) 576-0300
 SEQ ID NO: 28:
 CHARACTERISTICS:
 amino acids
 acid
 inear
 protein

1.5%; Score 8; DB 4; Length 39;
 rity 100.0%; Pred. No. 9.5;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 125
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Db 3 APAAAAA 10

RESULT 124

US-09-117-121-30
 ; Sequence 30, Application US/09117121
 ; Patent No. 6307020
 ; GENERAL INFORMATION:
 ; APPLICANT: Hew, Choy
 ; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
 ; TITLE OF INVENTION: and Nucleic Acids
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/117,121
 ; FILING DATE: 20-NOV-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/CA97/00062
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Kenneth A.
 ; REGISTRATION NUMBER: 31,677
 ; REFERENCE/DOCKET NUMBER: 016252-001610US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 54 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-117-121-30

Query Match 1.5%; Score 8; DB 4; Length 54;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 APAAAAA 125

Db 3 APAAAAA 10
 |||||

RESULT 125

US-08-199-776-4
 ; Sequence 4, Application US/08199776
 ; Patent No. 5594120
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenner, Michael B.
 ; APPLICANT: Parker, Christina M.
 ; TITLE OF INVENTION: No. 5594120e1 integrin alpha subunit
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02210
 ; COMPUTER READABLE FORM:

```
; Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
CAUTION DATA:
NUMBER: US/08/199,776
;
ION: 514
T INFORMATION:
er, Elizabeth R.
N NUMBER: 36,637
CKET NUMBER: B0801/7020
TION INFORMATION:
617-720-3500
17-720-2441
SEQ ID NO: 4:
ACTERISTICS:
amino acids
o acid
S: single
linear
: peptide
YES
NO
: internal
CE:
Homo sapiens
1.5%; Score 8; DB 1; Length 55;
arity 100.0%; Pred. No. 13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
EED 333
|||||
EED 43
ication US/08663731
23
TION:
renner, Michael B.
arker, Christina M.
NTION: No. 6057423el integrin alpha subunit
UENCES: 25
E ADDRESS:
Wolf, Greenfield and Sacks, P.C.
0 Atlantic Avenue
on
SA
ABLE FORM:
; Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
CAUTION DATA:
NUMBER: US/08/663,731
;
ION:
TION DATA:
NUMBER: 08/199,776
;
T INFORMATION:
er, Elizabeth R.
N NUMBER: 36,637
CKET NUMBER: B0801/7020
TION INFORMATION:
617-720-3500
17-720-2441
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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-663-731-4
Query Match 1.5%; Score 8; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 326 LEKEEED 333
|||||
Db 36 LEKEEED 43
RESULT 127
US-08-879-338-4
; Sequence 4, Application US/08879338A
; Patent No. 6063906
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha
; TITLE OF INVENTION: Subunit
; FILE REFERENCE: B0801/7080/ERP
; CURRENT APPLICATION NUMBER: US/08/879,338A
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: US 08/663,731
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: US 08/199,776
; EARLIER FILING DATE: 1994-02-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-879-338-4
Query Match 1.5%; Score 8; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 326 LEKEEED 333
|||||
Db 36 LEKEEED 43
RESULT 128
US-09-293-238B-4
; Sequence 4, Application US/09293238B
; Patent No. 6455042
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibod
; TITLE OF INVENTION: Beta 7 Integrin
; FILE REFERENCE: L0560/7005/ERP
; CURRENT APPLICATION NUMBER: US/09/293,238B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: US 08/879,338
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: US 08/663,731
; PRIOR FILING DATE: 1996-06-14
```

NUMBER: US 08/199,776
3: 1994-02-18
NOS: 31
Q for Windows Version 3.0

sapien

1.5%; Score 8; DB 4; Length 55;
city 100.0%; Pred. No. 13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

SED 333
|||
SED 43

cation PC/TUS9502044
ION:

ION: Novel integrin alpha subunit
ENCES: 25
ADDRESS:
Wolf, Greenfield and Sacks, P.C.
Atlantic Avenue

3LE FORM:

Floppy disk
3M PC compatible
STEM: PC-DOS/MS-DOS
atent in Release #1.0, Version #1.25
TION DATA:
NUMBER: PCT/US95/02044
herewith

ON DATA:
NUMBER: 08/199,776
18 February 1994
INFORMATION:
Elizabeth R.
NUMBER: 36,637
XET NUMBER: B0801/7020
ON INFORMATION:
17-720-3500
7-720-2441
SEQ ID NO: 4:
TERISTICS:
mino acids
acid
: single
inear
peptide
YES
internal
3:
omo sapiens

1.5%; Score 8; DB 5; Length 55;
city 100.0%; Pred. No. 13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

SED 333
|||
SED 43

RESULT 130
5496550-8
; Patent No. 5496550
; APPLICANT: WALLACH, MICHAEL; PUGATSCH, THEA; MENCHER, DAVID
; TITLE OF INVENTION: METHOD OF REDUCING THE OUTPUT OF EIMERIA
; OOCYSTS FROM A NEWBORN CHICK
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/108,763
; FILING DATE: 17-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 642,219
; FILING DATE: 16-JAN-1991
; APPLICATION NUMBER: 310,603
; FILING DATE: 14-FEB-1989
; APPLICATION NUMBER: 155,245
; FILING DATE: 12-FEB-1988
; APPLICATION NUMBER: 896,611
; FILING DATE: 14-AUG-1986
; SEQ ID NO: 8:
; LENGTH: 62
5496550-8

Query Match 1.5%; Score 8; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAAP 127
|||
Db 37 AAAAAAAP 44

RESULT 131
US-09-621-976-3951
; Sequence 3951, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3951
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -70...-1
US-09-621-976-3951

Query Match 1.5%; Score 8; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAAP 127
|||
Db 30 AAAAAAAP 37

RESULT 132
US-09-540-236-2315
; Sequence 2315, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ION: FOR DIAGNOSTICS AND THERAPEUTICS
2709.2005-001
ION NUMBER: US/09/540.236
DATE: 2000-04-04
NOS: 3840

arrhalis

1.5%: Score 8; DB 4; Length 96;
arity 100.0%; Pred. No. 22; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

ASS 24

ASS 79

ication US/07814220

10

ION:

aceci, Thomas

th, Thomas E.

umanaki, Maria B.W.

ATION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

JENCES: 43

ADDRESS:

WHITHAM, CURTIS & WHITHAM

ston Intl. Center, 11800 Sunrise Valley Dr.,

ite 900

on

3A

ABLE FORM:

1: Floppy disk

IBM PC compatible

(STEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

ATION DATA:

NUMBER: US/07/814.220

: 23-DEC-1991

ION: 435

ION DATA:

NUMBER: US 07/588,437

: 25-SEP-1990

ION INFORMATION:

am, Michael E.

NUMBER: 32,635

CKET NUMBER: CIT.016

ION INFORMATION:

703-391-2510

33-391-9035

SEQ ID NO: 2:

ACTERISTICS:

amino acids

o acid

linear

: protein

1.5%: Score 8; DB 2; Length 98;

arity 100.0%; Pred. No. 22; Indels 0;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AATA 158

|||||

AATA 15

RESULT 134
US-07-812-421-2
; Sequence 2, Application US/07812421
; Patent No. 5932697
; GENERAL INFORMATION:
; APPLICANT: Caceci, Thomas
; APPLICANT: Toth, Thomas E.
; APPLICANT: Szumanski, Maria B.W.
; TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
; STREET: Suite 900
; CITY: Reston
; STATE: VA
; COUNTRY: USA
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/812,421
; FILING DATE: 23-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/588,437
; FILING DATE: 25-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitham, Michael E.
; REGISTRATION NUMBER: 32,635
; REFERENCE/DOCKET NUMBER: CIT.016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-391-2510
; TELEFAX: 703-391-9035
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-812-421-2

Query Match 1.5%; Score 8; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158
|||||
Db 8 AAAAAATA 15

RESULT 135
US-08-702-344-16
; Sequence 16, Application US/08702344
; Patent No. 572315
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: LaVallie, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

Genetics Institute, Inc.
CambridgePark Drive
Irvine
California 92618
S.A.

FILE FORM:
FLOPPY disk
BM PC compatible
STEM: PC-DOS/MS-DOS
attentIn Release #1.0, Version #1.30
ATTION DATA:
NUMBER: US/08/702,344

ON: 536

INFORMATION:

Scott A.

NUMBER: 32,724

TON INFORMATION:

(617) 498-8224

17) 876-5851

SEQ ID NO: 16:

CTERISTICS:

amino acids

acid

linear

protein

1.5%; Score 8; DB 1; Length 116;

ity 100.0%; Pred. No. 26;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

PAL 438

|||

PAL 68

plication US/09621976

3

ON:

rt, S.

iano, J.Y.

ON: ESTs and Encoded Human Proteins.

GENSET.054PR2

TON NUMBER: US/09/621,976

ATE: 2000-07-21

NOS: 19335

.pm

sapiens

ON: Xaa = *,Trp

ON: Xaa = Ala,Pro

ON: Xaa = Asp,His

1.5%; Score 8; DB 4; Length 117;

ity 100.0%; Pred. No. 26;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAAP 127
|||
Db 2 AAAAAAAP 9

RESULT 137

US-09-072-596-243

; Sequence 243, Application US/09072596

; Patent No. 6458366

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Dillan, Davin C.

; APPLICANT: Campos-Neto, Antonio

; APPLICANT: Houghton, Raymond

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Twardzik, Daniel R.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Hendrickson, Ronald C.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

; NUMBER OF SEQUENCES: 350

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/072,596

; FILING DATE: 05-MAY-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.417C9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 243:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 123 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-072-596-243

Query Match 1.5%; Score 8; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 GGGGGAGG 266
|||
Db 107 GGGGGAGG 114

RESULT 138

US-09-072-967-248

; Sequence 248, Application US/09072967

; Patent No. 6592877

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Dillan, Davin C.

; APPLICANT: Campos-Neto, Antonio

; APPLICANT: Houghton, Raymond

; APPLICANT: Vedvick, Thomas S.

wardzik, Daniel R.
odes, Michael J.
endrickson, Ronald C.
NTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TION: AND DIAGNOSIS OF TUBERCULOSIS
UENCES: 355

E ADDRESS:
SEED and BERRY LLP
00 Columbia Center, 701 Fifth Avenue
le
hington
SA
-7092

ABLE FORM:
: Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:

NUMBER: US/09/072,967
: 05-MAY-1998
ION:

T INFORMATION:
David J.
N NUMBER: 31,392
CKET NUMBER: 210121.411C9

TION INFORMATION:
(206) 622-4900
206) 682-6031
SEQ ID NO: 248:

ACTERISTICS:
3 amino acids
o acid
S: single
linear
: protein

1.5%; Score 8; DB 4; Length 123;
arity 100.0%; Pred. No. 27;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

GAGG 266
|||
GAGG 114

plication US/09198452A
94
ION:

ION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
ION: thereof and uses thereof, in particular for the diagnosis, prevention
ION: and treatment of infection

9710-003-999
TION NUMBER: US/09/198,452A
DATE: 1998-11-24
D NOS: 6849

mydia pneumoniae
1.5%; Score 8; DB 4; Length 125;
arity 100.0%; Pred. No. 27;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATAP 159
|||
ATAP 96

RESULT 140
US-09-252-991A-30453
; Sequence 30453, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30453
; LENGTH: 130
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30453

Query Match 1.5%; Score 8; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 PPPAPVAA 142
|||
Db 43 PPPAPVAA 50

RESULT 141
US-09-489-039A-8788
; Sequence 8788, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8788
; LENGTH: 133
; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8788

Query Match 1.5%; Score 8; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATTAAAA 22
|||
Db 18 AATTAAAA 25

RESULT 142
US-09-252-991A-21247
; Sequence 21247, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

N NUMBER: US 60/074,788
E: 1998-02-18
N NUMBER: US 60/094,190
E: 1998-07-27
NOS: 33142

omonas aeruginosa

1.5%; Score 8; DB 4; Length 137;

ity 100.0%; Pred. No. 30; Mismatches 0; Indels 0; Gaps 0;

PSR 316

PSR 134

7 plication US/09489039A

ON:

Bretton et. al

ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

ON: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

2709.2004001

ION NUMBER: US/09/489,039A

ATE: 2000-01-27

N NUMBER: US 60/117,747

E: 1999-01-29

NOS: 14342

iella pneumoniae

1.5%; Score 8; DB 4; Length 146;

ity 100.0%; Pred. No. 32; Mismatches 0; Indels 0; Gaps 0;

AAA 155

AAA 75

2 plication US/09252991A

ON:

J. Rubenfield et al.

ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

107196.136

ION NUMBER: US/09/252,991A

ATE: 1999-02-18

N NUMBER: US 60/074,788

E: 1998-02-18

N NUMBER: US 60/094,190

E: 1998-07-27

NOS: 33142

omonas aeruginosa

1.5%; Score 8; DB 4; Length 148;

ity 100.0%; Pred. No. 32;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 APRAAAAA 155

Db 117 APRAAAAA 124

RESULT 145

US-09-489-039A-10001

; Sequence 10001, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Bretton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 10001

; LENGTH: 149

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10001

Query Match 1.5%; Score 8; DB 4; Length 149;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 GSGGGAGG 266

Db 94 GSGGGAGG 101

RESULT 146

US-09-433-241A-4

; Sequence 4, Application US/09433241A

; Patent No. 6525244

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Ralfalski, Antoni

; TITLE OF INVENTION: Plant Histidinol-Phosphate Aminotransferase Homoc

; FILE REFERENCE: BB1256 US NA

; CURRENT APPLICATION NUMBER: US/09/433,241A

; CURRENT FILING DATE: 1999-11-04

; PRIOR APPLICATION NUMBER: 60/107,273

; PRIOR FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 4

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Oryza sp.

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (88)

; OTHER INFORMATION: Xaa = ANY AMINO ACID

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (136)

; OTHER INFORMATION: Xaa = ANY AMINO ACID

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (137)

; OTHER INFORMATION: Xaa = ANY AMINO ACID

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (138)

; OTHER INFORMATION: Xaa = ANY AMINO ACID

US-09-433-241A-4

1.5%; Score 8; DB 4; Length 162;
arity 100.0%; Pred. No. 35;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
|||||
AAAA 63

location US/09140749
95
ION:
k, Peter
house, Mark A.
er, Samar
; Alfred W.K.
; Ighian, Sean V.
ION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
2318-205
TION NUMBER: US/09/140,749
DATE: 1998-08-26
TION NUMBER: U.S. 08/791,115
DATE: 1997-01-30
TION NUMBER: U.S. 60/057,750
DATE: 1997-08-26
TION NUMBER: U.S. 60/083,563
DATE: 1998-04-30
D NOS: 64
tin Ver. 2.0

musculus

1.5%; Score 8; DB 4; Length 194;
arity 100.0%; Pred. No. 41;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAP 127
|||||
AAAP 39

26
Application US/09252991A
95
ION:
c J. Rubenfield et al.
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
TION NUMBER: US/09/252,991A
DATE: 1999-02-18
ON NUMBER: US 60/074,788
TE: 1998-02-18
ON NUMBER: US 60/094,190
TE: 1998-07-27
D NOS: 33142

domonas aeruginosa
26

1.5%; Score 8; DB 4; Length 202;
arity 100.0%; Pred. No. 42;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 AAAAAAP 127
Db 92 AAAAAAP 99
|||||

RESULT 149
US-08-463-115-92
; Sequence 92, Application US/08463115
; Patent No. 5703221
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,115
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: Four
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 5703221ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-115-92

Query Match 1.5%; Score 8; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 133 PPPPPAPV 140
Db 197 PPPPPAPV 204
|||||

RESULT 150
US-08-465-388-92
; Sequence 92, Application US/08465388
; Patent No. 5753488
; GENERAL INFORMATION:

1:33:39 2004

us-09-976-740-43.olig.ra

P

LIAM JOHN MARTIN
ION: ISOLATED STEALTH VIRUSES
ION: AND RELATED VACCINES

ENCES: 104

ADDRESS:

Lyon & Lyon

West Fifth Street

te 4700

geles

fornia

S.A.

2066

BLE FORM:

3.5" Diskette, 1.44 Mb

Storage

BM Compatible

STEM: IBM P.C. DOS 5.0

astSeq Version 1.5

ATION DATA:

NUMBER: US/08/465,388

June 5, 1995

DN: 435

ION DATA:

ION DATA: including application

ION DATA: described below:

Four

NUMBER: 08/157,811

No. 575348ember 23, 1993

NUMBER: 07/887,502

May 22, 1992

NUMBER: 07/704,814

May 23, 1991

NUMBER: 07/763,039

September 20, 1991

INFORMATION:

g, Richard J.

NUMBER: 32,327

CKET NUMBER: 213/300

ION INFORMATION:

(213) 489-1600

(3) 955-0440

310

SEQ ID NO: 92:

TERISTICS:

amino acids

acid

single

near

1.5%; Score 8; DB 1; Length 218;

ity 100.0%; Pred.No.46;

servative 0; Mismatches 0; Indels 0; Gaps 0;

PV 140

||

PV 204

rch 30, 2004, 15:04:24

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 CompuGen Ltd.

n search, using sw model

ch 30, 2004, 14:54:16 ; Search time 60 Seconds
 (without alignments)
 2533.509 Million cell updates/sec

09-976-740-43

AGPALPPPTAAATAA.....HIKVLQGHFDDDDPDGFLG 538

30

cp 60.0 , Gapext 60.0

5107 seqs, 282547505 residues

s satisfying chosen parameters: 1586107

th: 0

ch: 2000000000

sting first 150 summaries

Genesep 29Jan04.*

genesep1980s.*

genesep1990s.*

genesep2000s.*

genesep2001s.*

genesep2002s.*

genesep2003as.*

genesep2003bs.*

genesep2004s.*

the number of results predicted by chance to have a
 than or equal to the score of the result being printed,
 i by analysis of the total score distribution.

SUMMARIES

Length	DB	ID	Description
0	538	4	AAB82806 Human low
3	217	2	Aaw49041 Human low
3	217	4	AAB82803 Human low
5	132	7	Ad59158 Human Pro
8	241	3	AAB58957 Breast an
4	550	4	AAB82807 Rabbit lo
1	232	4	AAB82799 Rabbit lo
1	252	4	AAB82800 Rabbit lo
1	317	4	AAB82798 Rabbit lo
3	61	3	AAB34365 Human sec
0	317	2	Aaw49038 Rabbit lo
4	316	4	AU31793 Novel hum
8	26	4	AAB82810 Human low
8	15	4	AAB82809 Human low
8	102	4	AAM39592 Human pol
8	102	4	Abb50215 Human tra
8	108	5	Abp58930 Human cel
8	114	4	Aam41378 Human pol
8	116	6	Ada55289 Human pro
2	104	4	Abb67522 Drosophil
2	2280	4	Abb61650 Drosophil
0	11	4	AAB82811 Human low
0	12	4	AAB82817 Rabbit lo
0	28	4	AAB82816 Rabbit lo
0	129	3	AAy51200 Human SCA

26	11	2.0	139	2	AA222382	Aar222382 Ant
27	11	2.0	189	5	ABG76914	Abg76914 Ric
28	11	2.0	270	4	ABG17272	Abg17272 Nov
29	11	2.0	892	7	AD018910	Ad018910 Hun
30	11	2.0	1109	7	ADC59312	Adc59312 Hun
31	11	2.0	1340	6	AAE37017	Aae37017 Hun
32	10	1.9	10	4	AAB82812	Aab82812 Hun
33	10	1.9	10	4	AAB82818	Aab82818 Rak
34	10	1.9	22	5	AU97858	Aau97858 Prc
35	10	1.9	75	4	ABB64202	Abb64202 Drc
36	10	1.9	96	4	ABB69039	Abb69039 Drc
37	10	1.9	112	6	ABR43149	Ab43149 Rye
38	10	1.9	132	3	AG34164	Ag34164 Zea
39	10	1.9	171	3	AG34163	Ag34163 Zea
40	10	1.9	238	6	ABU17208	Abu17208 Prc
41	10	1.9	254	6	ADA36364	Ada36364 Ac1
42	10	1.9	257	2	AAy25630	AAy25630 Phl
43	10	1.9	257	7	ADC34880	Adc34880 Tin
44	10	1.9	285	2	AAy25633	AAy25633 Phl
45	10	1.9	285	7	ADC34883	Adc34883 Tin
46	10	1.9	320	3	AG34499	Ag34499 Ara
47	10	1.9	322	3	AA42629	Aa42629 Hum
48	10	1.9	401	3	AG34498	Ag34498 Ara
49	10	1.9	402	5	ABP54691	Abp54691 Met
50	10	1.9	436	2	AAy32114	AAy32114 Mai
51	10	1.9	436	5	ABP51652	Abp51652 Mai
52	10	1.9	448	3	AG34497	Ag34497 Ara
53	10	1.9	581	5	ABG66745	ABG66745 Hum
54	10	1.9	588	6	ABU22735	Abu22735 Prc
55	10	1.9	613	6	ABU15059	Abu15059 Prc
56	10	1.9	635	3	AA18192	Aa18192 Pla
57	10	1.9	660	4	AB62471	Ab62471 Drc
58	10	1.9	660	6	ABU47568	Abu47568 Prc
59	10	1.9	660	6	ABU47065	Abu47065 Prc
60	10	1.9	687	4	ABG25510	ABG25510 Nov
61	10	1.9	725	4	ABG17677	ABG17677 Nov
62	10	1.9	806	4	AB60866	Ab60866 Drc
63	10	1.9	1101	3	AB07036	Ab07036 Mou
64	10	1.9	1250	2	AAW59361	Aaw59361 Dro
65	10	1.9	1250	4	AB65508	Ab65508 Dro
66	10	1.9	1250	4	AB65470	Ab65470 Dro
67	10	1.9	1277	4	AB67536	Ab67536 Cor
68	10	1.9	1301	4	AB65129	Ab65129 Dro
69	10	1.9	1390	5	ABU65152	Abu65152 Hum
70	10	1.9	1461	5	ABP73792	Abp73792 Can
71	10	1.9	1887	5	AB08801	Ab08801 Yea
72	10	1.9	1887	5	AB08807	Ab08807 Yea
73	10	1.9	1887	5	AB08803	Ab08803 Yea
74	10	1.9	1887	5	AB08805	Ab08805 Yea
75	10	1.9	1887	5	AB08802	Ab08802 Yea
76	10	1.9	1887	5	AB08806	Ab08806 Yea
77	10	1.9	1887	5	AB08804	Ab08804 Yea
78	10	1.9	1887	6	ABR52621	ABR52621 Pro
79	10	1.9	1894	6	ABU88253	Abu88253 Nov
80	10	1.9	1894	6	ABU90132	Abu90132 Nov
81	10	1.9	1894	6	ABU96434	Abu96434 Nov
82	10	1.9	1894	6	ABU99043	Abu99043 Nov
83	10	1.9	1894	6	ABU8258	Abu8258 Nov
84	10	1.9	1894	6	ABU91964	Abu91964 Nov
85	10	1.9	1894	6	ABU85268	Abu85268 Nov
86	10	1.9	1894	6	ABO00407	ABO00407 Nov
87	10	1.9	1894	6	ABU88958	Abu88958 Nov
88	10	1.9	1894	6	ABO06454	ABO06454 Nov
89	10	1.9	1894	6	ABU95514	Abu95514 Nov
90	10	1.9	1894	6	ABU95204	Abu95204 Nov
91	10	1.9	1894	6	ABU90752	Abu90752 Nov
92	10	1.9	1894	6	ABU93914	Abu93914 Nov
93	10	1.9	1894	6	ABU86188	Abu86188 Nov
94	10	1.9	1894	6	ABU82043	Abu82043 Nov
95	10	1.9	1894	6	ABU07904	Abu07904 Nov
96	10	1.9	1894	6	ABU94224	Abu94224 Nov
97	10	1.9	1894	6	ABO00097	ABO00097 Nov
98	10	1.9	1894	6	ABU87108	Abu87108 Nov

1.9 1894 6 ABU91349 Novel hum
 1.9 1894 6 ABU90442 Novel hum
 1.9 1894 6 ABU97033 Novel hum
 1.9 1894 6 ABO05229 Novel hum
 1.9 2012 4 AAB76534 Coryneb
 1.9 2993 4 AAG92485 Coryneb
 1.7 43 3 AAG34648 Arabidops
 1.7 49 3 AAG52678 Arabidops
 1.7 51 3 AAG52700 Arabidops
 1.7 52 4 ABUS2912 Human ute
 1.7 66 3 AAG01387 Human sec
 1.7 68 3 AAG34705 Arabidops
 1.7 68 3 AAG28554 Arabidops
 1.7 68 3 AAG52668 Arabidops
 1.7 68 3 AAG52680 Arabidops
 1.7 68 3 AAG21112 Arabidops
 1.7 69 3 AAG41928 Arabidops
 1.7 70 3 AAG34561 Arabidops
 1.7 74 3 AAG34647 Arabidops
 1.7 76 2 AAR22394 Antigen t
 1.7 79 3 AAG34372 Arabidops
 1.7 80 3 AAG52677 Arabidops
 1.7 81 3 AAG52679 Arabidops
 1.7 82 3 AAG52699 Arabidops
 1.7 84 3 AAG34371 Arabidops
 1.7 84 6 ABR69624 Human CGD
 1.7 87 3 AAG34646 Arabidops
 1.7 93 3 AAG52676 Arabidops
 1.7 95 3 AAG52698 Arabidops
 1.7 96 3 AAG13034 Arabidops
 1.7 99 3 AAG21111 Arabidops
 1.7 99 3 AAG28553 Arabidops
 1.7 99 3 AAG34704 Arabidops
 1.7 99 3 AAG52667 Arabidops
 1.7 99 3 AAG52671 Arabidops
 1.7 100 3 AAG41927 Arabidops
 1.7 101 3 AAG34560 Arabidops
 1.7 105 4 ABG25320 Novel hum
 1.7 109 3 AAG34350 Zea may
 1.7 111 4 AAM19703 Peptide #
 1.7 111 4 ABB71018 Drosophil
 1.7 111 4 ABB39430 Peptide #
 1.7 111 4 ABB32953 Peptide #
 1.7 111 4 ABB24202 Protein #
 1.7 111 4 AAM72722 Human bon
 1.7 111 4 AAM60110 Human bra
 1.7 111 4 ABG54420 Human liv
 1.7 111 5 ABG42546 Human pep
 1.7 112 2 AAY18127 Clone 1 o
 1.7 112 3 AAG34703 Arabidops
 1.7 112 3 AAG52670 Arabidops
 1.7 112 3 AAG21110 Arabidops

ALIGNMENTS

lard; protein; 538 AA.

(first entry)

ity lipoprotein binding protein 2 (LBP-2).

poprotein binding protein 2; LBP-2; LDL; human;
 s; antiarteriosclerotic; therapy; diagnosis; vaccine.

XX PD 07-SEP-2001.
 XX PF 28-FEB-2001; 2001WO-US0006356.
 XX PR 02-MAR-2000; 2000US-00517849.
 XX PR 14-JUL-2000; 2000US-00616289.
 XX PA (BOST-) BOSTON HEART FOUND INC.
 XX PI Lees AM, Lees RS, Law SW, Arjona AA;
 XX DR WPI; 2001-565505/63.
 XX DR N-PSDB; AAB26499.
 XX PT New isolated low density lipoprotein binding polypeptide for trea
 XX PS diagnosing and/or identifying therapeutic agents for atherosclero
 XX Claim 13(j); Fig 7A; 143pp; English.

The present sequence is that of novel human low density lipoprote
 binding protein 2 (LBP-2). The amino acid sequence was deduced fr
 coding region of isolated genomic DNA (see AAB26499). It differs
 sequence predicted from an LBP-2 cDNA clone (see AAB82803) by the
 presence of an additional 321 amino acids at the N-terminus (the
 clone is 5' truncated). Human LBP-2 is an example of claimed LBP
 polypeptides of the invention that are capable of binding to nati
 methylated low density lipoproteins. Also claimed are biological
 fragments and analogues of LBPs, polynucleotides encoding LBPs, a
 as expression vectors, cells and methods of producing the LBPs.
 CC Polypeptides having amino acid residues 329-343, 329-354, 344-354
 CC -538 (see AAB82809-12) of the present sequence are claimed. Method
 CC determining if an animal is at risk for atherosclerosis, methods
 CC evaluating an agent for use in treating atherosclerosis, and meth
 CC treating a cell having an abnormality in structure or metabolism
 CC are claimed. Pharmaceutical compositions comprising an LBP polypep
 CC nucleic acid, and vaccine compositions, are also claimed

XX Sequence 538 AA;

Query Match 100.0%; Score 538; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; G;

QY 1 MAGPPALPPETAAATTAATAASSSSAASPHYQWILDTIDSLRSRKARPDLEICRI
 DB 1 MAGPPALPPETAAATTAATAASSSSAASPHYQWILDTIDSLRSRKARPDLEICRI
 QY 61 RHGPEPERTRAELEKLIQORAVLRVSYKGSISYRNAARVQPPRRGATPPAPPRPR
 DB 61 RHGPEPERTRAELEKLIQORAVLRVSYKGSISYRNAARVQPPRRGATPPAPPRPR
 QY 121 AAAAAAPPTTAPPPPPAPVAAAAPARAAPRAAAAATAPPSPGPAQPGRAQAAAP
 DB 121 AAAAAAPPTTAPPPPPAPVAAAAPARAAPRAAAAATAPPSPGPAQPGRAQAAAP
 QY 181 PPAPAPPAVAPPAGPRAPPAPPAAREPLPPPPPPQPPAPPQPPPPPPPPPPPP
 DB 181 PPAPAPPAVAPPAGPRAPPAPPAAREPLPPPPPPQPPAPPQPPPPPPPPPPPP
 QY 241 RAGGAARPVSLREVRYLGGSGGAGGRLTRGRVQGLLEEEAAARGRLERLALAI
 DB 241 RAGGAARPVSLREVRYLGGSGGAGGRLTRGRVQGLLEEEAAARGRLERLALAI
 QY 301 DRPGRAPPAASARPSRKEGGERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDE
 DB 301 DRPGRAPPAASARPSRKEGGERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDE
 QY 361 HHQLNGERGQSAKERVKEWTFCGPHQDDEGRGAPGSGTTRQVFSMAAMNKEGGT
 DB 361 HHQLNGERGQSAKERVKEWTFCGPHQDDEGRGAPGSGTTRQVFSMAAMNKEGGT
 QY 421 TGPDSPSPVPLPGPKPALPGADGTPGCPGPKRKEKPSDPVETVMDVVEYFTEAGFI

|||||
 ?SVPLPPGKPAUFGADGTFPGPGGKPKSPDVEWTVMDVVEYFTEAGFPEQA 480
 DEIDGKSLMLMORTDVLTLGLSIRLGPALKIYEHKIKVLQOQHEDDDPDGFLG 538
 DEIDGKSLMLMORTDVLTLGLSIRLGPALKIYEHKIKVLQOQHEDDDPDGFLG 538

ard; protein; 217 AA.

(first entry)

ity lipoprotein binding protein LBP-2.

oprotein binding protein; LDL binding protein 2; LBP-2;
 1; atherosclerosis; diagnosis; therapy; vaccine.

Location/Qualifiers

8..33 "Claim 2"
 /note= "Claim 2"
 8..22 "Claim 2"
 /note= "Claim 2"
 23..33 "Claim 2"
 /note= "Claim 2"
 208..217 "Claim 2"
 /note= "Claim 2"

97WO-US021857.

96US-0031930P.
 97US-0048547P.

HEART FOUND INC.

RS, Law SW, Arjona AA;

5/28.
 8.

coding low density lipoprotein binding proteins and
 - transformed cells, proteins, and modulators of binding,
 tment and diagnosis of atherosclerosis and for identifying
 ik.

47pp; English.

le comprises novel human low density lipoprotein (LDL)
 LBP-2 that is capable of binding both native and methyl
 acid sequence was deduced from an isolated cDNA clone (see
 clones (see AAV32834-39) and encoded rabbit and human
 037-42) are claimed. An abnormality in an aspect of LBP
 structure is diagnostic of a risk for atherosclerosis. The
 des: methods for determining if an animal is at risk for
 (e.g. for prenatal screening); methods for treating
 (including gene therapy) using e.g. LBP polypeptides to
 hereby prevent formation of atherosclerotic plaque; and
 ating a cell having an abnormality in LBP structure or
 pharmaceutical and vaccine compositions are also provided, as
 nant vectors and host cells used to produce recombinant

Query Match 40.3%; Score 217; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 2.8e-182;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gs

QY 322 EERVLEKEEEDDEDEDEDDVSEGSEVPESDRPAGAHQHLNGERGPQSAKERVK
 DB 1 EERVLEKEEEDDEDEDEDDVSEGSEVPESDRPAGAHQHLNGERGPQSAKERVK
 QY 382 PCGPHQODEGRGAPGSGTRQVFSMAAMNKEGGTASVATGPDSPVPLPPGKAL
 DB 61 PCGPHQODEGRGAPGSGTRQVFSMAAMNKEGGTASVATGPDSPVPLPPGKAL
 QY 442 DGTFFGCGPPGKPKSPDVEWTVMDVVEYFTEAGFPEQATAFQEQEIDGKSLMLMQR
 DB 121 DGTFFGCGPPGKPKSPDVEWTVMDVVEYFTEAGFPEQATAFQEQEIDGKSLMLMQR
 QY 502 LTGLSIRLGPALKIYEHKIKVLQOQHEDDDPDGFLG 538
 DB 181 LTGLSIRLGPALKIYEHKIKVLQOQHEDDDPDGFLG 217

RESULT 3

AAB82803
 ID AAB82803 standard; protein; 217 AA.

XX AC AAB82803;

XX DT 12-NOV-2001 (first entry)

XX DE Human low density lipoprotein binding protein 2 (LBP-2).

XX KW Low density lipoprotein binding protein 2; LBP-2; LDL; human;
 XX KW atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine
 XX OS Homo sapiens.

XX EN WO200164874-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006356.

XX PR 02-MAR-2000; 2000US-00517849.

XX PR 14-JUL-2000; 2000US-00616289.

XX PA (BOST-) BOSTON HEART FOUND INC.

XX PI Lees AM, Lees RS, Law SW, Arjona AA;

XX DR WPI; 2001-565505/63.

XX DR N-PSDB; AAH26494.

XX FT New isolated low density lipoprotein binding polypeptide for treat:
 XX FT diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX PS Claim 13(g); Fig 7B; 143pp; English.

XX CC The present sequence is that of the N-terminal portion of novel hu
 CC density lipoprotein binding protein 2 (LBP-2). The amino acid sequ
 CC deduced from an isolated partial cDNA clone (see AAH26494). A full
 CC sequence is given in AAB82806. Human LBP-2 is an example of claim
 CC polypeptides of the invention that are capable of binding to native
 CC methylated low density lipoproteins. Also claimed are biologically
 CC fragments and analogues of LBP, polynucleotides encoding LBP, as
 CC as expression vectors, cells and methods of producing the LBP. Met
 CC of determining if an animal is at risk for atherosclerosis, method
 CC evaluating an agent for use in treating atherosclerosis, and method
 CC treating a cell having an abnormality in structure or metabolism of
 CC are claimed. Pharmaceutical compositions comprising an LBP polypept
 CC nucleic acid, and vaccine compositions, are also claimed

XX SQ Sequence 217 AA;

40.3%; Score 217; DB 4; Length 217;
 rity 100.0%; Pred. No. 2.8e-182;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 .EKEBEDDEDDEDDVSEGEVPSDRPAGAHQHLNGRGPSAKERVKEWT 381
 .EKEBEDDEDDEDDVSEGEVPSDRPAGAHQHLNGRGPSAKERVKEWT 60
 IQQDEGRGPAGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVPLPPGKPALPGA 441
 IQQDEGRGPAGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVPLPPGKPALPGA 120
 *GCPGRKXKPSDPVWTVMDVVEYFTEAGFPQATFQOEIDGKSLLMQRTDV 501
 *GCPGRKXKPSDPVWTVMDVVEYFTEAGFPQATFQOEIDGKSLLMQRTDV 180
 !IRLGPALKIYEHKIKVLOQGHFEDDDPDGFLG 538
 !IRLGPALKIYEHKIKVLOQGHFEDDDPDGFLG 217
 iard; protein; 132 AA.
 (first entry)
 XP_031299, SEQ ID NO 5049.
 neuronal tissue; gene therapy;
 al nerve injury; chronic constriction injury; CCI;
 njury; SNI; Chung.
 2.
 002WO-US025765.
 001US-0312147P.
 001US-0346382P.
 001US-0333347P.
 SPITAL CORP.
 AG.
 Iso D, Befort K, Costigan M;
 12/26.
 1299.
 n comprising two or more isolated polypeptides, useful for
 dicament for treating pain in an animal.
 1017pp; English.
 discloses a composition comprising two or more isolated rat
 nucleotides or a polynucleotide which represents a fragment,
 allelic variation of the nucleic acid sequence. Also
 vector comprising the novel polynucleotide, a host cell
 a vector, a method for identifying a nucleotide sequence
 essentially regulated in an animal subjected to pain and a
 n the method, an array, a method for identifying an agent
 s or decreases the expression of the polynucleotide sequence
 entially expressed in neuronal tissue of a first animal
 pain, a method for identifying a compound which regulates
 a of a polynucleotide sequence which is differentially
 an animal subjected to pain, a method for identifying a
 regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composi
 CC method for identifying a compound or small molecule that regulate
 CC activity in an animal of one or more of the polypeptides given in
 CC specification, a method for identifying a compound useful in trea
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compo
 CC modulates its activity is useful for preparing a medicament for t
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constr
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. ge
 CC therapy). The sequence presented is a human protein (shown in Tab
 CC the specification) which is differentially expressed during pain.
 CC The sequence data for this patent did not form part of the printer
 CC specification, but was obtained in electronic form directly from
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 132 AA;
 Query Match 24.5%; Score 132; DB 7; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.1e-107;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; G
 QY 407 MAAMNKEGGTASVATGPDSPSPVPLPPGKPALPGADCTPFGCPGKKEKPSDPVW
 Db 1 MAAMNKEGGTASVATGPDSPSPVPLPPGKPALPGADCTPFGCPGKKEKPSDPVW
 QY 467 VVEYFTEAGFPQATFQOEIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHKIKV
 Db 61 VVEYFTEAGFPQATFQOEIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHKIKV
 QY 527 HFEDDDPDGFLG 538
 Db 121 HFEDDDPDGFLG 132
 RESULT 5
 AAB58957
 ID AAB58957 standard; protein; 241 AA.
 XX
 AC AAB58957;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Breast and ovarian cancer associated antigen protein sequence SEQ
 XX
 KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressi
 KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic
 KW antidiabetic; antiinflammatory; antitumor; antitumor; anticonvuls
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disord
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.
 OS Homo sapiens.
 XX
 PN WO200055173-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005881.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-611515/58.
 DR N-PSDB; AAF21860.
 XX
 PT New human breast and ovarian cancer associated gene sequences and
 PT polypeptides encoded by these genes, useful in the prevention, tre
 PT and diagnosis of cancer, immune disorders, cardiovascular disorder

seases.

1112; 1299pp; English.

.614 - AAF22031 represent DNA sequences encoding human breast and ovarian cancer. Included in the invention are 2032 - AAF22040 and AAB59129 which are used in the characterisation of the DNA and protein sequences of the breast and ovarian cancer associated DNA, protein, agonist sequences exhibit cytostatic; immunosuppressive; nontropic; antiviral; antiallergic; hepatotropic; antidiabetic; cytotoxic; antitumor; anticonvulsant; antibacterial; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly human cancer. The nucleic acid sequences, proteins, agonists and also be used in the diagnosis, prevention and treatment of cancer. e.g. Addison's disease, allergies, autoimmune disease, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, rheumatoid arthritis and ulcerative colitis; disorders such as myocardial ischaemia; wound healing; diseases such as cerebral anoxia and epilepsy; and diseases

4;

city 20.8%; Score 112; DB 3; Length 241; Identity 100.0%; Pred. No. 7e-90;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

APRSKRGGEERVLKEKEDEDDDDDDVSEGEVPESDRPAQHQHQLNG 366

APRSKRGGEERVLKEKEDEDDDDDDVSEGEVPESDRPAQHQHQLNG 69

AKERYKWTGCGPHQDGEGRGAPGSGTRQVFSMAAMNKEGGTAS 418

AKERYKWTGCGPHQDGEGRGAPGSGTRQVFSMAAMNKEGGTAS 121

urd; protein; 550 AA.

(first entry)

ity lipoprotein binding protein 2 (LBP-2).

oprotein binding protein 2; LBP-2; LDL; rabbit; atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine.

iculus.

01WO-US006356.

000US-00517849.

000US-00616289.

HEART FOUND INC.

RS, Law SW, Arjona AA;

15/63.

10.

ow density lipoprotein binding polypeptide for treating, or identifying therapeutic agents for atherosclerosis.

PS Claim 13(k); Fig 2a; 143pp; English.
XX The present sequence is that of a full-length sequence of novel ra
CC low density lipoprotein binding protein 2 (LBP-2). The amino acid
CC sequence is deduced from an isolated cDNA clone (see AAB26500). Ra
CC LBP-2 is an example of claimed polypeptides of the invention, term
CC LBP-2, that are capable of binding to native and methylated low den
CC lipoproteins. Also claimed are biologically active fragments and
CC analogues of LBP-2, polynucleotides encoding LBP-2, as well as expe
CC vectors, cells and methods of producing the LBP-2. Polypeptides hav
CC amino acid residues 338-353, 338-365, 354-365 or 444-453 (see AAB8
CC 18) of the present sequence are claimed. Methods for evaluating an a
CC animal is at risk for atherosclerosis, methods for treating a ce
CC for use in treating atherosclerosis, and methods for treating a ce
CC having an abnormality in structure or metabolism of LBP are also c
CC as are pharmaceutical compositions comprising an LBP polypeptide o
CC nucleic acid, and vaccine compositions
XX
SQ Sequence 550 AA;

Query Match 18.4%; Score 99; DB 4; Length 550;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Ga

QY 19 AAAASSAASPHYQEWILDTIDSLRSRKARPDLEICRMVRRRHGPEPTRAELEK
Db 20 AAAASSAASPHYQEWILDTIDSLRSRKARPDLEICRMVRRRHGPEPTRAELEK

QY 79 QRAVLRSYKGSISYRNAARVQPPRGATPPAPPRG 117

Db 80 QRAVLRSYKGSISYRNAARVQPPRGATPPAPPRG 118

RESULT 7

AAB82799

ID AAB82799 standard; protein; 232 AA.

XX AAB82799;

DT 12-NOV-2001 (first entry)

DE Rabbit low density lipoprotein binding protein 2 (LBP-2).

KW Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine

OS Oryctolagus cuniculus.

FN WO200164874-A2.

XX 07-SEP-2001.

PF 28-FEB-2001; 2001WO-US006356.

PR 02-MAR-2000; 2000US-00517849.

PR 14-JUL-2000; 2000US-00616289.

XX (BOST-) BOSTON HEART FOUND INC.

PI Lees AM, Lees RS, Law SW, Arjona AA;

XX WPI; 2001-565505/63.

DR N-PSDB; AAB26489.

PT New isolated low density lipoprotein binding polypeptide for treat;
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

PS Claim 13(c); Fig 3; 143pp; English.

XX The present sequence is that of a partial sequence of novel rabbit
CC density lipoprotein binding protein 2 (LBP-2). The amino acid sequ
CC deduced from an isolated cDNA clone (see AAB26489). Full-length ra
CC LBP-2 is given in AAB82807. Rabbit LBP-2 is an example of claimed

of the invention, termed LBPs, that are capable of binding methylated low density lipoproteins. Also claimed are active fragments and analogues of LBPs, polynucleotides, , as well as expression vectors, cells and methods of LBPs. Methods of determining if an animal is at risk for is, methods for evaluating an agent for use in treating is, and methods for treating a cell having an abnormality in metabolism of LBP are also claimed, as are pharmaceutical comprising an LBP polypeptide or nucleic acid, and vaccine

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AA:
14.1%; Score 76; DB 4; Length 232;
arity 100.0%; Pred. No. 3.2e-58;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
NTVMDVVVFTEAGPPEQATAFQOEIDGKSLLMQRTDVLVTGLSIRGLPALXIYE 517
|||||
NTVMDVVVFTEAGPPEQATAFQOEIDGKSLLMQRTDVLVTGLSIRGLPALXIYE 211
|||||

ZLQQGHFEDDDP 533
|||||
ZLQQGHFEDDDP 227
|||||

```

lard; protein; 252 AA.

(first entry)

ity lipoprotein binding protein 3 (LBP-3).

ipoprotein binding protein 3; LBP-3; LDL; rabbit;
 LS; antiarteriosclerotic; therapy; diagnosis; vaccine.

miculus.

20

2001WO-US006356.

2000US-00517849.

2000US-00616289.

V HEART FOUND INC.

3 RS, Law SW, Arizona AA;

505/63.

190.

low density lipoprotein binding polypeptide for treating, and/or identifying therapeutic agents for atherosclerosis.

Fig 4; 143pp; English.

sequence is that of a partial sequence of novel rabbit low density lipoprotein binding protein 3 (LBP-3). The amino acid sequence is based on an isolated cDNA clone (see AAH26490). A full-length rabbit LBP-3 is given in AAB82801. Rabbit LBP-3 is an unmodified polypeptides of the invention, termed LBPs, that are added to native and methylated low density lipoproteins. These are biologically active fragments and analogues of LBPs, which are encoding LBPs, as well as expression vectors, cells, and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in atherosclerosis, and methods for treating a cell having an atherosclerosis, and methods for treating a cell having an atherosclerosis, are also described.

CC disorders, wound healing, and infectious diseases. The proteins ca
 CC be used as a food additive or preservative to increase or decrease
 CC storage capabilities. AAC59557 to AAC59565 and AAB34298 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 61 AA;

Query Match 11.3%; Score 61; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 1.6e-45;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 456 PSDPVEVTVMVVEYFTAGPPEQATAFQEQEIDGKSLLLMORTDVLTLGLSIRLGP
 DB 1 PSDPVEVTVMVVEYFTAGPPEQATAFQEQEIDGKSLLLMORTDVLTLGLSIRLGP

QY 516 Y 516
 DB 61 Y 61

RESULT 11
 AAW49038
 ID AAW49038 standard; protein; 317 AA.

XX AC AAW49038;
 XX 09-NOV-1998 (first entry)
 XX Rabbit low density lipoprotein binding protein LBP-2.
 XX Low density lipoprotein binding protein; LDL binding protein 2; LB
 XX receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine.
 XX Oryctolagus cuniculus.

Key	Location/Qualifiers
FT Misc-difference 10	/note= "encoded by TAG"
FT Protein	66..317
FT Protein	/note= "Claim 1"
FT Protein	86..317
FT Peptide	/note= "Claim 1"
FT Peptide	105..132
FT Peptide	/note= "Claim 2"
FT Peptide	105..120
FT Peptide	/note= "Claim 2"
FT Peptide	121..132
FT Peptide	/note= "Claim 2"
FT Peptide	211..220
FT Peptide	/note= "Claim 2"

WO9823282-A1.

04-JUN-1998.

26-NOV-1997; 97WO-US021857.

27-NOV-1996; 96US-0031930P.

03-JUN-1997; 97US-0048547P.

(BOST-) BOSTON HEART FOUND INC.

Lees AM, Lees RS, Law SM, Arjona AA;

WPI; 1998-322455/28.

N-PSDB; AAV32835.

Nucleic acid encoding low density lipoprotein binding proteins and
 related vectors - transformed cells, proteins, and modulators of b
 useful for treatment and diagnosis of atherosclerosis and for iden
 subjects at risk.

Claim 1; Fig 2; 47pp; English.

14.1%; Score 76; DB 4; Length 317;
 city 100.0%; Pred. No. 4.1e-58;
 iservative 0; Mismatches 0; Indels 0; Gaps 0;

VMDVVEYFTAGPPEQATAFQEQEIDGKSLLLMORTDVLTLGLSIRLGPALKIYE 517
 VMDVVEYFTAGPPEQATAFQEQEIDGKSLLLMORTDVLTLGLSIRLGPALKIYE 296

QQGHFEDDDP 533
 QQGHFEDDDP 312

ard; protein; 61 AA.

First entry)

protein sequence encoded by gene 9 SEQ ID NO:126.

i protein; diagnosis; neuroprotective; cytotstatic;
 immunomodulatory; muscular active general; vulnerary;
 al; nephrotropic; antiinfective; gynaecological;
 al; gene therapy; detection; cancer; chromosome marker;
 itification; neural disorder; immune disorder;
 ler; reproductive disorder; gastrointestinal disorder;
 der; cardiovascular disorder; renal disorder;
 disorder; wound healing; infectious disease; preservative;

000WO-US006822.

99US-0126054P.

99US-0169916P.

GENOME SCI INC.

in SM, Komatsoulis G;

16/55.

proteins and gene sequences encoding them, useful for
 enting, and treating disorders such as cancer,
 sorders and immune system disorders.

ie 396-397; 429pp; English.

ide sequences given in AAC59566 to AAC59614 encode the
 proteins given in AAB34299 to AAB34347. AAB34348 to
 ent human secreted polypeptide sequences and proteins
 hem, which are given in the exemplification of the present
 in secreted proteins have activities based on the tissues
 genes are expressed in. Example of activities include:
 a; cytotstatic; cardioactive; immunomodulatory; muscular
 ; vulnerary; gastrointestinal; nephrotropic; antinefractive;
 and antibacterial. The polynucleotides can be used for
 of various disorders such as cancer, chromosome
 as chromosome markers, and for numerous other diagnostic
 poses. The secreted proteins can be used to treat
 as neural, immune, muscular, reproductive,
 al, pulmonary, cardiovascular, renal, and proliferative

and antibodies to the polypeptides are useful in the presence of or predisposition to a disease associated with the polypeptide. The polypeptides are also useful for identifying agonists and antagonists that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for treatment of a pathology related to aberrant expression or interactions of the polypeptide. Vectors comprising the encoding the polypeptides and cells genetically engineered to express the polypeptides are also useful for producing the proteins. The proteins are also useful for producing the proteins. The proteins

4.8%; Score 26; DB 4; Length 26;
rity 100.0%; Pred. No. 5e-15;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DDEDEEDDVSEGSEVPESD 354
|||||
DDEDEEDDVSEGSEVPESD 26

ard; peptide; 15 AA.

first entry)

ity lipoprotein binding protein 2 (LBP-2) peptide.

poprotein binding protein 2; LBP-2; LDL; human;
s; antiarteriosclerotic; therapy; diagnosis; vaccine.

001WO-US006356.

000US-00517849.
000US-00616289.

HEART FOUND INC.

RS, Law SW, Arjona AA;

05/63.

ow density lipoprotein binding polypeptide for treating,
/or identifying therapeutic agents for atherosclerosis.

age; 143pp; English.

quence is that of a peptide comprising amino acid residues
al human low density lipoprotein binding protein 2 (LBP-2,
Human LBP-2 is an example of claimed LBP polypeptides of
that are capable of binding to native and methylated low
teins (LDLs). Also claimed are biologically active
analogues of LBPs, polynucleotides encoding LBPs, as well
ectors, cells and methods of producing the LBPs.
iving the present amino acid sequence are among those
is of determining if an animal is at risk for
; methods for evaluating an agent for use in treating
; and methods for evaluating a cell having an abnormality in
metabolism of LBP are also claimed, as are pharmaceutical
mprising an LBP polypeptide or nucleic acid, and vaccine
Note: the present sequence is not shown in the
ut is derived from the human LBP-2 sequence given in
AA82806)

2.8%; Score 15; DB 4; Length 15;
city 100.0%; Pred. No. 1.5e-05;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DDEDEEDD 343
|||||
DDEDEEDD 15

AAM39592
ID AAM39592 standard; protein; 102 AA.

XX
AC AAM39592;

XX
DT 22-OCT-2001 (first entry)

XX
DE Human polypeptide SEQ ID NO 2737.

XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; car
peripheral nervous system; neuropathy; central nervous system; CNS
Alzheimer's; Parkinson's disease; Huntington's disease; haemostati
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammatory
leukaemia.

XX
OS Homo sapiens.

XX
PN WO200153312-A1.

XX
PD 26-JUL-2001.

XX
PF 26-DEC-2000; 2000WO-US034263.

XX
PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wan
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Z
PI Zhou P, Goodrich R, Drmanac RT;

XX
DR WPI; 2001-442253/47.

DR N-FSDB; AAI58748.

XX
PT Novel nucleic acids and polypeptides, useful for treating disorder
as central nervous system injuries.

XX
PS Example 4; SEQ ID NO 2737; 10078pp; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) a
encoded polypeptides (AAM38642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polynucleotides are
in gene therapy. A composition containing a polypeptide or polynuc
of the invention may be used to treat diseases of the peripheral n
system, such as peripheral nervous injuries, peripheral neuropathy
localised neuropathies and central nervous system diseases, such a
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophi
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: Immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemo
and thrombolytic activity, cancer diagnosis and therapy, drug scre
assays for receptor activity, arthritis and inflammation, leukaemi
C.N.S disorders. Note: The sequence data for this patent did not f
part of the printed specification

XX
SQ Sequence 102 AA;

Query Match 2.8%; Score 15; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 482 AFQEQEIDGKSLIM 496

Db 51 AFQEQEIDGKSLIM 65

14-APR-2003 (first entry)
Human cell factor signal inhibitor 11.88.
Human; cell factor signal inhibitor 11.88; recombinant production
gene therapy; malignant tumour; cancer; blood disease; HIV infect
human immunodeficiency virus; immune disorder; inflammatory condi
cytostatic; antiinflammatory; immunomodulator.
Homo sapiens.
CN1361159-A.
31-JUL-2002.
26-DEC-2000; 2000CN-00136316.
26-DEC-2000; 2000CN-00136316.
(BODE-) BODE GENE DEV CO LTD SHANGHAI.
Mao Y, Xie Y;
WPI: 2002-751578/82.
N-PSDB; AB257768.
New polypeptide human cell factor signal inhibitor 11.88 and
polynucleotides encoding this polypeptide.
Claim 1; Page 28 (Disclosure); 34pp; Chinese.
The invention relates to human cell factor signal inhibitor 11.88
(ABP58930) and nucleic acids encoding it (AB257768). The protein
molecular weight of 11.88 kD. The invention also relates to a met
the recombinant production of the protein, an antagonist of the p
the use of the protein, gene and antagonist in therapeutic
applications. Cell factor signal inhibitor 11.88 can be used in t
treatment of a variety of diseases such as malignant tumours, bloo
diseases, HIV (human immunodeficiency virus) infection, immune di
and inflammatory conditions. The present sequence represents huma
factor signal inhibitor 11.88
SQ Sequence 108 AA;
Query Match 2.8%; Score 15; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 482 AFQEQEIDGKSLLLM 496
Db 57 AFQEQEIDGKSLLLM 71
RESULT 18
AAM41378
ID AAM41378 standard; protein; 114 AA.
XX
AC AAM41378;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 6309.
XX
KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; can
peripheral nervous system; neuropathy; central nervous system; CNS
Alzheimer's; Parkinson's disease; Huntington's disease; haemostati
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammatory
leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.

lard; protein; 102 AA.
(first entry)
ption factor TRFX-66.
e; inflammation; neurological disease;
disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
re; antiinflammatory; gene therapy.
1001WO-US008117.
1000US-018896P.
GENOMICS INC.
laughn MR, Yue H, Lal P, Lu DAM, Patterson C;
indman O, Tang YT, Mathur P, Shah P, Au-Young J;
96/64.
39.
ption factor polypeptides, used to treat diseases
h altered activity and expression of TRFX, and to screen
able of modulating its activity.
210; 327pp; English.
quence is the protein sequence for a human transcription
anscription factor and its coding sequence are useful in
treatment and prevention of diseases associated with
sion of the transcription factor e.g. cell proliferative,
lammatory, neurological and developmental disorders. A
ific disorders/diseases are given in the specification,
eriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
emia, asthma, autoimmune thyroiditis, bronchitis, atopic
abetes mellitus, emphysema, Goodpasture's syndrome, gout,
e, multiple sclerosis, osteoarthritis, pancreatitis,
umatoid arthritis, systemic lupus erythematosus, ulcerative
is, Alzheimer's disease, Huntington's disease, Parkinson's
e, and viral, bacterial, fungal and protozoal infections
A;
2.8%; Score 15; DB 4; Length 102;
rity 100.0%; Pred. No. 7.3e-05;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
EIDGKSLLLM 496
EIDGKSLLLM 65
ard; protein; 108 AA.

00WO-US034263.
 99US-00471275.
 00US-00488725.
 00US-00552317.
 00US-00598042.
 00US-00620312.
 00US-00653450.
 00US-00662191.
 00US-00693036.
 00US-00727344.
 NC.
 Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 Mehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 ch R, Dmanac RT;
 33/47.
 34.
 acids and polypeptides, useful for treating disorders such
 ous system injuries.
 ID NO 6309; 10078pp; English.
 relates to human nucleic acids (AAI57798-AAI61369) and the
 ptides (AAM38642-AAM42213) with nootropic,
 unt and cytosolic activity. The polynucleotides are useful
 n. A composition containing a polypeptide or polynucleotide
 n may be used to treat diseases of the peripheral nervous
 ; peripheral nervous injuries, peripheral neuropathy and
 pathies and central nervous system diseases, such as
 rkinson's disease, Huntington's disease, amyotrophic
 is, and Shy-Drager Syndrome. Other uses include the
 the activities such as: Immune system suppression,
 i activity, chemotactic/chemokinetic activity, haemostatic
 c activity, cancer diagnosis and therapy, drug screening,
 ptor activity, arthritis and inflammation, leukaemias and
 Note: The sequence data for this patent did not form
 nted specification
 2.8%; Score 15; DB 4; Length 114;
 ity 100.0%; Pred.No. 8e-05;
 ervative 0; Mismatches 0; Indels 0; Gaps 0;
 IDGKSLLLM 496
 IDGKSLLLM 77
 ard; protein; 116 AA.
 (first entry)
 SEQ ID 2857.
 i-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 uman; secretory protein; membrane proteins; cancer;
 sease; osteoporosis; neurological disease.

XX 19-MAR-2003.
 XX 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakanatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamec
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA53650.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secret
 PT and/or membrane proteins, useful for developing medicines for dise
 PT which the gene is involved, or as target molecules for gene therap
 XX
 PS Claim 14; SEQ ID NO 2857; 205pp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX
 SQ Sequence 116 AA;
 Query Match 2.8%; Score 15; DB 6; Length 116;
 Best Local Similarity 100.0%; Pred.No. 8.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Ga
 Qy 482 AFQEQEIDGKSLLLM 496
 Db 65 AFQEQEIDGKSLLLM 79
 |||||
 |||||
 RESULT 20
 ABB67522
 ID ABB67522 standard; protein; 104 AA.
 XX
 AC ABB67522;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 29358.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 FN WC200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL11625.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or r

relates to an isolated nucleic acid detection reagent encoding 1000 or more genes from *Drosophila*. The invention is in the fields of molecular biology and in elucidating cell signaling and interactions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention includes DNA sequences (AB116176-AB130511), expressed DNA (11840-AB116175) and encoded proteins (ABB57737-ABB57738). Sequence data for this patent did not form part of the invention, but was obtained in electronic format directly

VPEPSD 11

urd; peptide; 12 AA.

(first entry)

ity lipoprotein binding protein 2 (LBP-2) peptide.

oprotein binding protein 2; LBP-2; LDL; rabbit;
; antiarteriosclerotic; therapy; diagnosis; vaccine.
iculus.

101WO-US006356.

:00US-00517849.

:00US-00616289.

HEART FOUND INC.

RS, Law SW, Arjona AA;

5/63.

w density lipoprotein binding polypeptide for treating,
or identifying therapeutic agents for atherosclerosis.

ge; 143pp; English.

quence is that of a peptide comprising amino acid residues
il rabbit low density lipoprotein binding protein 2 (LBP-2,
Rabbit LBP-2 is an example of claimed LBP polypeptides of
hat are capable of binding to native and methylated low
teins (LDLs). Also claimed are biologically active
nalogues of LBPs, polynucleotides encoding LBPs, as well
ectors, cells and methods of producing the LBPs.
ving the present amino acid sequence are among those
s of determining if an animal is at risk for

, methods for evaluating an agent for use in treating
, and methods for treating a cell having an abnormality in
abolism of LBP are also claimed, as are pharmaceutical
mprising an LBP polypeptide or nucleic acid, and vaccine
ote: the present sequence is not shown in the
ut is derived from the rabbit LBP-2 sequence given in
AAB82807)

2.0%; Score 11; DB 4; Length 12;

ity 100.0%; Pred. No. 0.041;

servative 0; Mismatches 0; Indels 0; Gaps 0;

VPEPSD 354

|||||

VPEPSD 12

rd; peptide; 28 AA.

(first entry)

XX

DE

XX

KW

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PR

XX

XX

PA

XX

XX

PI

XX

XX

XX

DR

XX

XX

FT

XX

FT

XX

XX

PS

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Rabbit low density lipoprotein binding protein 2 (LBP-2) peptide.

Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;

atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine

Oryctolagus cuniculus.

WO200164874-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US006356.

02-MAR-2000; 2000US-00517849.

14-JUL-2000; 2000US-00616289.

(BOST-) BOSTON HEART FOUND INC.

Lees AM, Lees RS, Law SW, Arjona AA;

WPI; 2001-565505/63.

New isolated low density lipoprotein binding polypeptide for treat
diagnosing and/or identifying therapeutic agents for atherosclerosis

Claim 14(c); Page; 143pp; English.

The present sequence is that of a peptide comprising amino acid re
338-365 of novel rabbit low density lipoprotein binding protein 2
see AAB82807). Rabbit LBP-2 is an example of claimed LBP polypepti
the invention that are capable of binding to native and methylated
density lipoproteins (LDLs). Also claimed are biologically active
fragments and analogues of LBPs, polynucleotides encoding LBPs, as
as expression vectors, cells and methods of producing the LBPs.

Polypeptides having the present amino acid sequence are among thos
claimed. Methods of determining if an animal is at risk for
atherosclerosis, methods for evaluating an agent for use in treati
atherosclerosis, and methods for treating a cell having an abnormal
structure or metabolism of LBP are also claimed, as are pharmaceut
compositions comprising an LBP polypeptide or nucleic acid, and va
compositions. Note: the present sequence is not shown in the
specification but is derived from the rabbit LBP-2 sequence given
figure 2A (see AAB82807)

Sequence 28 AA;

Query Match 2.0%; Score 11; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.083;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 344 VSEGSSEVPEPSD 354

|||||

Db 18 VSEGSSEVPEPSD 28

RESULT 25

AAY51200

ID AAY51200 standard; protein; 129 AA.

XX AAY51200;

AC AAY51200;

XX 04-APR-2000 (first entry)

XX Human SCA7 protein fragment 2.

DE SCA7; human; spinocerebellar ataxia type 7; SCA1; SCA2; SCA3; SCA6;

KW repeat expansion detection; RED analysis; detection.
XX Homo sapiens.

OS Homo sapiens.

XX CA2245310-A.

PN CA2245310-A.

XX

98CA-02245310.
97US-0056170P.
MINNESOTA.
um LP;
181/09.
individuals at risk of developing spinocerebellar ataxia type
; trinucleotide repeat regions of spinocerebellar ataxia
age 46-47; 66pp; English.
describes a novel method for identifying individuals at
oping spinocerebellar ataxia type 7 (SCA7). The method
yzing the CAG repeat region of a SCA7 gene to detect CAG
; individuals at risk have at least 30 CAG repeats and those
ive less than 19 CAG repeats. The method is useful for
individuals at risk of developing SCA7 and also those at risk
SCA1, 2, 3 or 6. The use of genomic DNA in the repeat
action (RED) analysis allows isolation of any potential
repeat expansion regardless of the expression pattern.
; different oligonucleotides in the RED assay allows any of
trinucleotide repeats to be detected, and the cyclized nature
on makes it extremely sensitive. This sequence represents a
e human SCA7 protein which is described in the method of
A;
2.0%; Score 11; DB 3; Length 129;
arity 100.0%; Pred. No. 0.29;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PPPPQQ 232
|||||
PPPPQQ 44
lard; protein; 139 AA.
revised)
first entry)
e bile; mucosal immune response; chicken; parasite.
a.
91WO-US006431.
90US-00581694.
CORP.
T AG.
Strausberg RL, Wilson SD, Pope SH, Strausberg SH;

DR WPI; 1992-114366/14.
XX N-PSDB; AAQ23082.
PT Vaccine against avian coccidiosis - comprising recombinant eimeri;
PT antigen mc-4C, mc-5C or mc-30C gene, etc., or microorganisms expr
PT them.
XX Claim 12; Page 65 + Fig 12; 94pp; English.
XX To identify antigens of E. tenella that elicit a mucosal immune r
CC during parasitic infection of chickens, E. tenella cDNA and genom
CC expression libraries in lambda phage were screened with chicken i
CC ble. Phage that produce antigens cross-reactive with the immune i
CC were identified. The DNA inserts from the positive phage were clon
CC bacteriophage M13 and subjected to sequence analysis. E. tenella
CC tc-11e (13.9 kb) was identified. (Updated on 25-MAR-2003 to corre
CC field.)
XX Sequence 139 AA;
SQ Query Match 2.0%; Score 11; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G
QY 118 APAAAAAAPP 128
|||||
Db 12 APAAAAAAPP 22
RESULT 27
ABG76914
ID ABG76914 standard; protein; 189 AA.
XX AC
XX ABG76914;
XX 05-NOV-2002 (first entry)
XX DT
XX Rice WRKY polypeptide #2.
DE
XX WRKY; plant; zinc-finger-type factor; WRKY; SAR; sunflower;
KW SA-dependent structure-activity analysis response; pathogen resist
KW maize; wheat; rice; soybean.
XX
OS Oryza sativa.
XX
XX US2002076775-A1.
XX PD
XX 20-JUN-2002.
XX PF 16-MAR-2001; 2001US-00810264.
XX PR 17-MAR-2000; 2000US-0190467P.
XX
XX (CRAN/) CRANE V C.
PA (FAMO/) FAMODU O.
PA (HUX/) HU X.
PA (LUGG/) LU G.
PA (ZHAN/) ZHANG L.
XX
PI Crane VC, Famodu O, Hu X, Lu G, Zhang L;
XX
XX WPI; 2002-582922/62.
DR N-PSDB; ABS59410.
XX
PT New isolated plant-specific zinc-finger-type factor polynucleotide
PT useful for e.g. regulating the SA-dependent structure-activity ana
PT response in a plant.
XX
PS Claim 9; Page 45-46; 66pp; English.
XX The invention relates to an isolated polynucleotide encoding a pla
CC specific zinc-finger-type factor (WRKY) protein. The DNA and prote
CC used to modulate the level of a WRKY protein in a plant and to reg

at structure-activity analysis (SAR) response in a plant. can be used to engineer plants to resist pathogens such as bacteria, insects and fungi, and to survive stresses. They may be a molecular probe to track inheritance of corresponding crosses and facilitate the plant breeding process, to identify and genetically map WRKY and other closely related genes and to find genes and their promoters that are in the WRKY domain. This sequence represents a WRKY polypeptide of

Query Match 2.0%; Score 11; DB 5; Length 189; Best Local Similarity 100.0%; Pred. No. 0.4; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APVAAA 143
|||||
APVAAA 114

ard; protein; 270 AA.

first entry)

agnostic protein #17263.

ome mapping; gene mapping; gene therapy; forensic; medical imaging; diagnostic; genetic disorder.

01WO-US008631.

000US-00540217.

000US-00649167.

INC.

u C, Tang YT;

12/73.

9.

polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations genetic disorders or other traits and to assess

ID NO 47631; 103pp; English.

relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, identification of (II). The polynucleotides are also used as expressed sequence tags for identifying expressed genes in gene therapy techniques to restore normal function or to treat disease states involving (II). (II) is used as a molecular weight marker and as a food additive and its binding partners are useful in medical imaging (II). (I) and (II) are useful for treating disorders of protein expression or biological activity. The polynucleotide sequences have applications in forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for patent did not appear in the printed specification, but was obtained from electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 270 AA;

Query Match 2.0%; Score 11; DB 4; Length 270; Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 APPAPAAPPA 189

Db 124 APPAPAAPPA 134

RESULT 29

ADD18910

ID ADD18910 standard; protein; 892 AA.

XX ADD18910;

XX 15-JAN-2004 (first entry)

XX Human disease related protein SeqID399.

XX human; disease state; cytostatic; antiinflammatory; ophthalmologic antiarteriosclerotic; vulnary; gene therapy; hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis inflammation; erythropoiesis; glycolysis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX N-PSDB; ADD18911.

XX New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, wound healing.

XX Claim 25; SEQ ID NO 399; 424pp; English.

XX This invention relates to novel human genes and gene product which implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmologic, antiarteriosclerotic or vulnary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition such as tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric

a disease includes cancer, ischaemic conditions, reperfusion
apathy, neonatal stress, pre-eclampsia, atherosclerosis,
conditions or wound healing. The present sequence is that of
ated protein of the invention.

AA;

2.0%; Score 11; DB 7; Length 892;

arity 100.0%; Pred. No. 1.4; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0;

PPPPQPQ 232

|||||||

PPPPQPQ 46

iard; protein; 1109 AA.

(first entry)

ide #2.

itamine disease; gene; genealogical polyglutamine disease;
iconvulsant.

A.

001JP-00236788.

000JP-00236839.

001JP-00108723.

USA DNA KENKYUSHO.

II PHARM CO LTD.

.53/49.

II.

line diagnostic marker for polyglutamine disease, useful
is, prevention and/or treatment, comprises a polyglutamine
and its encoded polypeptide.

ID NO 4; 72pp; Japanese.

discloses polyglutamine disease related genes and their
ptides. Also claimed is a recombinant vector
preparation of the polynucleotides and resultant
diagnostic methods and a kit. The genes and encoded
are useful in the diagnosis, prevention and treatment of
polyglutamine disease. The sequence presented is a
the invention.

AA;

2.0%; Score 11; DB 7; Length 1109;
arity 100.0%; Pred. No. 1.7;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

0PQPQP 235

|||||||

0PQPQP 501

ID

XX

AC

XX

XX

DT

XX

DE

XX

XX

KW

KW

KW

KW

KW

XX

OS

XX

XX

PN

XX

XX

PD

XX

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PF

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PR

PR

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PR

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PR

PR

XX

XX

PA

XX

PI

PI

PI

PI

PI

PI

PI

XX

XX

DR

DR

XX

XX

PT

PT

PT

PT

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

XX

Query Match

Best Local Similarity 100.0%; Pred. No. 2;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

2.0%; Score 11; DB 6; Length 1340;

100.0%; Pred. No. 2;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

225 QPPPPQPQP 235

|||||||

729 QPPPPQPQP 739

QY

DB

ID

XX

AC

XX

XX

DT

XX

DE

XX

XX

KW

KW

KW

KW

KW

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OS

XX

PN

XX

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PD

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XX

PF

XX

XX

PR

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PR

PR

PR

PR

PR

PR

XX

XX

PA

XX

PI

PI

PI

PI

PI

PI

PI

XX

XX

DR

DR

XX

XX

PT

PT

PT

PT

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

XX

Query Match

Best Local Similarity 100.0%; Pred. No. 2;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

2.0%; Score 11; DB 7; Length 1109;

arity 100.0%; Pred. No. 1.7;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

0PQPQP 235

|||||||

0PQPQP 501

QY

DB

DE Rabbit low density lipoprotein binding protein 2 (LBP-2) peptide.
 XX
 KW Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
 XX atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine
 XX
 OS Oryctolagus cuniculus.
 XX
 FN WO200164874-A2.
 XX
 PD 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006356.
 PF
 XX
 XX poprotein binding protein 2; LBP-2; LDL; human;
 PR S; antiarteriosclerotic; therapy; diagnosis; vaccine.
 PR 02-MAR-2000; 2000US-00517849.
 XX
 XX 14-JUL-2000; 2000US-00616289.
 XX
 PA (BOST-) BOSTON HEART FOUND INC.
 XX
 XX
 PI Lees AM, Lees RS, Law SW, Arjona AA;
 XX
 XX WPI; 2001-565505/63.
 XX
 PT New isolated low density lipoprotein binding polypeptide for treat
 XX diagnosing and/or identifying therapeutic agents for atherosclerosis
 PS Claim 14 (c); Page; 143pp; English.
 XX
 CC The present sequence is that of a peptide comprising amino acid re
 CC 444-453 of novel rabbit low density lipoprotein binding protein 2
 CC see AAB82807). Rabbit LBP-2 is an example of claimed LBP polypepti
 CC the invention that are capable of binding to native and methylated
 CC density lipoproteins (LDLs). Also claimed are biologically active
 CC fragments and analogues of LBPs, polynucleotides encoding LBPs, as
 CC as expression vectors, cells and methods of producing the LBPs.
 CC Polypeptides having the present amino acid sequence are among those
 CC claimed. Methods of determining if an animal is at risk for
 CC atherosclerosis, methods for evaluating an agent for use in treati
 CC atherosclerosis, and methods for treating a cell having an abnormal
 CC structure or metabolism of LBP are also claimed, as are pharmaceut
 CC compositions comprising an LBP polypeptide or nucleic acid, and va
 CC compositions. Note: the present sequence is not shown in the
 CC specification but is derived from the rabbit LBP-2 sequence given
 CC figure 2A (see AAB82807)
 XX
 SQ Sequence 10 AA;
 Query Match 1.9%; Score 10; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Gaps
 Matches 10; Conservative 0;
 QY 432 PPGKPALEGA 441
 Db 1 PPGKPALEGA 10
 RESULT 34
 AAU97858
 ID AAU97858 standard; protein; 22 AA.
 XX
 AC AAU97858;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Protein inhibitor of activated STAT, piassy, acidic domain.
 KW K+ channel associated protein; KchAP; chaperone protein; agonist;
 KW antagonist; cardiac arrhythmia; hypertension; angina; asthma; diab
 KW renal insufficiency; urinary incontinence; irritable colon; epilep
 KW cerebrovascular ischaemia; autoimmune disease; acidic domain;
 KW protein inhibitor of activated STAT; PIASy.
 XX
 OS Unidentified.
 XX

ard; peptide; 10 AA.
 first entry)
 ity lipoprotein binding protein 2 (LBP-2) peptide.
 poprotein binding protein 2; LBP-2; LDL; human;
 S; antiarteriosclerotic; therapy; diagnosis; vaccine.
 001WO-US006356.
 000US-00517849.
 000US-00616289.
 HEART FOUND INC.
 RS, Law SW, Arjona AA;
 05/63.
 ow density lipoprotein binding polypeptide for treating,
 /or identifying therapeutic agents for atherosclerosis.
 age; 143pp; English.
 quence is that of a peptide comprising amino acid residues
 el human low density lipoprotein binding protein 2 (LBP-2,
 Human LBP-2 is an example of claimed LBP polypeptides of
 that are capable of binding to native and methylated
 oteins (LDLs). Also claimed are biologically active
 analogues of LBPs, polynucleotides encoding LBPs, as well
 vectors, cells and methods of producing the LBPs.
 aving the present amino acid sequence are among those
 is of determining if an animal is at risk for
 s, methods for evaluating an agent for use in treating
 etabolism of LBP are also claimed, as are pharmaceutical
 comprising an LBP polypeptide or nucleic acid, and vaccine
 Note: the present sequence is not shown in the
 but is derived from the human LBP-2 sequence given in
 AAB82806)
 1.9%; Score 10; DB 4; Length 10;
 city 100.0%; Pred. No. 0.27;
 iservative 0; Mismatches 0; Indels 0; Gaps 0;
 DGFLG 538
 |||||
 DGFLG 10
 ard; peptide; 10 AA.
 first entry)

developmental biology and in elucidating cell signalling and reactions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention of mic DNA sequences (ABL16176-ABL30511), expressed DNA (1840-ABL16175) and the encoded proteins (ABB57737-ABB57737) sequence data for this patent did not form part of the invention, but was obtained in electronic format directly from the public domain.

1.9%; Score 10; DB 4; Length 96;
 rity 100.0%; Pred. No. 1.7;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAPPP 129
 |||||
 AAPPP 32

ard; protein; 112 AA.

First entry)

5 isoform A protein SEQ ID NO:3.

am perenne; Lol p 5; Phl p 5; Poa p 5; allergen;
 immunotherapy; immunophylactic treatment; hayfever;
 se; ryegrass pollen; immunological; pollen; allergy.

1.

002WO-AU001261.

001AU-00007792.

ELBOURNE.

ugh MB, Bhalla PL, Swoboda I;

16/34.

combinant allergen which lacks or comprises reduced epitopes and/or exhibits reduced binding capacity for IgE, having type I allergic disease, particularly sensitivity to an.

1; 66pp; English.

vention describes a modified recombinant allergen in a form and which is associated with allergic disease sensitive subjects. The modified recombinant allergen amino acid sequence modified from the naturally occurring sequence such that the allergen lacks or comprises reduced epitopes and/or exhibits reduced binding capacity for IgE, reduced IgE production stimulatory activity while maintaining antigenicity. Also described: (1) a composition of modified allergen which lacks or comprises reduced numbers and/or exhibits reduced binding capacity for IgE and/or reduced IgE production stimulatory activity while retaining T-activity, and one or more pharmaceutical carriers and/or (2) prophylaxis or treatment of an allergic disease subject, by administering a modified allergen defined as recombinant allergen is useful in the immunotherapy of allergic diseases such as type I

allergic disease, particularly sensitivity to ryegrass pollen, and treating sensitivity to ryegrass pollen or pollen from an immunologic relative of ryegrass in a mammal sensitive to such pollen. The present invention may also be used to modify IgE response to the grass pollen allergen. The present invention also provides a method for the treatment of allergic disease by study the mechanism of immunotherapy of Lolium perenne allergy, to modified derivatives or analogues useful in immunotherapy, and in manufacture of a medicament for the treatment or prophylaxis of allergic disease in sensitive individuals. The present sequence represents a ryegrass isoform A protein, which is given in the exemplification of the present invention.

XX Sequence 112 AA;

Query Match 1.9%; Score 10; DB 6; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 PPLPPPPQPP 218
 |||||
 DB 96 PPLPPPPQPP 105

RESULT 38

AAG34164

ID AAG34164 standard; protein; 132 AA.

XX AC AAG34164;

XX AC AAG34164;

DT 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 41527.

DE Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; protein termination sequence; corn.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 28-APR-1999; 99US-0130891P.

XX 30-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 04-MAY-1999; 99US-0132407P.

XX 05-MAY-1999; 99US-0132484P.

XX 06-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

XX 06-MAY-1999; 99US-0132487P.

XX 07-MAY-1999; 99US-0132863P.

XX 11-MAY-1999; 99US-0134256P.

XX 14-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

XX 14-MAY-1999; 99US-0134221P.

XX 18-MAY-1999; 99US-0134370P.

XX 18-MAY-1999; 99US-0134768P.

XX 19-MAY-1999; 99US-0134941P.

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99US-0161993P.
99US-0162142P.

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1.9%; Score 10; DB 3; Length 132;
city 100.0%; Pred. No. 2.3;
perservative 0; Mismatches 0; Indels

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AAAP	127
AAAP	130

ard; protein; 171 AA.

first entry)

in fragment SEQ ID NO: 41526.

ification; signal transduction pathway; metabolic pathway; assay; genetic mapping; gene expression control; promoter; nuclease; corn.

. mays.

200EP-00301439.

99US-01121825P.
99US-01123160P.
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PR	21-JUL-1999	99US-01450882P
PR	22-JUL-1999	99US-01450852P
PR	22-JUL-1999	99US-01450872P
PR	22-JUL-1999	99US-01450892P
PR	22-JUL-1999	99US-01451922P
PR	23-JUL-1999	99US-01451452P
PR	23-JUL-1999	99US-01452182P
PR	23-JUL-1999	99US-01452242P
PR	26-JUL-1999	99US-01452762P
PR	27-JUL-1999	99US-01459132P
PR	27-JUL-1999	99US-01459182P
PR	28-JUL-1999	99US-01459192P
PR	28-JUL-1999	99US-01459512P
PR	02-AUG-1999	99US-01463862P
PR	02-AUG-1999	99US-01463882P
PR	02-AUG-1999	99US-01463892P
PR	03-AUG-1999	99US-01470382P
PR	04-AUG-1999	99US-01472042P
PR	05-AUG-1999	99US-01473022P
PR	05-AUG-1999	99US-0171922P

99US-0147260P.
99US-0147303P.
99US-0147416P.
99US-0147493P.
99US-0147935P.
99US-0148171P.
99US-0148319P.
99US-0148341P.
99US-0148565P.
99US-0148684P.
99US-0149368P.
99US-0149175P.
99US-0149426P.
99US-0149722P.
99US-0149723P.
99US-0149929P.
99US-0149902P.
99US-0149930P.
99US-0150566P.
99US-0150884P.
99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0151303P.
99US-0151438P.
99US-0151930P.
99US-0152363P.
99US-0153070P.
99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0154779P.
99US-0155139P.
99US-0155486P.
99US-0155659P.
99US-0156458P.
99US-0156596P.
99US-0157117P.
99US-0157753P.
99US-0157865P.
99US-0158029P.
99US-0158232P.
99US-0158369P.
99US-0159233P.
99US-0159294P.
99US-0159295P.
99US-0159329P.
99US-0159330P.
99US-0159331P.
99US-0159637P.
99US-0159638P.
99US-0159584P.
99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-0160770P.
99US-0160814P.
99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0160989P.
99US-0161404P.
99US-0161405P.
99US-0161406P.
99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161922P.
99US-0161993P.
99US-0162142P.

1.9%; Score 10; DB 3; Length 171;

Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G:
QY 118 AAAAAAAAAAP 127
|||||
Db 160 AAAAAAAAAAP 169
RESULT 40
ABU17208
ID ABU17208 standard; protein; 238 AA.
XX
AC ABU17208;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #2735.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug d
XX
OS Acinetobacter baumannii.
XX
PN WC200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WC-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
XX
N-PSDB; ACA21078.
XX
PT New antisense nucleic acids, useful for identifying proteins or s
PT for homologous nucleic acids required for cellular proliferation
PT isolate candidate molecules for rational drug discovery programs.
XX
Claim 25; SEQ ID NO 45132; 1766pp; English.
XX
The invention relates to an isolated nucleic acid comprising any
the 6213 antisense sequences given in the specification where exp
of the nucleic acid inhibits proliferation of a cell. Also includ
(1) a vector comprising a promoter operably linked to the nucleic
encoding a polypeptide whose expression is inhibited by the antis
nucleic acid; (2) a host cell containing the vector; (3) an isolat
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically b
the polypeptide; (5) producing the polypeptide; (6) inhibiting cel
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the act
the gene product or that has an activity against a biological pat
required for proliferation, or that inhibits cellular proliferati
identifying a gene required for cellular proliferation or the bio
pathway in which a proliferation-required gene or its gene product
or a gene on which the test compound that inhibits proliferation
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which th
product is overexpressed or underexpressed; (12) determining the
to which each of the strains is present in a culture or collection
strains; or (13) identifying the target of a compound that inhibit
proliferation of an organism. The antisense nucleic acids are usef
identifying proteins or screening for homologous nucleic acids rec
for cellular proliferation to isolate candidate molecules for rati
drug discovery programs, or for screening homologous nucleic acid

oliferation in cells other than *S. aureus*, *S. typhimurium*, or *P. aeruginosa*. The present sequence is encoded by one of a set of three genes. Note: The sequence data for this form part of the printed specification, but was obtained from a direct submission to WIPO at the International Bureau of Intellectual Property.

1.9%; Score 10; DB 6; Length 238;
100.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||
AAAPA 141

Protein; 254 AA.

First entry

baumannii protein #3525.

baumannii; bacterial disease; antibacterial; vaccine;
agent.

baumannii.

99US-00328352.

98US-0088701P.

THERAPEUTICS CORP.

1 D;

2/54.

38.

baumannii proteins and nucleic acids, useful as reagents for a bacterial disease, as components of antibacterial agents for antibacterial drugs, or as biocontrol agents for

NO 7651; 328pp; English.

relates to isolated *Acinetobacter baumannii* nucleic acids. The present sequence is encoded by one of a set of three genes. Note: The sequence data for this form part of the printed specification, but was obtained from a direct submission to WIPO at the International Bureau of Intellectual Property.

1.9%; Score 10; DB 6; Length 254;
100.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||

Db 148 PAPVAAAAA 157

RESULT 42

AAAY25630

ID AAY25630 standard; protein; 257 AA.

XX

AC AAY25630;

XX

DT 30-SEP-1999 (first entry)

XX

DE Phleum sp. allergen Phl p 5 protein fragment #11.

XX

KW Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; insect; s
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; hon
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea
KW mite; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX

OS Phleum sp.

XX

PN WO9934826-A1.

XX

PD 15-JUL-1999.

XX

PF 11-JAN-1999; 99WO-GB0000080.

XX

PR 09-JAN-1998; 98GB-00000445.

XX

PR 21-SEP-1998; 98GB-00020474.

XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX

PI Larche M, Kay AB;

XX

XX WPI; 1999-458255/38.

XX

PT Desensitizing patients to polypeptide allergens.

XX

PS Example 6; Page 64; 117pp; English.

XX

This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a polypeptide derived from the allergen where restriction to a MHC Class II molecule is able to induce a late phase response in an individual who possesses the MHC class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and insect (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honey bee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larva, Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (timothy grass) Phl p 5 allergen

SQ Sequence 257 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 PPLPPPPPP 218

|||||

DB 231 PPLPPPPPP 240

XX

RESULT 43

ADC34880

ID ADC34880 standard; protein; 257 AA.

XX

(first entry)

allergen Phl p 5.

igen; hyporesponsive; desensitisation; immunomodulator;
timothy grass.

32.

2002WO-GB005548.

2001US-0338385P.

SSIA LTD.

lger PW;

267/49.

an individual to a selected polypeptide antigen comprises a composition containing polypeptide antigens in an amount as a state of hyporesponsiveness to the antigen to allow on.

age 33-34; 57pp; English.

relates to a novel method for desensitising an individual polypeptide antigen. The method comprises administering a at contains polypeptide antigens in an amount that the individual a state of hyporesponsiveness to the antigen sensitisation to one or more polypeptide antigens. The method on has immunomodulator activity, and may have a use in gene composition and method are useful in manufacturing a desensitising an individual to a selected polypeptide generating in the individual a state of hyporesponsiveness to allow desensitisation to one or more polypeptide present sequence is used in the exemplification of the

A;

urity 100.0%; Pred. No. 3.9; Length 257;

inservative 0; Mismatches 0; Indels 0; Gaps 0;

PPQPP 218

PPQPP 240

ard; protein; 285 AA.

first entry)

ergen Phl p 5a protein fragment #3.

patibility complex; class II; desensitising; human; s; tree, weed; pollen; fungi; mould; food; insect; sting; ider; mite; housefly; fruit fly; sheep blow fly; honeybee; ; grain weevil; silkworm; bee moth; larvae; mealworm; cat; tle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig; vaccine; treatment; prevention; hypersensitivity.

OS Phleum sp.
XX WO9934826-A1.
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-GB000080.
XX PF 09-JAN-1998; 98GB-00000445.
XX PR 21-SEP-1998; 98GB-00020474.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Larche M, Kay AB;
XX WPI; 1999-458255/38.
XX
XX Desensitizing patients to polypeptide allergens.
XX
XX Example 6; Page 64-65; 117pp; English.
XX
XX This invention describes a novel method of desensitizing a patient polypeptide allergen and comprises administering to the patient a derived from the allergen where restriction to a MHC Class II mol. possessed by the patient can be demonstrated for the peptide and peptide is able to induce a late phase response in an individual possesses the MHC Class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree a (including ragweed) pollens, fungi and moulds, foods, stinging in the chironomidae (non-biting midges), spiders and mites, housefly, fly, sheep blow fly, screw worm fly, grain weevil, silkworm, hone non-biting midge larvae, bee moth larvae, mealworm, cockroach, la Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be produce immunological vaccines which may be used to prevent and/o conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 5a allergen
XX Sequence 285 AA;
SQ
Query Match 1.9%; Score 10; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 209 PPLPPFPQPP 218
Db 259 PPLPPFPQPP 268
RESULT 45
ADC34883
ID ADC34883 standard; protein; 285 AA.
XX
XX ADC34883;
AC
XX 18-DEC-2003 (first entry)
DT
XX
XX Timothy grass allergen Phl p 5a.
DE
XX
XX
XX
XX allergen; antigen; hyporesponsive; desensitisation; immunomodulator; gene therapy; timothy grass.
KW
XX
XX Phleum sp.
OS
XX
XX WO2003047618-A2.
PN
XX
XX 12-JUN-2003.
PD
XX
XX 05-DEC-2002; 2002WO-GB005548.
PF
XX
XX 05-DEC-2001; 2001US-0338385P.
PR
XX
XX (CIRC-) CIRCASSIA LTD.

PR 99US-0145086P.
 PR 99US-0145088P.
 PR 99US-0145089P.
 PR 99US-0145087P.
 PR 99US-0145089P.
 PR 99US-0145192P.
 PR 99US-0145145P.
 PR 99US-0145218P.
 PR 99US-0145224P.
 PR 99US-0145276P.
 PR 99US-0145913P.
 PR 99US-0145918P.
 PR 99US-0145919P.
 PR 99US-0145951P.
 PR 99US-0146386P.
 PR 99US-0146388P.
 PR 99US-0146389P.
 PR 99US-0147038P.
 PR 99US-0147204P.
 PR 99US-0147302P.
 PR 99US-0147192P.
 PR 99US-0147260P.
 PR 99US-0147303P.
 PR 99US-0147416P.
 PR 99US-0147493P.
 PR 99US-0147935P.
 PR 99US-0148171P.
 PR 99US-0148319P.
 PR 99US-0148341P.
 PR 99US-0148565P.
 PR 99US-0148684P.
 PR 99US-0149368P.
 PR 99US-0149175P.
 PR 99US-0149426P.
 PR 99US-0149722P.
 PR 99US-0149723P.
 PR 99US-0149929P.
 PR 99US-0149902P.
 PR 99US-0149930P.
 PR 99US-0150566P.
 PR 99US-0150884P.
 PR 99US-0151065P.
 PR 99US-0151066P.
 PR 99US-0151080P.
 PR 99US-0151303P.
 PR 99US-0151438P.
 PR 99US-0151930P.
 PR 99US-0152363P.
 PR 99US-0153070P.
 PR 99US-0153758P.
 PR 99US-0154018P.
 PR 99US-0154039P.
 PR 99US-0154779P.
 PR 99US-0155139P.
 PR 99US-0155486P.
 PR 99US-0155659P.
 PR 99US-0156458P.
 PR 99US-0156596P.
 PR 99US-0157117P.
 PR 99US-0157753P.
 PR 99US-0157865P.
 PR 99US-0158029P.
 PR 99US-0158232P.
 PR 99US-0158369P.
 PR 99US-0159233P.
 PR 99US-0159294P.
 PR 99US-0159295P.
 PR 99US-0159329P.
 PR 99US-0159330P.
 PR 99US-0159331P.
 PR 99US-0159637P.
 PR 99US-0159638P.
 PR 99US-0159584P.

PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161931P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 1.0%; Score 10; DB 3; Length 320;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 222 QQQQPPPPQP 231
 Db 288 QQQQPPPPQP 297

RESULT 47

AAB42629
 ID AAB42629 standard; protein; 322 AA.

XX AAB42629;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF2393 polypeptide sequence SEQ ID NO:4786.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatoto
 KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprote
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; ca
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabeti
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypert
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID;
 KW cholesterol ester storage; systemic lupus erythematosus; infectio
 KW severe combined immunodeficiency; malaria; autoimmune disorder; a
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound
 KW bone damage; cartilage damage; antinflammatory disease; coagulat
 KW thrombosis; contraceptive.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

PA (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

DR N-PSDB; AAC76838.

acids and peptides derived from open reading frame X,
 including e.g. cancers, proliferative disorders,
 and disorders and cardiovascular disease.

3968-3969; 5507pp; English.

77606 encode the proteins given in AAB40237 to AAB43397,
 the human ORFX open reading frames 1 to 3161. The ORFX
 activities such as: cytostatic; hepatotropic; vulnery;
 antiparkinsonian; nootropic; neuroprotective; osteopathic;
 antiarthritic; immunosuppressant; immunostimulant;
 hydrolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 immunosuppressive; antiinflammatory; antibacterial;
 fungicidal; antirheumatic; antithyroid; and antianaemic. The
 are used for determining the presence of or predisposition
 to or treating pathological conditions associated with an
 disorder. The nucleic acids can be used to express ORFX
 in therapy vectors. The proteins and nucleic acids may be
 used in the treatment of cancers, proliferative disorders, neurodegenerative
 diseases, arthritis, graft vs host disease, cardiovascular disease,
 lupus, hypertension, hypothyroidism, cholesterol ester
 deficiency, bacterial or fungal infection, malaria, autoimmune
 disease, allergies, aplastic anaemia, burns, wounds, bone and
 joint, nocturnal haemoglobinuria, antiinflammatory disease; to
 inhibit thrombosis; and as a contraceptive

1;

1.9%; Score 10; DB 3; Length 322;

Identity 100.0%; Pred. No. 4.7;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAP 127

|||||

AAAP 300

Word; protein; 401 AA.

first entry

Liana protein fragment SEQ ID NO: 41986.

Location; signal transduction pathway; metabolic pathway;
 assay; genetic mapping; gene expression control; promoter;
 function.

Liana.

00EP-00301439.

99US-0121825P.

99US-0123180P.

99US-0123548P.

99US-0125788P.

99US-0126264P.

99US-0126785P.

99US-0127462P.

99US-0128234P.

99US-0128714P.

99US-0129845P.

99US-0130077P.

99US-0130449P.

PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 07-MAY-1999; 99US-0132487P.
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 PR 14-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 18-MAY-1999; 99US-0134370P.
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 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
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 PR 18-JUN-1999; 99US-0139457P.
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 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
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 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 23-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140911P.
 PR 30-JUN-1999; 99US-0141267P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
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 PR 15-JUL-1999; 99US-0144005P.
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 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
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 PR 19-JUL-1999; 99US-0144334P.
 PR 19-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144352P.

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 99US-0149175P.
 99US-0149426P.
 99US-0149722P.
 99US-0149723P.
 99US-0149929P.
 99US-0149902P.
 99US-0149930P.
 99US-0150566P.
 99US-0150884P.
 99US-0151065P.
 99US-0151066P.
 99US-0151080P.
 99US-0151303P.
 99US-0151438P.
 99US-0151930P.
 99US-0152363P.
 99US-0153070P.
 99US-0153758P.
 99US-0154018P.
 99US-0154039P.
 99US-0154779P.
 99US-0155139P.
 99US-0155486P.
 99US-0155659P.
 99US-0156458P.
 99US-0156596P.
 99US-0157117P.
 99US-0157753P.
 99US-0157865P.
 99US-0158029P.
 99US-0158232P.
 99US-0158369P.
 99US-0159293P.
 99US-0159284P.
 99US-0159295P.
 99US-0159329P.
 99US-0159330P.
 99US-0159331P.

PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 1.9%; Score 10; DB 3; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G;

QY 222 QQQPPPPQP 231
 |||||
 Db 369 QQQPPPPQP 378

RESULT 49
 ABP54691
 ID ABP54691 standard; protein; 402 AA.
 XX
 AC ABP54691;
 XX
 DT 30-DEC-2002 (first entry)
 XX
 DE Metastatic colorectal cancer-associated polypeptide.
 XX
 KW Colorectal cancer; metastasis; differential expression; cytostatic
 diagnosis; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 387
 FT /note= "encoded by CGN"
 XX
 PN WO200268677-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 27-FEB-2002; 2002WO-US006001.
 XX
 PR 27-FEB-2001; 2001US-0272206P.
 PR 02-APR-2001; 2001US-0281149P.
 PR 17-APR-2001; 2001US-0284555P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 XX
 PI Mack DH, Markowitz SD;
 XX
 DR WPI: 2002-698677/75.
 DR N-PSDB; ABP81557.
 XX

New genes that are up- or down-regulated in colorectal cancer, use
 PT diagnosing colorectal cancer in a subject, or for identifying modu
 PT of colorectal cancer-associated proteins and genes for treating
 PT colorectal cancer.

252; 260pp; English.

ence is the protein sequence of a human polypeptide
ne that exhibits increased expression in colon cancer-
ases compared to normal colon tissue. It is an example of
ptides that are encoded by genes which are differentially
tastic colorectal cancer cells. Such polypeptides are
ostic and prognostic assays, for raising antibodies useful
herapy, and in screening for modulator compounds of
lue

1;

1.9%; Score 10; DB 5; Length 402;

city 100.0%; Pred.No. 5.6;

servative 0; Mismatches 0; Indels 0; Gaps 0;

APAAP 187

|||||

APAAP 245

ird; protein; 436 AA.

irst entry)

n.

rotein; Id protein; maize; corn; flower induction;
n; transgenic plant.

Location/Qualifiers

98. .118

/note= "zinc finger 1"

199. .219

/note= "zinc finger 2"

99WO-US007157.

99US-00056226.

PRING HARBOR LAB.

Sundaresan V;

17/54.

9.

oral induction gene, used for producing plants with
of transition from the vegetative to the flowering stage.

80pp; English.

represents the maize chromosome 1 indeterminate (Id)
a zinc finger regulatory protein that plays a crucial role
from vegetative to reproductive development, controlling
of other genes required for floral development. Loss of Id
prolonged vegetative development. Understanding the
is regulation provides a basis for producing specialized
l to flower and produce seed independent of native internal
hromental effects. Methods are provided for producing
ected times of transition from the vegetative to the

CC flowering stage. They can result in either earlier cessation of
CC vegetative growth and initiation of flowering, or in later floweri
CC the absence of floral induction. The plants can be induced to flow
CC set seed prior to adverse weather. Similarly, flower induction can
CC prolonged for short-season plants grown in areas with long periods
CC warm weather. As a result of the extra vegetative mass and carbohy
CC these plants can produce more and/or larger flowers and, consequen
CC more seed. Plants can even be prevented from flowering, thus provi
CC nutritious silage biomass. They can also be used to eliminate the
CC for detasseling in the production of hybrids

XX Sequence 436 AA;

Query Match

Best Local Similarity 1.9%; Score 10; DB 2; Length 436;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 210 PLPPPPQPPA 219

|||||

Db 45 PLPPPPQPPA 54

RESULT 51

ABP51652
ID ABP51652 standard; protein; 436 AA.

XX AC ABP51652;

XX DT 30-SEP-2002 (first entry)

XX DE Maize indeterminate 1 (Id1) protein SEQ ID NO:10.

XX KW Lolium perenne; perennial ryegrass; indeterminate protein; plant;
XX life cycle; growth phase; flower.

XX OS Zea mays.

XX PN WO200238768-A1.

XX PD 16-MAY-2002.

XX PF 07-NOV-2001; 2001WO-AU001432.

XX PR 08-NOV-2000; 2000AU-00001313.

XX PA (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.

XX PI Spangenberg G, Liu B, Truman D;

XX DR WPI; 2002-575206/61.

XX Novel polypeptide referred to as indeterminate 1 from ryegrass or
PT species, useful for modifying plant life cycles and growth phases
PT flowering processes, plant architecture, inflorescence, flower
PT development.

XX Example 2; Fig 7; 80pp; English.

XX The present invention describes a substantially purified or isolat
CC polypeptide (I) from a ryegrass (Lolium) or fescue (Festuca) spec
CC from indeterminate 1 (Id1) and Id1-like proteins, its functionall
CC fragments and variants. Polynucleotide sequences (II) encoding (I)
CC used for modifying plant life cycles and/or growth phases such as
CC flowering processes, flowering and plant architecture, inflorescen
CC flower development. (II) can also be used as a genetic marker. (I)
CC (II) can be used for facilitating immunological screening of cDNA
CC expression libraries. (II) is useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species,
CC hybridisation probes to screen libraries from the desired plant. (I
CC useful in amplification protocols to amplify longer nucleic acid o
CC nucleic acid fragments encoding homologous genes for DNA or RNA. (I
CC also useful as a molecular genetic marker for quantitative trait lo
CC (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assist

particularly in ryegrasses and fescues. (II) is also used as
static markers in forage and turf grass improvement e.g.,
for herbage quality traits, flowering intensity, flowering
of tillers, leafiness, bushiness, seasonal growth pattern,
flower architecture, plant stature. The present sequence
maize indeterminate 1 (ID1) which is given in comparison
in the table below. The protein isolated from Lolium perenne (perennial
the exemplification of the present invention

1A;
1.9%; Score 10; DB 5; Length 436;
arity 100.0%; Pred.No. 6;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

PPPPA 219

|||||

PPPPA 54

dard; protein; 448 AA.

(first entry)

haliana protein fragment SEQ ID NO: 41985.

ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

haliana.

2000EP-00301439.

99US-0121825P.

99US-012180P.

99US-0123548P.

99US-0125789P.

99US-0126264P.

99US-0126785P.

99US-0127462P.

99US-0128234P.

99US-0128714P.

99US-0129845P.

99US-0130077P.

99US-013049P.

99US-0130510P.

99US-0130891P.

99US-0131449P.

99US-0132048P.

99US-0132407P.

99US-0132484P.

99US-0132485P.

99US-0132486P.

99US-0132487P.

99US-0132863P.

99US-0134256P.

99US-0134218P.

99US-0134219P.

99US-0134370P.

99US-0134768P.

99US-0134941P.

99US-0135124P.

99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 04-JUN-1999; 99US-0137528P.
PR 03-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.

99US-0146389P.
 99US-0147038P.
 99US-0147204P.
 99US-0147302P.
 99US-0147192P.
 99US-0147260P.
 99US-0147303P.
 99US-0147416P.
 99US-0147493P.
 99US-0147935P.
 99US-0148171P.
 99US-0148313P.
 99US-0148341P.
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 99US-0149175P.
 99US-0149426P.
 99US-0149722P.
 99US-0149723P.
 99US-0149929P.
 99US-0149902P.
 99US-0149930P.
 99US-0150884P.
 99US-0150566P.
 99US-0151065P.
 99US-0151066P.
 99US-0151080P.
 99US-0151303P.
 99US-0151438P.
 99US-0151930P.
 99US-0152363P.
 99US-0153070P.
 99US-0153758P.
 99US-0154018P.
 99US-0154039P.
 99US-0154779P.
 99US-0155139P.
 99US-0155486P.
 99US-0155659P.
 99US-0156458P.
 99US-0156596P.
 99US-0157117P.
 99US-0157753P.
 99US-0157865P.
 99US-0158029P.
 99US-0158232P.
 99US-0158369P.
 99US-0159293P.
 99US-0159294P.
 99US-0159295P.
 99US-0159329P.
 99US-0159330P.
 99US-0159331P.
 99US-0159617P.
 99US-0159638P.
 99US-0159584P.
 99US-0160741P.
 99US-0160767P.
 99US-0160768P.
 99US-0160770P.
 99US-0160814P.
 99US-0160815P.
 99US-0160980P.
 99US-0160981P.
 99US-0160989P.
 99US-0161404P.
 99US-0161405P.
 99US-0161406P.
 99US-0161359P.
 99US-0161360P.
 99US-0161361P.
 99US-0161920P.

PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.
 Query Match 1.9%; Score 10; DB 3; Length 448;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
 QY 222 QQQQPPPPPP 231
 Db 416 QQQQPPPPPP 425
 RESULT 53
 ABG66745
 ID ABG66745 standard; protein; 581 AA.
 XX
 AC ABG66745;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Human novel polypeptide #80.
 XX
 KW Human; inflammatory condition; shock; sepsis; immune response; can
 wound healing; central nervous system disease; haematopoiesis;
 peripheral nervous system disease; amyotrophic lateral sclerosis;
 myeloid cell disorder; lymphoid cell disorder; platelet disorder;
 cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
 bone degenerative disorder; periodontal disease; reperfusion injury;
 lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
 allergic condition; thrombolysis; thrombosis; coagulation disorder
 fungal infection.
 KW
 XX Homo sapiens.
 OS
 XX
 PN W0200244340-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 30-NOV-2001; 2001WO-US047004.
 XX
 PR 30-NOV-2000; 2000US-00728952.
 XX
 PA (HYSE-) HYSBQ INC.
 XX
 PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang I
 Yamazaki V, Ujwal ML, Drmanac RT;
 XX
 DR WPI; 2002-508509/54.
 DR N-PSDB; ABK94969.
 XX
 PT Novel nucleic acids and polypeptides for diagnosis, treatment of
 inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
 disorders, cancer and promoting wound healing.
 XX
 PS Claim 10; Page 655-656; 672pp; English.
 XX
 CC The invention relates to human novel polynucleotides and associated
 polypeptides. The polynucleotides and polypeptides are useful for
 treating inflammatory conditions such as arthritis, nephritis, Crohn
 disease, ischaemia-reperfusion injury, shock, sepsis, immune response
 and cancer and for promoting wound healing. The sequences are used
 to induce the proliferation of neural cells and regeneration of nerve
 brain tissue, and are useful for the treatment of central and peripheral
 nervous system diseases and neuropathies, such as Alzheimer's disease
 Parkinson's disease, Huntington's disease and amyotrophic lateral
 sclerosis. The sequences are involved in chemotactic or chemokinetic
 activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
 cell disorders and platelet disorders such as thrombocytopenia, tissue
 regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 growth, tissue repair, healing of burns, incisions, ulcers, treatment
 osteoporosis, osteoarthritis, bone degenerative disorders and pericardial
 disease. The sequences of the invention are also useful for gut

regeneration and treatment of lung or liver fibrosis,
injury in various tissues, immune deficiencies and disorders
are combined immunodeficiency (SCID), bacterial or fungal
autoimmune disorders e.g. multiple sclerosis and myasthenia
gravis conditions such as asthma, thrombolytic or thrombotic
disorders. Sequences ABG66666-ABG666758 represent human
sequences of the invention

AA;

Query Match 1.9%; Score 10; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

POQPP 234
|||||
POQPP 97

hard; protein; 588 AA.

(first entry)

ed by Prokaryotic essential gene #8262.

Prokaryotic essential gene; cell proliferation; drug design.

alleles.

2.

2002WO-US009107.

2001US-00815242.

2001US-00948993.

2001US-0342923P.

2002US-00072851.

2002US-0362699P.

A PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

26/02.
205.

nucleic acids, useful for identifying proteins or screening
nucleic acids required for cellular proliferation to
late molecules for rational drug discovery programs.

ID NO 50659; 1766pp; English.

relates to an isolated nucleic acid comprising any one of
sense sequences given in the specification where expression
of acid inhibits proliferation of a cell. Also included are:
comprising a promoter operably linked to the nucleic acid
typeptide whose expression is inhibited by the antisense
(2) a host cell containing the vector; (3) an isolated
its fragment whose expression is inhibited by the
eic acid; (4) an antibody capable of specifically binding
ie.(5) producing the polypeptide; (6) inhibiting cellular
or the activity of a gene in an operon required for
(7) identifying a compound that influences the activity of
act or that has an activity against a biological pathway
proliferation, or that inhibits cellular proliferation; (8)
gene required for cellular proliferation or the biological

pathway in which a proliferation-required gene or its gene product
or a gene on which the test compound that inhibits proliferation
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which t
product is overexpressed or underexpressed; (12) determining the
to which each of the strains is present in a culture or collecti
strains; or (13) identifying the target of a compound that inhibi
proliferation of an organism. The antisense nucleic acids are use
identifying proteins or screening for homologous nucleic acids re
for cellular proliferation to isolate candidate molecules for rat
drug discovery programs, or for screening homologous nucleic acid
required for proliferation in cells other than S. aureus, S. typh
K. pneumoniae or P. aeruginosa. The present sequence is encoded b
the target prokaryotic essential genes. Note: The sequence data f
patent did not form part of the printed specification, but was ob
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX Sequence 588 AA;

Query Match 1.9%; Score 10; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 118 APAAAAAAP 127

Db 476 APAAAAAAP 485

RESULT 55

ABU15059

ID ABU15059 standard; protein; 613 AA.

XX AC ABU15059;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #596.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug d

XX OS Escherichia coli.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA18929.

XX XX New antisense nucleic acids, useful for identifying proteins or s

XX PT for homologous nucleic acids required for cellular proliferation t

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 42983; 1766pp; English.

XX XX The invention relates to an isolated nucleic acid comprising any

XX CC the 6213 antisense sequences given in the specification where exp

XX CC of the nucleic acid inhibits proliferation of a cell. Also include

XX CC (1) a vector comprising a promoter operably linked to the nucleic

ypeptide whose expression is inhibited by the antisense
(2) a host cell containing the vector; (3) an isolated
its fragment whose expression is inhibited by the
eic acid; (4) an antibody capable of specifically binding
e;(5) producing the polypeptide; (6) inhibiting cellular
or the activity of a gene in an operon required for
(7) identifying a compound that influences the activity of
ct or that has an activity against a biological pathway
roliferation, or that inhibits cellular proliferation; (8)
gene required for cellular proliferation or the biological
ch a proliferation-required gene or its gene product lies
hich the test compound that inhibits proliferation of an
(9) manufacturing an antibiotic; (10) profiling a
ivity; (11) a culture comprising strains in which the gene
repressed or underexpressed; (12) determining the extent
of the strains is present in a culture or collection of
3) identifying the target of a compound that inhibits the
of an organism. The antisense nucleic acids are useful for
oteins or screening for homologous nucleic acids required
roliferation to isolate candidate molecules for rational
programs, or for screening homologous nucleic acids
roliferation in cells other than *S. aureus*, *S. typhimurium*,
or *P. aeruginosa*. The present sequence is encoded by one of
karyotic essential genes. Note: The sequence data for this
form part of the printed specification, but was obtained
format directly from WIFO at
ub/published_pct_sequences

A;

1.9%; Score 10; DB 6; Length 613;

rity 100.0%; Pred. No. 8;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

EDED 342

|||||

EDED 200

ard; protein; 635 AA.

first entry)

ciparum chromosome 2 related protein SEQ ID NO:49.

ciparum; chromosome 2; human malaria parasite; vaccine;
malaria; protozoacide; infection; insecticide.

ciparum.

99WO-US026796.

98US-0107131P.

J S.

I D.

R M.

J C.

rucci D, Gardner M, Venter JC;

47/31.

ed by chromosome 2 of the human malarial parasite.
ciparum, useful as antimalarial vaccines and in thediagnosis of *P. falciparum* infection.

Disclosure; Page 115-116; 577pp; English.

The present invention describes proteins and their fragments (I) &
by chromosome 2 of the human malarial parasite, *Plasmodium falciparum*.
Also described are: (i) nucleotide sequences (ii) encoding (i); at
vaccines against *P. falciparum* infection comprising (i) or (ii).
(ii) are useful for the development of vaccines against *P. falciparum*.
infection. (i) and polyclonal antisera or a monoclonal antibody &
immunogens comprising the sequences of (i), are useful in the detection
of infection with *P. falciparum*. Furthermore, (i) (especially when
are refined or secreted or membrane proteins) can aid the identification
of drugs to treat or prevent *P. falciparum* infection, or they can
to identify drug resistance in *P. falciparum*. Sequencing of the
Plasmodium chromosome 2 and the subsequent identification of proteins
encoded by it will help to expand our understanding of proteins &
a process hampered by the complexity of the parasitic lifecycle, &
provide new targets for vaccine and drug development. Parasite resistance
to drugs and mosquito resistance to insecticides have led to a resurgence
of malaria in many parts of the world, and there is a pressing need
for vaccines and new drugs. AAT70078 to AAA70287 and AAB18144 to AAB18144
represent nucleotide and protein sequences given in the present
invention, but which are not specifically mentioned within the
specification

XX Sequence 635 AA;

Query Match 1.9%; Score 10; DB 3; Length 635;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 334 DDEDEDEDD 343

|||||

Db 577 DDEDEDEDD 586

RESULT 57

ABB62471

ID ABB62471 standard; protein; 660 AA.

XX ABB62471;

AC ABB62471;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 14205.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-ESDB; ABL06574.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX Genes from *Drosophila* and for elucidating cell signaling and cell-cell

XX interactions.

XX Disclosure; SEQ ID NO 14205; 21pp + Sequence Listing; English.

relates to an isolated nucleic acid detection reagent detecting 1000 or more genes from *Drosophila*. The invention is supplemental biology and in elucidating cell signalling and interactions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention omic DNA sequences (ABL16176-ABL30511), expressed DNA 501840-ABL16175) and the encoded proteins (ABBS7737- a sequence data for this patent did not form part of the fication, but was obtained in electronic format directly ftp.wipo.int/pub/published_pct_sequences

AA;

1.9%; Score 10; DB 4; Length 660;

arity 100.0%; Pred. No. 8.5; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 150

hard; protein; 660 AA.

(first entry)

ad by Prokaryotic essential gene #33095.

Prokaryotic essential gene; cell proliferation; drug design.

chi.

?

2002WO-US009107.

2001US-00815242.

2001US-00948993.

2001US-0342923P.

2002US-00072851.

2002US-0362699P.

A PHARM INC.

lio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

ck JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

25/02.

38.

nucleic acids, useful for identifying proteins or screening nucleic acids required for cellular proliferation to late molecules for rational drug discovery programs.

ID NO 75492; 1766pp; English.

relates to an isolated nucleic acid comprising any one of sense sequences given in the specification where expression acid inhibits proliferation of a cell. Also included are: comprising a promoter operably linked to the nucleic acid -peptide whose expression is inhibited by the antisense (2) a host cell containing the vector; (3) an isolated its fragment whose expression is inhibited by the leic acid; (4) an antibody capable of specifically binding le; (5) producing the polypeptide; (6) inhibiting cellular or the activity of a gene in an operon required for

proliferation; (7) identifying a compound that influences the act the gene product or that has an activity against a biological pat required for proliferation, or that inhibits cellular proliferati identifying a gene required for cellular proliferation or the bio pathway in which a proliferation-required gene or its gene produc or a gene on which the test compound that inhibits proliferation organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which t product is overexpressed or underexpressed; (12) determining the to which each of the strains is present in a culture or collectio strains; or (13) identifying the target of a compound that inhibi proliferation of an organism. The antisense nucleic acids are use identifying proteins or screening for homologous nucleic acids re for cellular proliferation to isolate candidate molecules for rat drug discovery programs, or for screening homologous nucleic acid required for proliferation in cells other than *S. aureus*, *S. typh* *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded b the target prokaryotic essential genes. Note: The sequence data f patent did not form part of the printed specification, but was ob in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 660 AA;

Query Match 1.9%; Score 10; DB 6; Length 660;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDEDEDEED 342

|||||

Db 238 DDEDEDEED 247

RESULT 59

ABU47065

ID ABU47065 standard; protein; 660 AA.

XX AC ABU47065;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #32592.

XX Antisense; prokaryotic essential gene; cell proliferation; drug d

XX OS *Salmomella typhimurium*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA50935.

XX PT New antisense nucleic acids, useful for identifying proteins or sc for homologous nucleic acids required for cellular proliferation t isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 74989; 1766pp; English.

forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

ID NO 48036; 103pp; English.

relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, inant production of (II). The polynucleotides are also used as expressed sequence tags for identifying expressed genes in gene therapy techniques to restore normal function or to treat disease states involving (II). (II) is used in tissue, as molecular weight markers and as a food additive and its binding partners are useful in medical imaging and protein expression or biological activity. The polynucleotide sequences have applications in forensics, gene mapping, identification of mutations or genetic disorders or other traits to assess biodiversity and other types of data and products dependent on DNA and sequences. ABG00010-ABG30377 represent novel human diagnostic sequences of the invention. Note: The sequence data for this invention appear in the printed specification, but was obtained in format directly from WIPO at pub/published_pct_sequences

AA;

1.9%; Score 10; DB 4; Length 725;

arity 100.0%; Pred. No. 9.2; Indels 0; Gaps 0; conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDEED 342
|||||||
DEDEED 141

dard; protein; 806 AA.

(first entry)

lanogaster polypeptide SEQ ID NO 9390.

developmental biology; cell signalling; insecticide; 1.

lanogaster.

2.

2001WO-US009231.

2000US-0191637P.

2000US-00614150.

RP NY.

Jams M, Li PWD, Myers EW;

860/75.

969.

nucleic acid detection reagent for detecting 1000 or more asophila and for elucidating cell signaling and cell-cell

XX Disclosure; SEQ ID NO 9390; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116176-AB130511), expressed DN sequences (AB101840-AB116175) and the encoded proteins (AB857737-AB872072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 806 AA;

Query Match 1.9%; Score 10; DB 4; Length 806;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Oy 20 AAASSSAASP 29

Db 214 AAASSSAASP 223

RESULT 63
ABB07036
ID ABB07036 standard; protein; 1101 AA.

AC ABB07036;

XX 21-JUN-2002 (first entry)

DE Mouse SRG3 (SWI3-related gene) protein sequence.

KW Mouse; SRG3; SWI3-related gene.

XX Mus sp.

Key Location/Qualifiers

Misc-difference 20 /note= "encoded by CGG"

XX KR191125-B1.

XX 15-JUN-1999.

XX 10-AUG-1996; 96KR-00033288.

XX 10-AUG-1996; 96KR-00033288.

XX (SUNG/) SUNG N.

XX Sung N, Park S, Chun S;

XX WPI; 2000-644520/62.

XX N-PSDB; ABL50888, ABL50889.

XX NEW SWI3-RELATED GENE PURIFIED FROM MOUSE AND THE PROTEIN EXPRESSED THAT.

XX Claim 2; Page 11-12; 15pp; Korean.

XX The present invention describes an SWI3-related gene, designated as CC which is isolated from mouse. The present sequence represents the CC SRG3 protein sequence

XX Sequence 1101 AA;

Query Match 1.9%; Score 10; DB 3; Length 1101;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QPPPP 229
 |||||
 QPPPP 1083

ard; protein; 1250 AA.

(first entry)

anogaster retinal degeneration B polypeptide (DmrdgB).

/rosine kinase binding protein; 6-transmembrane domain;
 iron; Pyk2 binding domain; synaptic vesicles;
 ar signalling; myasthenia gravis; stroke; neuroblastoma;
 ia; Alzheimer's; Huntington's; Parkinson's; depression;
 pain epilepsy.

anogaster.

Location/Qualifiers

≥ 1055
 /note= "encoded by TA"
 ≥ 1133
 /note= "encoded by TCC"
 ≥ 1134
 /note= "encoded by ACC"
 ≥ 1149
 /note= "encoded by CA"

97WO-US017374.

96US-0027337P.

INC.

EW YORK MEDICAL CENT.

GD, Schlessinger J;

36/22.
 36.

id encoding human retinal degradation polypeptide - and
 vectors, transformed cells, proteins and antibodies, used
 neurological disease and to identify specific modulators with
 peutic activity.

je 48-50; 59pp; English.

quence represents the D.melanogaster retinal degeneration B
 3), which is a non-receptor tyrosine kinase binding
 A that encodes this protein had previously been identified
 al, Journal of cell biology, volume 122: 1013-1022, 1993.
 is a false stop codon sequencing error in this reference,
 he sequence to be incorrectly interrupted as a member of the
 domain family of proteins, thus the Pyk-2 binding domain
 identified. DmrdgB contains both a PIT domain, and a Pyk2
 and is thus concerned with PI transfer and regulating
 er signalling respectively. This protein is seen to be
 gnalling transduction pathways and therefore would be
 nosis, treatment, and prevention of the following diseases:
 vis; neuroblastoma; thrombocytopaenia; stroke; Alzheimer's;
 parkinson's; depression; schizophrenia; pain epilepsy

AA;

Query Match 1.9%; Score 10; DB 2; Length 1250;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 329 EEEEDDEDE 338
 |||||
 Db 324 EEEEDDEDE 333

RESULT 65

ABB65508
 ID ABB65508 standard; protein; 1250 AA.

XX AC ABB65508;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 23316.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL09611.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or
 PT genes from Drosophila and for elucidating cell signalling and cell-
 PT interactions.

XX PS Disclosure; SEQ ID NO 23316; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The inven
 CC useful in developmental biology and in elucidating cell signalling
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of
 CC printed specification, but was obtained in electronic format direc
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1250 AA;

Query Match 1.9%; Score 10; DB 4; Length 1250;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 329 EEEEDDEDE 338
 |||||
 Db 324 EEEEDDEDE 333

RESULT 66

ABB65470
 ID ABB65470 standard; protein; 1250 AA.

XX AC ABB65470;

(first entry)
lanogaster polypeptide SEQ ID NO 23202.
evolutionary biology; cell signalling; insecticide;
1.
lanogaster.
2.
2001WO-US009231.
2000US-0191637P.
2000US-00614150.
RP NY.
Jams M, Li PWD, Myers EW;
960/75.
573.
nucleic acid detection reagent for detecting 1000 or more
osophila and for elucidating cell signaling and cell-cell
EQ ID NO 23202; 21pp + Sequence Listing; English.
relates to an isolated nucleic acid detection reagent
ecting 1000 or more genes from Drosophila. The invention is
olopmental biology and in elucidating cell signalling and
rations in higher eukaryotes for the development of
therapeutics and pharmaceutical drugs. The invention
omic DNA sequences (AB116176-AB130511), expressed DNA
01840-AB116175) and the encoded proteins (AB1857737-
sequence data for this patent did not form part of the
fication, but was obtained in electronic format directly
ftp.wipo.int/pub/published_pct_sequences
AA;
arity 1.9%; Score 10; DB 4; Length 1250;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDDEDE 338
|||||
DDDEDE 333
iard; protein; 1277 AA.
(first entry)
am glutamicum MCT protein SEQ ID NO:54.
am glutamicum; brevibacterium lactofermentum; MCT;
struction and membrane transport protein; petroleum spill;
egradation; gram positive aerobic bacterium; marker;
a; microorganism; fine chemical production; transformation;
i; genetic engineering.
am glutamicum.
2.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-IB000926.
XX PR 25-JUN-1999; 99US-0141031P.
PR 08-JUL-1999; 99DE-01031454.
PR 08-JUL-1999; 99DE-01031478.
PR 08-JUL-1999; 99DE-01031563.
PR 09-JUL-1999; 99DE-01032122.
PR 09-JUL-1999; 99DE-01032124.
PR 09-JUL-1999; 99DE-01032125.
PR 09-JUL-1999; 99DE-01032128.
PR 09-JUL-1999; 99DE-01032180.
PR 09-JUL-1999; 99DE-01032182.
PR 09-JUL-1999; 99DE-01032190.
PR 09-JUL-1999; 99DE-01032191.
PR 09-JUL-1999; 99DE-01032209.
PR 09-JUL-1999; 99DE-01032212.
PR 09-JUL-1999; 99DE-01032227.
PR 09-JUL-1999; 99DE-01032228.
PR 09-JUL-1999; 99DE-01032229.
PR 09-JUL-1999; 99DE-01032230.
PR 14-JUL-1999; 99DE-01032927.
PR 14-JUL-1999; 99DE-01033005.
PR 14-JUL-1999; 99DE-01033006.
PR 27-AUG-1999; 99DE-01040764.
PR 27-AUG-1999; 99DE-01040765.
PR 27-AUG-1999; 99DE-01040766.
PR 27-AUG-1999; 99DE-01040830.
PR 27-AUG-1999; 99DE-01040831.
PR 27-AUG-1999; 99DE-01040832.
PR 31-AUG-1999; 99DE-01040833.
PR 31-AUG-1999; 99DE-01041378.
PR 31-AUG-1999; 99DE-01041379.
PR 31-AUG-1999; 99DE-01041395.
PR 03-SEP-1999; 99DE-01042077.
PR 03-SEP-1999; 99DE-01042078.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042088.
PA (BADI) BASF AG.
XX PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX DR WPI; 2001-071496/08.
XX DR N-PSDB; AAF67769.
XX PT Corynebacterium glutamicum nucleic acids encoding membrane constru
PT and membrane transport proteins or their portions, useful for typ
PT identifying C. glutamicum or related bacteria, and as markers for
PT transformation.
XX PS Claim 20; Page 242-246; 1119pp; English.
XX CC AAF67743 to AAF68080 encode the Corynebacterium glutamicum membra
CC construction and membrane transport (MCT) proteins given in AAB76
CC AAB76847. The MCT nucleic acids and proteins are useful in the
CC identification of microorganisms which can be used to produce fin
CC chemicals, for modulating fine chemical production in C. glutamic
CC related bacteria (e.g. Brevibacterium lactofermentum), the typing
CC identification of C. glutamicum or related bacteria, as reference
CC for mapping C. glutamicum genome, and as markers for transformati
CC AAF68082 and AAF68082 represent sequencing primers which are used
CC example from the present invention
XX SQ Sequence 1277 AA;
Query Match 1.9%; Score 10; DB 4; Length 1277;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY 137 PAPVAAAPAA 146

|||||
AAAPA 993

ard; protein; 1301 AA.

first entry)

anogaster polypeptide SEQ ID NO 2179.

velopental biology; cell signalling; insecticide;

anogaster.

001WO-US009231.

000US-0191637P.

000US-00614150.

P NY.

ams M, Li PWD, Myers EW;

60/75.

32.

nucleic acid detection reagent for detecting 1000 or more
sophila and for elucidating cell signaling and cell-cell

2 ID NO 2179; 21pp + Sequence Listing; English.

relates to an isolated nucleic acid detection reagent
acting 1000 or more genes from Drosophila. The invention is
lomental biology and in elucidating cell signalling and
rations in higher eukaryotes for the development of
therapeutics and pharmaceutical drugs. The invention
nic DNA sequences (ABL16176-ABL30511), expressed DNA
01840-ABL16175) and the encoded proteins (ABB57737-
sequence data for this patent did not form part of the
ication, but was obtained in electronic format directly
p.wipo.int/pub/published_pct_sequences

AA;

1.9%; Score 10; DB 4; Length 1301;

city 100.0%; Pred. No. 15;

iservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 22

AAAAA 1276

ard; protein; 1390 AA.

first entry)

rotein.

KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic;
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vacc.
KW human.

XX Homo sapiens.

XX WO2002/2757-A2.

XX 19-SEP-2002.

XX 08-MAR-2002; 2002WO-US006908.

XX 08-MAR-2001; 2001US-0274101P.

XX 08-MAR-2001; 2001US-0274194P.

XX 08-MAR-2001; 2001US-0274281P.

XX 08-MAR-2001; 2001US-0274322P.

XX 09-MAR-2001; 2001US-0274845P.

XX 12-MAR-2001; 2001US-0275235P.

XX 13-MAR-2001; 2001US-0275578P.

XX 13-MAR-2001; 2001US-0275579P.

XX 14-MAR-2001; 2001US-0275601P.

XX 14-MAR-2001; 2001US-0276000P.

XX 16-MAR-2001; 2001US-0276778P.

XX 19-MAR-2001; 2001US-0276994P.

XX 20-MAR-2001; 2001US-0277239P.

XX 20-MAR-2001; 2001US-0277321P.

XX 20-MAR-2001; 2001US-0277327P.

XX 21-MAR-2001; 2001US-0277791P.

XX 22-MAR-2001; 2001US-0277833P.

XX 23-MAR-2001; 2001US-0278152P.

XX 26-MAR-2001; 2001US-0278894P.

XX 27-MAR-2001; 2001US-0278999P.

XX 27-MAR-2001; 2001US-0279036P.

XX 28-MAR-2001; 2001US-0279344P.

XX 30-MAR-2001; 2001US-0277338P.

XX 30-MAR-2001; 2001US-0279995P.

XX 30-MAR-2001; 2001US-0280233P.

XX 02-APR-2001; 2001US-0280802P.

XX 02-APR-2001; 2001US-0280822P.

XX 02-APR-2001; 2001US-0280900P.

XX 04-APR-2001; 2001US-0281194P.

XX 13-APR-2001; 2001US-0283675P.

XX 30-APR-2001; 2001US-0287424P.

XX 02-MAY-2001; 2001US-0288066P.

XX 03-MAY-2001; 2001US-0288342P.

XX 03-MAY-2001; 2001US-0288528P.

XX 15-MAY-2001; 2001US-0291130P.

XX 16-MAY-2001; 2001US-0291099P.

XX 16-MAY-2001; 2001US-0291240P.

XX 30-MAY-2001; 2001US-0294485P.

XX 31-MAY-2001; 2001US-0294889P.

XX 31-MAY-2001; 2001US-0294899P.

XX 18-JUN-2001; 2001US-0299027P.

XX 19-JUN-2001; 2001US-0299303P.

XX 19-JUN-2001; 2001US-0299310P.

XX 10-JUL-2001; 2001US-0304354P.

XX 31-JUL-2001; 2001US-0309198P.

XX 16-AUG-2001; 2001US-0312903P.

XX 10-SEP-2001; 2001US-0318462P.

XX 12-SEP-2001; 2001US-0318770P.

XX 27-SEP-2001; 2001US-0325430P.

XX 18-OCT-2001; 2001US-0330380P.

XX 31-OCT-2001; 2001US-0335301P.

XX 14-NOV-2001; 2001US-0332172P.

XX 14-NOV-2001; 2001US-0332271P.

XX 14-NOV-2001; 2001US-0332272P.

XX 14-NOV-2001; 2001US-0333184P.

XX 21-NOV-2001; 2001US-0333272P.

XX 21-NOV-2001; 2001US-0332094P.

XX 03-DEC-2001; 2001US-0337426P.

XX 03-DEC-2001; 2001US-0338092P.

XX 04-DEC-2001; 2001US-0337185P.

2002US-0345705P.
2002US-00092900.

EN CORP.

Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
Gangolli E, Vernet CM, Guo X, Tchernev V;
Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Catterton E, Burgess C, Leite M, Zhong H, Alsbrook JP;
Ieger DK;
332/78.
119.

ides and polynucleotides, useful for preventing or treating
sociated with aberrant NOVX expression or activity e.g.,
tension, atherosclerosis, cardiomyopathy or bronchial

323; 1103pp; English.

n describes novel human NOVX polypeptides which have
aridant, antiarteriosclerotic, antiasthmatic and hypotensive
rmaceutical compositions comprising the NOVX proteins or
molecules or NOVX antibodies are useful for preventing or
sorder associated with aberrant NOVX expression or activity
ypertension, atherosclerosis, cardiomyopathy or bronchial
roducts of the invention can be used for gene therapy or in
J65041-ABU65218 represent the NOVX polypeptides encoded by
7185

AA;

arity 1.9%; Score 10; DB 5; Length 1390;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

QPQPPP 235

QPQPPP 986

dard; protein; 1461 AA.

(first entry)

ans essential protein SEQ ID NO 7629.

ction; DNA replication; cell division; growth;
; Candida albicans; fungicide; antifungal.

ans.

2.

2001WO-US049486.

2000US-0259128P.

2001US-00792024.

2001US-0314050P.

A PHARM INC.

ang B, Boone C, Bussey H, Ohlsen KL;

DR

XX WPI; 2002-566694/60.

XX N-PSDB; ABZ32342.

PT Constructing strains for identifying gene products as effective t
PT for therapeutic intervention, by inactivating in the strain one a
PT a gene and placing other allele of the gene under conditional exp
XX Claim 44; SEQ ID NO 7629; 167pp + Sequence Listing; English.

XX The invention relates to constructing (M1) a strain of diploid fu
CC cells in which both alleles of a gene are modified, comprising mo
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterolo
CC promoter, so that expression of the second allele is regulated by
CC promoter. (M1) is useful for constructing a strain of diploid fun
CC cells in which both alleles of a gene are modified. The diploid f
CC cells having both alleles modified are useful for identifying a g
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a
CC that contributes to the resistance of a diploid fungus to an anti
CC agent, an antifungal agent that inhibits the growth of a diploid
CC and for identifying a therapeutic agent for treatment of a mammal
CC disease. (M1) is useful for identifying a compound which modulate
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell divi
CC activity. The method is useful for identifying a compound having a
CC ability to inhibit growth or proliferation of C. albicans cells a
CC treating infection by C. albicans. The present sequence is that o
CC essential Candida albicans protein used in the method of the inve
CC Note: The sequence data for this patent is not represented in the
CC specification but is based on sequence information supplied to De
CC the European Patent Office

XX Sequence 1461 AA;

Query Match 1.9%; Score 10; DB 5; Length 1461;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

OY 334 DDEDEDEDD 343

Db 1436 DDEDEDEDD 1445

RESULT 71

ABB08801
ID ABB08801 standard; protein; 1887 AA.

XX AC ABB08801;

XX 27-MAY-2002 (first entry)

DE Yeast fatty acid synthetase SEQ ID NO 1.

XX Yeast; fatty acid synthetase; ethyl caproate; fermentation; enzym

XX Saccharomyces cerevisiae.

XX JP2002027989-A.

XX 29-JAN-2002.

XX 17-JUL-2000; 2000JP-00215908.

XX 17-JUL-2000; 2000JP-00215908.

XX (YAMA-) YAMAGUCHI KEN.

XX (YAMA-) YAMAGUCHI TLO YG.

XX WPI; 2002-248227/30.

XX N-PSDB; ABL54551.

ast for improved productivity of ethyl caproate, and for
, comprises a mutated fatty acid synthetase gene.

8-12; 28pp; Japanese.

relates to recombinant yeast with improved productivity of
by introducing mutations into fatty acid synthetase
e yeast is used for improved productivity of ethyl caproate
sing the fermentation characteristic features of yeast. The
ce is that of the yeast fatty acid synthetase gene

AA;

1.9%; Score 10; DB 5; Length 1887;

ity 100.0%; Pred. No. 20;

servative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146

|||||

AAAPA 134

ard; protein; 1887 AA.

first entry)

id synthetase mutant G1250Q.

id synthetase; ethyl caproate; fermentation; enzyme;

cerevisiae.

Location/Qualifiers

a 1250

/note= "Wild-type Gly substituted by Gln"

000JP-00215908.

000JP-00215908.

CHI KEN.

CHI TLO YG.

27/30.

ast for improved productivity of ethyl caproate, and for
, comprises a mutated fatty acid synthetase gene.

28pp; Japanese.

relates to recombinant yeast with improved productivity of
by introducing mutations into fatty acid synthetase
e yeast is used for improved productivity of ethyl caproate
sing the fermentation characteristic features of yeast. The
ce is that of the yeast fatty acid synthetase mutant. Note:
quence is not shown in the specification but is derived
, fatty acid synthetase sequence given as SEQ ID NO 1, Page

AA;

1.9%; Score 10; DB 5; Length 1887;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 137 PAPVAAAAPA 146

Db 125 PAPVAAAAPA 134

RESULT 73

ABB08803

ID ABB08803 standard; protein; 1887 AA.

XX

AC ABB08803;

XX

DT 27-MAY-2002 (first entry)

XX

DE Yeast fatty acid synthetase mutant G1250A.

XX

KW Yeast; fatty acid synthetase; ethyl caproate; fermentation; enzyme
mutant; mutein.

KW

OS Saccharomyces cerevisiae.

OS

XX Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1250

FT /note= "Wild-type Gly substituted by Ala"

XX

PN JP2002027989-A.

XX

PD 29-JAN-2002.

XX

PF 17-JUL-2000; 2000JP-00215908.

XX

PR 17-JUL-2000; 2000JP-00215908.

XX

PA (YAMA-) YAMAGUCHI KEN.

PA (YAMA-) YAMAGUCHI TLO YG.

XX

DR WPI; 2002-248227/30.

XX

PT Recombinant yeast for improved productivity of ethyl caproate, and
producing food, comprises a mutated fatty acid synthetase gene.

PT

XX

PS Claim 1; Page; 28pp; Japanese.

XX

CC The invention relates to recombinant yeast with improved productiv
ethyl caproate by introducing mutations into fatty acid synthet
(ABB08801). The yeast is used for improved productivity of ethyl c
without decreasing the fermentation characteristic features of yea
CC present sequence is that of the yeast fatty acid synthetase mutant
CC The present sequence is not shown in the specification but is deri
CC from the yeast fatty acid synthetase sequence given as SEQ ID NO 1
CC 8-12 (ABB08801)

XX

SQ Sequence 1887 AA;

Query Match

Best Local Similarity 1.9%; Score 10; DB 5; Length 1887;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 137 PAPVAAAAPA 146

Db 125 PAPVAAAAPA 134

RESULT 74

ABB08805

ID ABB08805 standard; protein; 1887 AA.

XX

AC ABB08805;

XX

DT 27-MAY-2002 (first entry)

cid synthetase mutant G1250C.
acid synthetase; ethyl caproate; fermentation; enzyme;
a.
cerevisiae.
Location/Qualifiers
ce 1250
/note= "Wild-type Gly substituted by Cys"
A.
2000JP-00215908.
2000JP-00215908.
UCHI KEN.
UCHI TLO YG.
227/30.
east for improved productivity of ethyl caproate, and for
i, comprises a mutated fatty acid synthetase gene.
; 28pp; Japanese.
relates to recombinant yeast with improved productivity of
e By introducing mutations into fatty acid synthetase
ne yeast is used for improved productivity of ethyl caproate
asing the fermentation characteristic features of yeast. The
ace is that of the yeast fatty acid synthetase mutant. Note:
sequence is not shown in the specification but is derived
t, fatty acid synthetase sequence given as SEQ ID NO 1, Page
1)
AA;
1.9%; Score 10; DB 5; Length 1887;
arity 100.0%; Pred. No. 20;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAA 146
|||||
AAAAA 134
iard; protein; 1887 AA.
(first entry)
cid synthetase mutant G1250T SEQ ID NO 5.
acid synthetase; ethyl caproate; fermentation; enzyme;
n.
cerevisiae.
Location/Qualifiers
ce 1250
/note= "Wild-type Gly substituted by Thr"
A.
The invention relates to recombinant yeast with improved producti-

29-JAN-2002.
17-JUL-2000; 2000JP-00215908.
17-JUL-2000; 2000JP-00215908.
(YAMA-) YAMAGUCHI KEN.
(YAMA-) YAMAGUCHI TLO YG.
WPI; 2002-248227/30.
N-PSDB; ABL54554.
Recombinant yeast for improved productivity of ethyl caproate, an
producing food, comprises a mutated fatty acid synthetase gene.
Claim 1; Page 20-27; 28pp; Japanese.
The invention relates to recombinant yeast with improved producti
ethyl caproate by introducing mutations into fatty acid synthetase
(ABB08801). The yeast is used for improved productivity of ethyl
CC without decreasing the fermentation characteristic features of ye
CC present sequence is that of the yeast fatty acid synthetase mutan
XX
XX Sequence 1887 AA;
Query Match 1.9%; Score 10; DB 5; Length 1887;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 137 PAPVAAAAPA 146
Db 125 PAPVAAAAPA 134
|||||
RESULT 76
ABB08806
ID ABB08806 standard; protein; 1887 AA.
XX
AC ABB08806;
XX
XX 27-MAY-2002 (first entry)
DT
XX
DE Yeast fatty acid synthetase mutant G1250Y.
XX
XX Yeast; fatty acid synthetase; ethyl caproate; fermentation; enzym
KW mutant; mutain.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1250
FT /note= "Wild-type Gly substituted by Tyr"
XX
BN JP2002027989-A.
XX
XX 29-JAN-2002.
PD
XX
PF 17-JUL-2000; 2000JP-00215908.
XX
PR 17-JUL-2000; 2000JP-00215908.
XX
PA (YAMA-) YAMAGUCHI KEN.
PA (YAMA-) YAMAGUCHI TLO YG.
XX
DR WPI; 2002-248227/30.
DR N-PSDB; ABL54554.
XX
PT Recombinant yeast for improved productivity of ethyl caproate, an
PT producing food, comprises a mutated fatty acid synthetase gene.
XX
PS Claim 1; Page 20-27; 28pp; Japanese.
XX
CC The invention relates to recombinant yeast with improved producti
ethyl caproate by introducing mutations into fatty acid synthetase
(ABB08801). The yeast is used for improved productivity of ethyl
CC without decreasing the fermentation characteristic features of ye
CC present sequence is that of the yeast fatty acid synthetase mutan
XX
XX Sequence 1887 AA;
Query Match 1.9%; Score 10; DB 5; Length 1887;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 137 PAPVAAAAPA 146
Db 125 PAPVAAAAPA 134
|||||
RESULT 76
ABB08806
ID ABB08806 standard; protein; 1887 AA.
XX
AC ABB08806;
XX
XX 27-MAY-2002 (first entry)
DT
XX
DE Yeast fatty acid synthetase mutant G1250Y.
XX
XX Yeast; fatty acid synthetase; ethyl caproate; fermentation; enzym
KW mutant; mutain.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1250
FT /note= "Wild-type Gly substituted by Tyr"
XX
BN JP2002027989-A.
XX
XX 29-JAN-2002.
PD
XX
PF 17-JUL-2000; 2000JP-00215908.
XX
PR 17-JUL-2000; 2000JP-00215908.
XX
PA (YAMA-) YAMAGUCHI KEN.
PA (YAMA-) YAMAGUCHI TLO YG.
XX
DR WPI; 2002-248227/30.
XX
PT Recombinant yeast for improved productivity of ethyl caproate, an
PT producing food, comprises a mutated fatty acid synthetase gene.
XX
PS Claim 1; Page; 28pp; Japanese.
XX
CC The invention relates to recombinant yeast with improved producti-

by introducing mutations into fatty acid synthetase
 yeast is used for improved productivity of ethyl caproate
 sing the fermentation characteristic features of yeast. The
 ce is that of the yeast fatty acid synthetase mutant. Note:
 quence is not shown in the specification but is derived
 fatty acid synthetase sequence given as SEQ ID NO 1, Page

AA;

1.9%; Score 10; DB 5; Length 1887;

ity 100.0%; Pred. No. 20; Indels 0; Gaps 0;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
 |||||
 AAAPA 134

lard; protein; 1887 AA.

first entry)

id synthetase mutant G1250F.

cid synthetase; ethyl caproate; fermentation; enzyme;

cerevisiae.

Location/Qualifiers

e 1250

/note= "Wild-type Gly substituted by Phe"

000JP-00215908.

000JP-00215908.

CHI KEN.

CHI TLO YG.

27/30.

ast for improved productivity of ethyl caproate, and for
 , comprises a mutated fatty acid synthetase gene.

28pp; Japanese.

relates to recombinant yeast with improved productivity of
 by introducing mutations into fatty acid synthetase
 e yeast is used for improved productivity of ethyl caproate
 sing the fermentation characteristic features of yeast. The
 ce is that of the yeast fatty acid synthetase mutant. Note:
 quence is not shown in the specification but is derived
 fatty acid synthetase sequence given as SEQ ID NO 1, Page

AA;

1.9%; Score 10; DB 5; Length 1887;

ity 100.0%; Pred. No. 20;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146

|||||
 125 PAFVAAAAPA 134

RESULT 78

ABR52621
 ID ABR52621 standard; protein; 1887 AA.

XX

AC ABR52621;

XX

DT 20-JUN-2003 (first entry)

XX

DE Protein sequence #SEQ ID 107.

XX

KW Multiprotein complex; eukaryote; drug target; diagnosis.

XX

OS Saccharomyces cerevisiae.

XX

PN EP1258494-A1.

XX

PD 20-NOV-2002.

XX

PF 20-DEC-2001; 2001EP-00130253.

XX

PR 15-MAY-2001; 2001EP-00111774.

XX

PA (CELL-) CELLZONE AG.

XX

PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;

PI Marzioch M, Schultz JD, Superti-Furga GD;

XX

DR WPI; 2003-250078/25.

XX

DR N-PSDB; ACC60663.

XX

PT New isolated protein complexes useful for diagnosing a disease or
 disorder, or as a target for an active agent of a pharmaceutical,
 PT preferably a drug target in the treatment or prevention of disease
 disorder.

XX

PS Disclosure; SEQ ID NO 107; 17pp + Sequence Listing; English.

XX

CC The invention relates to multiprotein complexes from eukaryotes. I
 of the invention and DNA sequences encoding them are given in rec
 CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complex
 CC obtainable by using a protein as a bait and isolating the set of I
 CC which is attached thereto from cells. Such protein complexes may c
 CC up to 30 distinct proteins. Protein complexes of the invention are
 CC for diagnosing a disease or disorder, or as a target for an active
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for t
 CC patent is not represented in the printed specification, but is bas
 CC sequence information supplied by the European Patent Office. The c
 CC document is available on CD-ROM

XX Sequence 1887 AA;

Query Match

Best Local Similarity 1.9%; Score 10; DB 6; Length 1887;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 137 PAFVAAAAPA 146

|||||

DB 125 PAFVAAAAPA 134

RESULT 79

ABU88253

ID ABU88253 standard; protein; 1894 AA.

XX

AC ABU88253;

XX

DT 07-JUL-2003 (first entry)

XX

secreted and transmembrane PRO polypeptide #1.
ed and transmembrane protein: PRO; gene therapy;
is factor-alpha release; TNF-alpha release;
roliferation; chondrocyte differentiation; tumour;
ur; lung tumour; colon tumour; breast tumour;
ur; rectal tumour; cervical tumour; liver tumour.

A1.

2002US-00183012.

97US-0059263P.
97US-0059266P.
97US-0062250P.
97US-0063486P.
97US-0063120P.
97US-0063121P.
97US-0063540P.
97US-0063541P.
97US-0063544P.
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PR 28-MAY-1998; 98US-0087098P.
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PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.

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1.9%; Score 10; DB 6; Length 1894;

identity 100.0%; Pred. No. 20;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

TAAAA 22

|||||

TAAAA 1060

ard; protein; 1894 AA.

first entry)

creted and transmembrane PRO protein #1.

erapy; tissue typing; tumour; chondrocyte proliferation;
 fferentiation; tumour necrosis factor-alpha release;
 ication.

XX
 PN US2003036147-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 02-JUL-2002; 20C2US-00187741.
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 PR 18-SEP-1997; 97US-0059263P.
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98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
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Db 1051 AAAATTAAAA 1060

RESULT 81

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ID ABU96434 standard; protein; 1894 AA.

XX AC ABU96434;

XX DT 25-JUL-2003 (first entry)

XX DE Novel human secreted and transmembrane protein #1.

XX KW Human; secreted and transmembrane protein; PRO; transgenic animal
knockout; chromosome identification; tissue typing; tumour;
XX KW chondrocyte proliferation; chondrocyte differentiation;
tumor necrosis factor-alpha release stimulator.

XX OS Homo sapiens.

XX PN US2003036144-A1.

XX PD 20-FEB-2003.

XX PF 01-JUL-2002; 2002US-00187601.

[illegible]


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(first entry)

creted and transmembrane protein #1.

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timulator; tumour; adrenal tumour; lung tumour;
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ur; liver tumour; TNF-alpha release;
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KW	chondrocyte stimulator; tumour; adrenal tumour; lung tumour;		
KW	colon tumour; breast tumour; prostate tumour; rectal tumour;		
KW	cervical tumour; liver tumour; chromosome identification.		
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OS	Homo sapiens.		
XX			
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PD	23-JAN-2003.		
XX			
PF	21-JUN-2002; 2002US-00176915.		
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TAAAA 22

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TAAAA 1060

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first entry)

creted and transmembrane PRO protein #1.

erapy; chromosome identification; tissue typing.

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 XX PD 13-FEB-2003.
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(first entry)

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first entry)

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Db 1051 AAAATTAAAA 1060

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KW	tumour.

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first entry)

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imulatur; chromosome mapping; gene mapping; tumour.

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Db 1051 AAAATTAAAA 1060

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XX AC ABU93914;
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KW tumour necrosis factor alpha.
XX Homo sapiens.
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XX 13-FEB-2003.

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 00US-00946374.
 00US-00052586.

ECH INC.

n J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 V, Watanabe CK, Wood WI, Zhang Z;

73/32.

and five nucleic acids encoding PRO polypeptides, useful
 cure of a medicament for diagnosing or treating tumor or
 or detecting expression of an associated gene.

Q ID NO 613; 707pp; English.

XX The invention relates to three hundred and five nucleic acids encod
 CC PRO polypeptides (secreted and transmembrane). The PRO nucleic aci
 CC polypeptides are useful for the manufacture of a medicament for
 CC diagnosing or treating tumour in a mammal, for measuring or detect
 CC expression of an associated gene, for stimulation of chondrocytes
 CC stimulating the release of tumour necrosis factor alpha (TNF-alpha)
 CC human blood. The present sequence represents the amino acid sequen
 CC secreted and transmembrane PRO protein. Note: The sequence data fr
 CC patent did not form part of the printed specification but was obtai
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030032199
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 SQ Sequence 1894 AA;
 Query Match 1.9%; Score 10; DB 6; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 20;
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 Db 1051 AAAATTAAAA 1060
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 XX
 DT 01-JUL-2003 (first entry)
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 XX
 KW Human; secreted and transmembrane protein; PRO; chromosome mapping
 KW gene mapping; transgenic animal; knockout animal; tissue typing; t
 KW chondrocyte cell proliferation; gene therapy;
 KW chondrocyte cell differentiation; tumour necrosis factor-alpha re
 XX
 OS Homo sapiens.
 XX
 PN US2003022300-A1.
 XX
 PD 30-JAN-2003.
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 PF 25-JUN-2002; 2002US-00180552.
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 PR 17-OCT-1997; 97US-0062250P.
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first entry)

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ping; gene mapping; tumor necrosis factor-alpha; blood;
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oliferation stimulator; tumour; tissue typing.

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XX PF 02-JUL-2002; 2002US-00188769.
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(first entry)

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Query Match 1.9%; Score 10; DB 6; Length 1894;
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QY 13 AAAATTAAAA 22
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 Db 1051 AAAATTAAAA 1060

RESULT 98

ABU87108
 ID ABU87108 standard; protein; 1894 AA.

XX
 AC ABU87108;

XX
 DT 02-JUL-2003 (first entry)

DE Novel human secreted and transmembrane protein #1.
 XX Human; secreted and transmembrane protein; PRO; cyostatic; gene t

KW

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ITAAAA 22

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(first entry)

secreted and transmembrane protein #1.

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 a therapy; TNF-alpha release;
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 differentiation; tumour; adrenal tumour; lung tumour;
 Breast tumour; prostate tumour; rectal tumour;
 ir; liver tumour.

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 XX 98US-0098014P.
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US2003036154-A1.

20-FEB-2003.

02-JUL-2002; 2002US-00187757.

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Query Match 1.9%; Score 10; DB 6; Length 1894;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gz

QY 13 AAAATTAAAA 22
Db 1051 AAAATTAAAA 1060

RESULT 100
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ID ABU90442 standard; protein; 1894 AA.

XX AC ABU90442;
XX AC ABU90442;
DT 11-AUG-2003 (first entry)
XX Novel human secreted and transmembrane PRO protein #1.
XX Human; gene therapy; tumour necrosis factor-alpha release; TNF;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW tissue typing.
XX Homo sapiens.
XX US2003036153-A1.
PN 20-FEB-2003.
XX 02-JUL-2002; 2002US-00187754.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.

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 98US-00168978.

1.9%; Score 10; DB 6; Length 1894;

ity 100.0%; Pred. No. 20;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

TAAAA 22

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TAAAA 1060

ard; protein; 1894 AA.

first entry)

creted and transmembrane PRO protein #1.

typing; tumour; chondrocyte stimulator; gene therapy;
 s factor-alpha release; affinity purification.

1.

002US-00199464.

97US-0059263P.
 97US-0059266P.
 97US-0062250P.
 97US-0063486P.
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 97US-0063564P.
 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.
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 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
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 PR 12-DEC-1997; 97US-0069335P.
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PR 18-SEP-1998; 98US-0101068P.
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 PR 01-OCT-1998; 98US-0102684P.
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 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98US-0103395P.

Query Match 1.9%; Score 10; DB 6; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
 Db 1051 AAAATTAAAA 1060

RESULT 102

ABO5229

ID ABO5229 standard; protein; 1894 AA.

XX AC ABO5229;
 XX AC

DT 12-AUG-2003 (first entry)
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DE Novel human secreted and transmembrane PRO protein #1.
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KW Human; gene therapy; tumour necrosis factor-alpha; tumour;
 OS chondrocyte stimulation; tissue typing.
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OS Homo sapiens.
 XX

PN US2003008352-A1.
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PD 09-JAN-2003.
 XX

PF 18-JUN-2002; 2002US-00174590.
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PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
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 PR 28-OCT-1997; 97US-0063540P.
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 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 11-DEC-1997; 97US-0066772P.
 PR 97US-0069335P.

ECH INC.

n J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
V, Watanabe CK, Wood WI, Zhang Z;

DR	WPI; 2003-341327/32.
XX	
XX	
PT	New PRO polypeptides and nucleic acids encoding the polypeptides,
PT	in gene therapy, chromosome identification, tissue typing, or as
PT	hybridization probes in chromosome and gene mapping.
XX	
PS	Disclosure; SEQ ID NO 613; 708pp; English.
XX	
CC	The invention relates to an isolated PRO polypeptide. The PRO nuc
CC	sequences are useful as hybridisation probes in chromosome and ge
CC	mapping, for stimulating the release of tumour necrosis factor-al
CC	stimulating proliferation or differentiation of chondrocyte cells
CC	detecting the presence of tumour in a mammal, or in generating an
CC	rNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC	polypeptides, in assays to identify other proteins or molecules i
CC	in binding reaction, to generate transgenic animals or knockout a
CC	which in turn are useful in the development and screening of
CC	therapeutically useful reagents, for chromosome identification an
CC	typing. The PRO polypeptides and nucleic acid molecules are also
CC	in gene therapy, and as molecular weight markers for protein
CC	electrophoresis purposes. The anti-PRO antibodies may be used in
CC	diagnostic assays for PRO, or for the affinity purification of PR
CC	recombinant cell culture or natural sources. The present sequence
CC	represents the amino acid sequence of a secreted and transmembran
CC	polypeptide
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XX	
QQ	Sequence 1894 AA;
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QQ	Query Match 1.9%; Score 10; DB 6; Length 1894;
XX	
PT	Best Local Similarity 100.0%; Pred.No. 20;
PT	Matches 10; Conservative 0; Mismatches 0; Indels 0; G;
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QY	13 AAAATTAAAA 22
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DB	1051 AAAATTAAAA 1060
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AC	AAAB76534;
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DT	11-APR-2001 (first entry)
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DE	
DE	Corynebacterium glutamicum MCT protein SEQ ID NO:50.
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KW	Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
KW	membrane construction and membrane transport protein; petroleum si
KW	hydrocarbon degradation; gram positive aerobic bacterium; marker;
KW	identification; microorganism; fine chemical production; transform
KW	genome mapping; genetic engineering.
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OS	Corynebacterium glutamicum.
XX	
PN	WO200100805-A2.
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XX	04-JAN-2001.
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PF	23-JUN-2000; 2000WO-IB000926.
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XX	25-JUN-1999; 99US-0141031P.
PPR	08-JUL-1999; 99DE-01031454.
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PPR	08-JUL-1999; 99DE-01031563.
PPR	09-JUL-1999; 99DE-01032122.
PPR	09-JUL-1999; 99DE-01032124.
PPR	09-JUL-1999; 99DE-01032125.
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PPR	09-JUL-1999; 99DE-01032182.
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PPR	09-JUL-1999; 99DE-01032191.

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99DE-01042078.
99DE-01042079.
99DE-01042088.

AG.

Kroeger B, Schroeder H, Zelder O, Haberhauer G;

486/08.
767.

A glutamicum nucleic acids encoding membrane construction transport proteins or their portions, useful for typing or glutamicum or related bacteria, and as markers for a.

a 224-231; 1119pp; English.

AF68080 encode the Corynebacterium glutamicum membrane and membrane transport (MCT) proteins given in AAB76510 to MCT nucleic acids and proteins are useful in the a of microorganisms which can be used to produce fine r modulating fine chemical production in C. glutamicum or cia (e.g. Brevibacterium lactofermentum), the typing or i of C. glutamicum or related bacteria, as reference points i glutamicum genome, and as markers for transformation. iAF68082 represent sequencing primers which are used in an the present invention

AA;

1.9%; Score 10; DB 4; Length 2012;
arity 100.0%; Pred. No. 21;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPPA 146
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AAAPPA 1675

iard; protein; 2993 AA.

(first entry)

protein fragment SEQ ID NO: 6239.

terium; amino acid synthesis; vitamin; saccharide;
ynthesis.

OS Corynebacterium glutamicum.
XX EP1108790-A2.
PN 20-JUN-2001.
PD 18-DEC-2000; 2000EP-00127688.
XX 16-DEC-1999; 99JP-00377484.
PF 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
PI MPI; 2001-376931/40.
DR N-FSDB; AAH67704.

PT Novel polynucleotides derived from Coryneform bacteria, for ident
mutation point of a gene, measuring expression of a gene, analyzi
expression profile or pattern of a gene and identifying homologou
XX Claim 17; SEQ ID NO 6239; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein
sequences from the Coryneform bacterium Corynebacterium glutamicu
are useful for identifying the mutation point of a gene derived f
mutant of coryneform bacterium, measuring expression amount and a
the expression profile or expression pattern of a gene derived fr
Coryneform bacterium, and identifying a homologue of a gene deriv
Coryneform bacterium. Coryneform bacteria are useful for produc
acids, nucleic acids, vitamins, saccharides and organic acids,
particularly L-lysine. The present sequence is a protein describe
exemplification of the invention. Note: The sequence data for thi
did not form part of the printed specification, but was obtained
XX electronic format directly from the European Patent Office
SQ Sequence 2993 AA;

Query Match 1.9%; Score 10; DB 4; Length 2993;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 137 PAPVAAAAPA 146
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Db 1696 PAPVAAAAPA 1705

RESULT 105
AAG34648

ID AAG34648 standard; protein; 43 AA.

XX AAG34648;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 42193.

XX Protein identification; signal transduction pathway; metabolic pat
KW hybridisation assay; genetic mapping; gene expression control; pr
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

99US-0123180P.
99US-0123548P.
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99US-0162142P.

1.7%; Score 9; DB 3; Length 43;
arity 100.0%; Pred. No. 6.8;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
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AAAPA 35

dard; protein; 49 AA.

(first entry)
haliana protein fragment SEQ ID NO: 66991.
ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
equence.
haliana.

200HEP-00301439.

99US-0121825P.
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PR	21-OCT-1999;	99US-0160767P.
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PR	21-OCT-1999;	99US-0160814P.
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PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
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PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match

1.7%; Score 9; DB 3; Length 49;

Best Local Similarity 100.0%; Pred.No.7.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G2

QY	138 APVAAAAPA 146
Db	27 APVAAAAPA 35

RESULT 107

AAGS2700

ID AAGS2700 standard; protein; 51 AA.

XX

AC AAGS2700;

XX

DT 18-OCT-2000 (first entry)

XX

DE DE

XX

KW Arabidopsis thaliana protein fragment SEQ ID NO: 67021.

KW Protein identification; signal transduction pathway; metabolic pat

KW hybridisation assay; genetic mapping; gene expression control; pro

XX

XX termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

XX

PR 25-FEB-1999; 99US-0121825P.

PR

PR 05-MAR-1999; 99US-0123180P.

PR

PR 09-MAR-1999; 99US-0123548P.

PR

PR 23-MAR-1999; 99US-0125788P.

PR

PR 25-MAR-1999; 99US-0128264P.

PR

PR 29-MAR-1999; 99US-0126785P.

PR

PR 01-APR-1999; 99US-0127462P.

PR

PR 06-APR-1999; 99US-0128234P.

PR

PR 08-APR-1999; 99US-0128714P.

PR

PR 16-APR-1999; 99US-0129845P.

PR

PR 19-APR-1999; 99US-0130077P.

PR

PR 21-APR-1999; 99US-0130449P.

PR

PR 23-APR-1999; 99US-0130510P.

PR

PR 23-APR-1999; 99US-0130891P.

PR

PR 28-APR-1999; 99US-0131449P.

PR

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99US-0160767P.
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99US-0162142P.

1.7%; Score 9; DB 3; Length 51;
city 100.0%; Pred. No. 7.8;
servative 0; Mismatches 0; Indels 0; Gaps 0;

APA 146
|||||
APA 35

ard; protein; 52 AA.

(first entry)

erived DXFzphutel_22n2 homologue #2.

arapy; vaccine; disease treatment; detection.

000WO-IB001496.
99US-0149499P.
99US-0156503P.

HUMAN GENOME PROJECT.

40/34.

having the sequences of clones isolated from libraries of
n tissues, useful in recombinant DNA methodologies.

age 519; 1095pp; English.

describes novel polynucleotides and polypeptides isolated
A libraries which can be used for gene therapy or in
polynucleotides of the invention and antibodies encoded by
ed in the prevention, diagnosis and treatment of diseases
h inappropriate polypeptide expression. The products of the
also be used to identify modulators of expression and
o down regulate expression and activity. The antibodies of
may also be used as diagnostic agents for detecting the
lypeptides in samples. This sequence represents a homologue
de described in the disclosure of the invention

XX
SQ Sequence 52 AA;

Query Match 1.7%; Score 9; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 7.9; Indels 0; Ga
Matches 9; Conservative 0; Mismatches 0; Indels 0; Ga

QY 330 EEEEDDEDE 338
|||||
Db 3 EEEEDDEDE 11

RESULT 109

AAG01387
ID AAG01387 standard; protein; 66 AA.

XX
AC AAG01387;

XX
DT 06-OCT-2000 (first entry)

XX
DE Human secreted protein, SEQ ID NO: 5468.

XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isol
KW gene therapy; chromosome mapping.

XX
OS Homo sapiens.

XX
PN EP1033401-A2.

XX
PD 06-SEP-2000.

XX
PF 21-FEB-2000; 2000EP-00200610.

XX
PR 26-FEB-1999; 99US-0122487P.

XX
PA (GEST) GENSET.

XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX
DR WPI; 2000-500381/45.

XX
DR N-PSDB; AAC01393.

XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedur

XX
PS Claim 13; SEQ ID NO 5468; 71pp + Sequence Listing; English.

XX
CC The present sequence is a polypeptide encoded by one of a large nu
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC prepared from total human RNAs or polyA+ RNAs derived from 30 diff
CC tissues. EST sequences usually correspond mainly to the 3' untrans
CC region (UTR) of the mRNA because they are often obtained from olig
CC primed cDNA libraries. Such ESTs are not well suited for isolating
CC sequences derived from the 5' ends of mRNAs and even in those case
CC longer cDNA sequences have been obtained, the full 5' UTR is rare
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and c
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5'
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory se
CC and to design expression and secretion vectors

XX
SQ Sequence 66 AA;

Query Match 1.7%; Score 9; DB 3; Length 66;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Ga

QY 221 PQQQQPPPP 229
|||||
Db 22 PQQQQPPPP 30

dard; protein; 68 AA.

(first entry)

Italiana protein fragment SEQ ID NO: 42272.

ification; signal transduction pathway; metabolic pathway; assay; genetic mapping; gene expression control; promoter; sequence.

haliana.

2000EP-00301439.

99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
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99US-0130077P.
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1.7%; Score 9; DB 3; Length 68;
rity 100.0%; Pred. No. 9.9;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAPA 146
|||||
AAPA 35

ard; protein; 68 AA.

first entry)

XX DE 99US-0149929P.
XX DE 99US-0149902P.
XX KW 99US-0150566P.
XX KW 99US-0150884P.
XX KW 99US-0151065P.
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XX PR 99US-0162142P.

Arabidopsis thaliana protein fragment SEQ ID NO: 33815.
Protein identification; signal transduction pathway; metabolic pat
hybridisation assay; genetic mapping; gene expression control; prc
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-00301439.

25-FEB-1999; 99US-0121825P.
05-MAR-1999; 99US-0123180P.
09-MAR-1999; 99US-0123548P.
23-MAR-1999; 99US-0125788P.
25-MAR-1999; 99US-0126264P.
29-MAR-1999; 99US-0126785P.
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AC AAG52668;

DT 18-OCT-2000 (first entry)

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XX	Protein identification; signal transduction pathway; metabolic pa
KW	hybridisation assay; genetic mapping; gene expression control; pr
KW	termination sequence.
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1.7; Score 9; DB 3; Length 68;
arity 100.0%; Pred.No. 9.9;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 146
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AAAA 35

dard; protein; 68 AA.

(first entry)

haliana protein fragment SEQ ID NO: 66994.

ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

haliana.

2000EP-00301439.

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Query Match 1.7%; Score 9; DB 3; Length 68;
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DT 17-OCT-2000 (first entry)
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KW termination sequence.
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99US-0162142P.

1.7%; Score 9; DB 3; Length 68;
arity 100.0%; Pred.No. 9.9;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
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AAAPA 35

dard; protein; 69 AA.

(first entry)

haliana protein fragment SEQ ID NO: 52226.

ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

haliana.

2000EP-00301439.

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Query Match 1.7%; Score 9; DB 3; Length 69;
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QY 138 APVAAAAPA 146
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 Db 27 APVAAAAPA 35

RESULT 116

AAG34561
 ID AAG34561 standard; protein; 70 AA.

XX AC AAG34561;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 42072.

XX KW Protein identification; signal transduction pathway; metabolic p
 hybridisation assay; genetic mapping; gene expression control; p
 termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

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PR 16-APR-1999; 99US-0129845P.

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1.7%; Score 9; DB 3; Length 70;
Identity 100.0%; Pred. No. 10;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 146
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AAAAA 35

indard; protein; 74 AA.

(first entry)

thaliana protein fragment SEQ ID NO: 42192.

cification; signal transduction pathway; metabolic pathway;
1 assay; genetic mapping; gene expression control; promoter;
sequence.

thaliana.

2000EP-00301439.

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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
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Query Match 1.7%; Score 9; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
Qy 138 APVAAAAAPA 146
Db 58 APVAAAAAPA 66
RESULT 118
AAR22394
ID AAR22394 standard; protein; 76 AA.
XX AC AAR22394;
XX 25-MAR-2003 (revised)
DT 17-AUG-1992 (first entry)
XX Antigen tc-10a.
XX Oocysts; MAB 12-07; sporozoite.
XX Eimeria tenella.
XX WO204460-A.
XX 19-MAR-1992.
XX 05-SEP-1991; 91WO-US006430.
XX 12-SEP-1990; 90US-00581693.
XX (GEMX) GENEX CORP.
XX Jacobson JW, Strausberg RL, Wilson SD, Pope SH, Strausberg SI
PI Ruff MD, Augustine PC, Danforth HD;
XX WPI; 1992-114365/14.
XX N-PSDB; AAQ23094.
XX Vaccine against avian coccidiosis - comprising recombinant eimer
PT antigen ac-18 or ac-6b gene, or microorganisms expressing them.
XX Claim 10; Page 39 + Fig 10; 56pp; English.
XX To identify antigens of E. tenella, expression libraries were pri
CC lambda vector, lambda gt11, using cDNA prep. from polyA mRNA is
CC from E. tenella oocysts. The cDNA expression library was screened
CC monoclonal antibody (MAB) 12-07 which was raised against the spo
CC stage of E. tenella. The library to be screened was plated on a l
CC allows lysis and plaque formation. During induction of the anti
CC encoded by the phage, the plaques were identified by screening t
CC filters with Mab 12-07. The cDNA inserts from the MAB 12-07 posi
CC phage were cloned into bacteriophage M13 and subjected to sequen
CC analysis. Following sequence analysis, E. tenella antigen tc-10a
CC identified. (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 76 AA;
SQ
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Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
Qy 118 APVAAAAAPA 126
Db 58 APVAAAAAPA 66

AAAAA 31

dard; protein; 79 AA.

(first entry)

haliana protein fragment SEQ ID NO: 41809.

ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

haliana.

2000EP-00301439.

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KA assay; genetic mapping; gene expression control; promoter;

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CS haliana.

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sequence.
thaliana.
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Query Match 1.7%; Score 9; DB 3; Length 82;
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pa
hybridisation assay; genetic mapping; gene expression control; pr
termination sequence.
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OS Arabidopsis thaliana.
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(first entry)

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 2001US-0327380P.
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 2001US-0348165P.
 2001US-0350219P.
 2001US-0344518P.

PR 09-NOV-2001; 2001US-0345143P.
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 PR 03-DEC-2001; 2001US-0336908P.
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 XX WPI; 2003-421159/39.
 DR N-PSDB; ACC90601.
 XX New human proteins associated with cell growth, differentiation,
 PT death (CGDD), useful for diagnosing, treating and preventing dis
 PT conditions associated with the aberrant CGDD expression e.g. can
 PT AIDS, or epilepsy.
 XX Claim 1; Page 274; 350pp; English.
 PS The invention relates to an isolated polypeptide associated with
 CC growth, differentiation and death (CGDD). Also disclosed are the
 CC polynucleotides encoding the polypeptides. The polypeptides and
 CC polynucleotides are useful in diagnosing, treating and preventing
 CC diseases or conditions associated with the decreased expression
 CC expression of CGDD. Such diseases include cell proliferative (e.
 CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington
 CC disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and
 CC reproductive disorders, or disorders of the placenta. They are a
 CC useful in assessing the effects of exogenous compounds on the ex
 CC of nucleic acid and amino acid sequences of CGDD. The CGDD or it
 CC fragments are useful in screening compounds for effectiveness as
 CC agonist or antagonist of the polypeptides, or in altering the ex
 CC of the target polynucleotide and compounds that specifically bind
 CC modulate the activity of the polypeptide. Microarrays consist
 CC polynucleotides of the invention are useful in monitoring or mea
 CC protein-protein interactions, drug-target interactions, and gene
 CC expression profiles. Sequences given in records AAR69601-AAR6965
 CC represent CGDD polypeptides of the invention
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 DT 18-OCT-2000 (first entry)
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 KW Protein identification; signal transduction pathway; metabolic pa
 KW hybridisation assay; Genetic mapping; gene expression control; pr
 KW termination sequence.
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 OS Arabidopsis thaliana.
 XX
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AAAPA 146
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AAAPA 79

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(first entry)

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assay; Genetic mapping; gene expression control; promoter;
sequence.

hallana.

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PF 25-FEB-2000; 2000EP-00301439.
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(first entry)

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XX PN EPI033405-A2.

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(first entry)

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assay; genetic mapping; gene expression control; promoter;
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Query Match 1.7%; Score 9; DB 3; Length 99;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; G:

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AAAPA 66

ward; protein; 99 AA.

(first entry)

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ification; signal transduction pathway; metabolic pathway;
assay; Genetic mapping; gene expression control; promoter;
sequence.

haliana.

2008EP-00301439.

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AAAPA 146
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AAAPA 66

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XX AC AAG52671;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 66981.
XX KW Protein identification; signal transduction pathway; metabolic pa
XX KW hybridisation assay; genetic mapping; gene expression control; pr
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
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Query Match 1.7%; Score 9; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 13;
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RESULT 134

ID AAG41927 standard; protein; 100 AA.

XX AC AAG41927;

XX DT 18-OCT-2000 (first entry)

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fication; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
quence.

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99US-0162142P.

arity 1.7%; Score 9; DB 3; Length 100;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
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AAAPA 66

idard; protein; 101 AA.

(first entry)
haliana protein fragment SEQ ID NO: 42071.
ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.
haliana.
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PR 16-SEP-1999; 99US-0154039P.
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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
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PR 26-OCT-1999; 99US-0161360P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.7%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 138 APVAAAAPA 146
Db 58 APVAAAAPA 66

RESULT 136
ABG25320
ID ABG25320 standard; protein; 105 AA.
XX AC ABG25320;
XX 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #25311.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.

2000US-00649167.
 } INC.
 Liu C, Tang YT;
 1362/73.
 1507.
 polynucleotide and encoded polypeptides, useful in
 forensics, gene mapping, identification of mutations
 for genetic disorders or other traits and to assess
 } ID NO 55679; 103pp; English.
 } relates to isolated polynucleotide (I) and polypeptide (II)
 } (I) is useful as hybridisation probes, polymerase chain
 } primers, oligomers, and for chromosome and gene mapping.
 } Invariant production of (II). The polynucleotides are also used
 } as expressed sequence tags for identifying expressed
 } useful in gene therapy techniques to restore normal
 } (II) or to treat disease states involving (II). (II) is
 } generating antibodies against it, detecting or quantitating a
 } in tissue, as molecular weight markers and as a food
 } (II) and its binding partners are useful in medical imaging
 } (II). (I) and (II) are useful for treating disorders
 } aberrant protein expression or biological activity. The
 } and polynucleotide sequences have applications in
 } forensics, gene mapping, identification of mutations
 } for genetic disorders or other traits to assess biodiversity
 } for other types of data and products dependent on DNA and
 } sequences. AB00010-AB03077 represent novel human diagnostic
 } sequences of the invention. Note: The sequence data for this
 } appear in the printed specification, but was obtained in
 } format directly from WIPO at
 } pub/published_pct_sequences
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 1.7%; Score 9; DB 4; Length 105;
 Identity 100.0%; Pred. No. 14;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PAPAA 186
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 PAPAA 55
 idard; protein; 109 AA.
 (first entry)
 ein fragment SEQ ID NO: 41779.
 ification; signal transduction pathway; metabolic pathway;
 assay; genetic mapping; gene expression control; promoter;
 sequence; corn.
 sp. mayas.
 2000EP-00301439.
 99US-0121825P.
 99US-0123180P.

09-MAR-1999; 99US-0123548P.
 23-MAR-1999; 99US-0125788P.
 25-MAR-1999; 99US-0126264P.
 29-MAR-1999; 99US-0126785P.
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PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 22-OCT-1999; 99US-0160980P.
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PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 28-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.7%; Score 9; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 138 APVAAAAPA 146
| | | | |
Db 69 APVAAAAPA 77

RESULT 138

AAM19703
ID AAM19703 standard; protein; 111 AA.

XX AC AAM19703;

XX DT 12-OCT-2001 (first entry)

XX DE Peptide #6137 encoded by probe for measuring cervical gene expres
XX KW Probe; human; microarray; gene expression; cervical epithelial ce
XX KW cervical cancer.

XX OS Homo sapiens.

XX XX WO200157278-A2.

XX PD 09-AUG-2001.

XX XX 30-JAN-2001; 2001WO-US000670.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

12el DK, Chen W, Rank DR;
3901/53.
derived single exon nucleic acid probes useful for analyzing
on in human cervical epithelial cells.
ID NO 24529; 487pp; English.
vention relates to human single exon nucleic acid probes
110068-AA128459). The present sequence is a peptide encoded
probe. The SNPs are derived from human Hela cells. The SNPs
o produce a single exon microarray, which can be used for
an gene expression in a sample derived from human cervical
ills. By measuring gene expression, the probes are therefore
iding and/or staging of diseases of the cervix, notably
er. Note: The sequence data for this patent did not form
rinted specification, but was obtained in electronic format
a WIPO at ftp.wipo.int/pub/published_pct_sequences
AA;
1.7%; Score 9; DB 4; Length 111;
arity 100.0%; Pred. No. 15;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAA 126
|||||
AAAAA 29
idard; protein; 111 AA.
(first entry)
lanogaster polypeptide SEQ ID NO 39846.
evelopmental biology; cell signalling; insecticide;
il.
lanogaster.
A2.
2001WO-US009231.
2000US-0191637P.
2000US-00614150.
DRP NY.
Adams M, Li PWD, Myers BW;
5860/75.
5121.
nucleic acid detection reagent for detecting 1000 or more
rosophila and for elucidating cell signalling and cell-cell
SEQ ID NO 39846; 21pp + Sequence Listing; English.
a relates to an isolated nucleic acid detection reagent
etecting 1000 or more genes from Drosophila. The invention is
velopmental biology and in elucidating cell signalling and
eractions in higher eukaryotes for the development of
therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed D
sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737
CC ABB72072). The sequence data for this patent did not form part o
CC printed specification, but was obtained in electronic format dir
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 111 AA;
Query Match 1.7%; Score 9; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 131 PAPPPPPPAP 139
DB 68 PAPPPPPPAP 76
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RESULT 140
ABB39430
ID ABB39430 standard; peptide; 111 AA.
XX
AC ABB39430;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #6936 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid p
XX Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
PT gene expression in human foetal liver.
XX
XX PS Claim 27; SEQ ID NO 32065; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for me
CC human gene expression in a sample derived from human foetal live
CC single exon nucleic acid probes may be used for predicting, meas
CC displaying gene expression in samples derived from human foetal l
CC present sequence is a peptide encoded by a single exon nucleic a
CC of the invention. Note: The sequence data for this patent did not
CC part of the printed specification, but was obtained in electroni
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 111 AA;
Query Match 1.7%; Score 9; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 118 AAAAAAAA 126
|||||

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AAAAA 29
iardi; protein; 111 AA.
(first entry)
encoded by probe for measuring placental gene expression.
cray; human; placenta; antenatal diagnosis;
ber.
2.
2001WO-US000663.
2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
ULAR DYNAMICS INC.
zel DK, Chen W, Rank DR;
397/53.
derived single exon nucleic acid probes useful for analyzing
on in human placenta.
ID NO 33222; 654pp; English.
vention relates to single exon nucleic acid probes (SENP:
A157546). The present sequence is a peptide encoded by one
ie probes are useful for producing a microarray for
asuring and displaying gene expression in samples derived
acenta. The probes are useful for antenatal diagnosis of
disorders
AA;
arity 1.7%; Score 9; DB 4; Length 111;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAA 126
|||||
AAAAA 29
iardi; protein; 111 AA.
(first entry)
encoded by probe for measuring heart cell gene expression.
xpersion; heart; microarray; vascular system;
c disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.
XX Homo sapiens.
OS
XX WO200157274-A2.
PN
XX
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX MPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in
PT hearts.
XX
XX Claim 15; SEQ ID NO 25972; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes
CC measuring human gene expression in a sample derived from human he
CC ABA21535-ABA41305). The present sequence is a protein encoded by
CC probe. The probes may be used for predicting, measuring and displ
CC gene expression in samples derived from the human heart via micro
CC By measuring gene expression, the probes are useful for predictin
CC diagnosing, grading, staging, monitoring and prognosing diseases
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. N
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly fro
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 111 AA;
Query Match 1.7%; Score 9; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 118 AAAAAAAAAA 126
|||||
DB 21 AAAAAAAAAA 29
RESULT 143
AAW72722
ID AAW72722 standard; protein; 111 AA.
XX
XX AC AAW72722;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 3302
XX
XX KW Human; bone marrow expressed exon; gene expression analysis; prob
XX microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX OS Homo sapiens.
XX
XX PN WO200157276-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000668.

DE 2000US-0180312P.
 PF 2000US-0207456P.
 PR 2000US-00608408.
 PR 2000US-00632366.
 PR 2000US-0234687P.
 PR 2000US-0236359P.
 PR 2000GB-00024263.
 XX TULAR DYNAMICS INC.
 PF 1zel DK, Chen W, Rank DR;
 XX 3900/53.
 DE -derived single exon nucleic acid probes useful for analyzing
 PF ion in human bone marrow.
 PR SEQ ID NO 33028; 658pp + Sequence Listing; English.
 XX invention provides a number of single exon nucleic acid
 CC are derived from genomic sequences expressed in the human
 CC they can be used to measure gene expression in bone marrow
 CC they may enable the improved diagnosis and treatment of cancers
 CC iona, leukaemia and myeloma. The present sequence is a
 CC ded by one of the probes of the invention
 CC AA;
 DE 1.7%; Score 9; DB 4; Length 111;
 PF 1arity 100.0%; Pred. No. 15;
 PR Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX AAAAA 126
 XX |||||
 XX AAAAA 29
 DE standard; protein; 111 AA.
 PF (first entry)
 DE expressed single exon probe encoded protein SEQ ID NO: 32215.
 PF expressed exon; gene expression analysis; probe: microarray;
 PR disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX 12.
 DE 2001WO-US000667.
 PF 2000US-0180312P.
 PR 2000US-0207456P.
 PR 2000US-00608408.
 PR 2000US-00632366.
 PR 2000US-0234687P.
 PR 2000US-0236359P.
 PR 2000GB-00024263.
 XX TULAR DYNAMICS INC.
 PF 1zel DK, Chen W, Rank DR;
 XX 3446/52.

PT Single exon nucleic acid probes for analyzing gene expression in
 PT brains.
 XX Example 4; SEQ ID NO 32215; 650pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic a
 CC probes which are derived from genomic sequences expressed in the
 CC brain. They can be used to measure gene expression in brain cell
 CC which may enable the diagnosis and improved treatment of nervous
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizo
 CC epilepsy and cancers. The present sequence is a protein encoded
 CC the probes of the invention
 XX Sequence 111 AA;
 SQ
 Query Match 1.7%; Score 9; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 118 AAAAAAAAA 126
 DB 21 AAAAAAAAA 29
 |||||
 |||||
 RESULT 145
 ID ABG54420 standard; peptide; 111 AA.
 XX AC ABG54420;
 XX DT 25-FEB-2003 (first entry)
 XX DE Human liver peptide, SEQ ID No 33068.
 XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 XX OS Homo sapiens.
 XX PN WO200157273-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488898/53.
 DR Human genome-derived single exon nucleic acid probes useful for
 XX gene expression in human adult liver.
 XX Claim 27; SEQ ID NO 33068; 658pp; English.
 CC The invention relates to a single exon nucleic acid probe (SENP)
 CC measuring human gene expression in a sample derived from human a
 CC liver, comprising one of 13109 defined nucleotide sequences giv
 CC specification (or complements/ fragments). The probe hybridises
 CC stringency to a nucleic acid molecule expressed in the human adu
 CC (I) may be used for predicting, measuring and displaying gene ex
 CC in samples derived from human adult liver. The genes identified
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia

ch coronary heart disease. ABG47348-ABG59930 represent human exon encoded peptides of the invention. Note: The sequence or this patent does not appear in the printed specification in electronic format directly from WIPO at pub/published_pct_sequences

AA;
arity 1.7%; Score 9; DB 4; Length 111;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 29

dard; peptide; 111 AA.

(first entry)

encoded by genome-derived single exon probe SEQ ID 32211.

exon probe; asthma; lung cancer; COPD; ILD;
active pulmonary disease; interstitial lung disease;
pathic pulmonary fibrosis; neurofibromatosis;
rosis; Gaucher's disease; Niemann-Pick disease;
lak syndrome; sarcoidosis; pulmonary haemosiderosis;
tiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
solar proteinosis; fibrocystic pulmonary dysplasia;
ry dyskinesia; pulmonary hypertension;
ane disease.

2.

2001WO-US000665.

2000US-0180312P.
2000US-0207456P.
2000US-0060840P.
2000US-0063236P.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.

JLAR DYNAMICS INC.

zel DK, Chen W, Rank DR;

183/15.

reassable set of single exon nucleic acid probes, used to expression in human lung samples.

ID NO 32211; 634pp; English.

relates to a spatially-addressable set of single exon probes for measuring gene expression in a sample derived ng comprising single exon nucleic acid probes having one of acid sequences mentioned in the specification, or their r the 12387 open reading frames derived from the 12614 included are a microarray comprising the novel set of probes d of probes which hybridise at high stringency to a nucleic d in the human lung; measuring gene expression in a sample human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human
CC mRNA, and (b) measuring the label detectably bound to each probe
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequenc
CC the eukaryote; and (b) detecting specific hybridisation of detect
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon
CC having a fragment identical to the predicted exon, the probe is i
CC in the above mentioned microarray; assigning exons to a single ge
CC comprising (a) identifying exons from genomic sequence by the met
CC above and (b) measuring the expression of each of the exons in se
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern
CC expression of the exons in the tissues and/or cell types indicate
CC the exons should be assigned to a single gene; a peptide comprisi
CC of 12011 sequences, mentioned in the specification, or encoded by
CC probes/open reading frames (ORF). The probes are used for gene ex
CC analysis, and for identifying exons in a gene, particularly using
CC lung derived mRNA and for the study of lung diseases such as asth
CC cancer, chronic obstructive pulmonary disease (COPD), interstitia
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibro
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Herm
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmona
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar protei
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary cili
CC dyskinesia, pulmonary hypertension and hyaline membrane disease.
CC present sequence is a peptide/protein encoded by a single exon pr
CC the invention. Note: The sequence data for this patent did not fc
CC of the printed specification, but was obtained in electronic form
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC
XX Sequence 111 AA;

Query Match 1.7%; Score 9; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Oy 118 AAAAAAAA 126
Db 21 AAAAAAAA 29

RESULT 147

AAAY18127
ID AAAY18127 standard; protein; 112 AA.

XX AC AAAY18127;

DT 11-AUG-1999 (first entry)

XX DE Clone 1 of A. thaliana strong light adapting protein.

XX KW Strong light adapting condition; light-resistant plant; transgeni

XX OS Arabidopsis thaliana.

XX FN JP11137253-A.

XX PD 25-MAY-1999.

XX PF 07-NOV-1997; 97JP-00306044.

XX PR 07-NOV-1997; 97JP-00306044.

XX PA (SUMO) SUMITOMO CHEM CO LTD.

XX DR WPI; 1999-364702/31.

XX DR N-PSDB; AAX77096.

XX PT Induction of gene to be expressed in plant under a strong light a
XX condition - useful for enabling plant to grow in desert.

XX PS Claim 3; Page 9; 16pp; Japanese.

XX

represents a clone of the protein of the invention. The
ates to a gene that is induced and expressed in a plant
g light adapting conditions, and is prepared by a procedure
of the following light irradiations (1) to (3) is made on a
, irradiated by a light of a light intensity of 60-100 mu
sisting of a continuous wave length component of a wave
i of 300-800 nm at 15 to 38 degrees C and the gene expression
induced in the cell of said plant: (1) A light of a light
300-700 nm E/sq. m s consisting of a continuous wave length
a wave length region of 300-800 nm at 15-38 degrees C for 1
al days; (2) a light of a light intensity of 200-600 mu
sisting of a continuous wave length component of a wave
i of 350-560 nm at 15-38 degrees C for several hours to
(3) a light of intensity 75-270 mu E/sq. m s consisting of
wave length component of a wave length region of 300-800 nm
es C for several hours to several days. The method can be
rating a transgenic plant that is able to grow in the desert

AA;

1.7%; Score 9; DB 2; Length 112;

arity 100.0%; Pred. No. 15;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146

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AAAPA 79

idard; protein; 112 AA.

(first entry)

haliana protein fragment SEQ ID NO: 42270.

ification; signal transduction pathway; metabolic pathway;
assay; Genetic mapping; gene expression control; promoter;
sequence.

haliana.

2000EP-00301439.

99US-0121825P.

99US-0123180P.

99US-0123548P.

99US-0125788P.

99US-0126264P.

99US-0126785P.

99US-0127462P.

99US-0128234P.

99US-0128714P.

99US-0129845P.

99US-0130077P.

99US-0130449P.

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11-MAY-1999; 99US-0134256P.
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23-JUL-1999; 99US-0145145P.

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1.7%; Score 9; DB 3; Length 112;
arity 100.0%; Pred.No.15;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
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AAAPA 79

dard; protein; 112 AA.

(first entry)
naliana protein fragment SEQ ID NO: 23547.
ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.
naliana.

2000EP-00301439.
99US-0121825P.
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01-JUL-1999; 99US-0141842P.
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02-JUL-1999; 99US-0142055P.
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Best Local Similarity 100.0%; Pred. No. 15;
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Db 71 APVAAAAPA 79

Search completed: March 30, 2004, 15:00:42
Job time : 69 secs

11:33:41 2004

us-09-976-740-43.olig.rpr

GenCore version 5.1.6
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in search, using sw model

rch 30, 2004, 14:58:32 ; Search time 20 Seconds
(without alignments)
2587.552 Million cell updates/sec

-09-976-740-43

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IGO

pop 60.0 , Gapext 60.0

3366 seqs, 96191526 residues

is satisfying chosen parameters: 283366

hth: 0

hth: 2000000000

isting first 150 summaries

[R 78.*

pir1:**

pir2:**

pir3:**

pir4:**

the number of results predicted by chance to have a
: than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

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2.0	445	2	T30604		hypothetical prote
2.0	808	2	C72858		AcOrf-66 protein -
2.0	892	2	T09193		ataxin 7 - human
1.9	257	2	S32101		PHLPSA protein - c
1.9	301	2	S62087		hrpf protein - pse
1.9	436	2	T01652		zinc finger protei
1.9	469	2	T37451		HBFG-2 (HFK-2) pro
1.9	544	2	T17547		proline-rich prote
1.9	557	2	S12359		nicotinic acetylch
1.9	613	1	RNECS		transcription init
1.9	613	2	F91122		RNA polymerase sig
1.9	613	2	E85967		RNA polymerase sig
1.9	615	1	RNEBST		transcription init
1.9	635	2	A71620		hypothetical prote
1.9	660	2	AB0893		RNA polymerase sig
1.9	678	2	A54514		glutamic acid-rich
1.9	762	2	H87302		chemotaxis protein
1.9	1054	2	A61221		probable calcium t
1.9	1100	2	T30967		transcription acti
1.9	1887	2	S61703		fatty-acid synthas
1.7	100	2	T17126		hypothetical prote
1.7	109	1	R6UTP1		acidic ribosomal p
1.7	109	2	T02716		acidic ribosomal p
1.7	109	2	T02039		acidic ribosomal p
1.7	112	2	E86141		protein T25K16.9
1.7	172	2	F86176		protein T19P19.9
1.7	178	2	AH1394		B. subtilis RNA po
1.7	183	2	F84636		hypothetical prote
1.7	217	2	T04353		DNA binding protei

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probable PP
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evx1 protei
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probable ph
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homeotic pr
HMS1 protei
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1.5 149 2 S39556 high mobility grou
 1.5 165 2 B87702 ribosomal protein
 1.5 172 2 S35568 sex-determining pr
 1.5 176 2 I48752 gene RRBetal prot
 1.5 177 2 AB3269 outer membrane lip
 1.5 178 2 S26481 calcium-binding pr
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 1.5 205 2 JQ2247 photosystem I chai
 1.5 205 2 S41002 hypothetical prote
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 1.5 233 2 D95860 probable transcrip
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 1.5 240 2 S09377 small nuclear ribo
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 1.5 243 2 A28993 auxin-induced prot
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 1.5 247 2 AG3513 channel protein vi
 1.5 249 2 T35724 cobalt transport i
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 1.5 261 2 S63604 homeobox protein G
 1.5 271 2 S34666 glycine-rich prote
 1.5 271 2 JC6553 transcription fact
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ALIGNMENTS

in 3L - Molluscum contagiosum virus 1
 : MC003L
 : num contagiosum virus 1
 : 9 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
 : 04
 : Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
 : 116, 1996
 : sequence of a human tumorigenic poxvirus: Prediction of specific host re
 : 220876; MUID:96325459; PMID:8670425
 : 04
 : lary; translated from GB/EMBL/DBJ
 : DNA
 : <SEN>
 : 5: EMBL:U60315; PIDN:AAC55131.1

2.0%; Score 11; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0;
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 Db 353 PPTTAPPPPP 363
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 RESULT 2
 C72858
 AcOrf-66 protein - Autographa californica nuclear polyhedrosis virus
 C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
 A:Note: dsDNA virus
 C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-No
 C:Accession: C72858
 R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D
 Virology 202, 586-605, 1994
 A:Title: The complete DNA sequence of Autographa californica nuclear
 A:Reference number: A72850; MUID:94303173; PMID:8030224
 A:Accession: C72858
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-808 <AYR>
 A:Cross-references: GB:L22858; NID:G510708; PIDN:AAA66696.1; PID:G559
 C:Genetics:
 A:Gene: AcOrf-66

Query Match 2.0%; Score 11; DB 2; Length 808;
 Best Local Similarity 100.0%; Pred. No. 0.45;
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QY 212 PPPQPAPPQP 222
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 Db 108 PPPQPAPPQP 118
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RESULT 3
 T09193
 ataxin 7 - human
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju
 C:Accession: T09193
 R:Del-Favero, J.; Krois, L.; Michalik, A.; Theuns, J.; Lofgren, A.; G
 Hum. Mol. Genet. 7, 177-186, 1998
 A:Title: Molecular genetic analysis of autosomal dominant cerebellar
 A:Reference number: Z16604; MUID:98087568; PMID:9425224
 A:Accession: T09193
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-892
 A:Cross-references: EMBL:AF032105; NID:G3192953; PIDN:AAC39765.1; PID
 A:Experimental source: cell type lymphoblast
 C:Genetics:
 A:Gene: SCA7
 A:Map position: 3

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 Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0;
 Matches 11; Conservative 0; Mismatches 0;

QY 222 QQQQPPPPQP 232
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 Db 36 QQQQPPPPQP 46
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RESULT 4
 S32101
 PHLP5A protein - common timothy (fragment)
 C:Species: Phleum pratense (common timothy)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Ma
 C:Accession: S32101
 R:Sufer, A.; Becker, W.M.; Petersen, A.; Schramm, G.; Schlaak, M.


```
33 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
39
40 Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.;
41 1990
42 and functional expression of a single alpha subunit of an insect nicot
43 r: S12359; MUID:91092283; PMID:1702381
44
45 rRNA
46 <MAR>
47 s: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
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49 ethylcholine receptor
50 protein; ion channel; neurotransmitter receptor; transmembrane protein
51 final sequence #status predicted <SIG>
52 nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT
53 transmembrane #status predicted <TM1>
54 transmembrane #status predicted <TM2>
55 transmembrane #status predicted <TM3>
56 transmembrane #status predicted <TM4>
57 site: carbohydrate (Asn) (covalent) #status predicted
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60 1.9%; Score 10; DB 2; Length 557;
61 larity 100.0%; Pred. No. 2.3;
62 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
63
64 ASSSAAS 28
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NA
<ERI>
 : GB:M14427; NID:g154402; PIDN:AAA27242.1; PID:g154406

nscription initiation factor sigma 70; transcription initiation factor
nding; sigma factor; transcription initiation
nscription initiation factor sigma region 1 homology <SR1>
transcription initiation factor sigma katF homology <KTF>

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DEDED 342
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DEDED 202

in PRB0250w - malaria parasite (Plasmodium falciparum)
ium falciparum
3 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000

ettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
zhberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
1132, 1998

e 2 sequence of the human malaria parasite Plasmodium falciparum.
 : A71600; MUID:99021743; PMID:9804551

ary; nucleic acid sequence not shown; translation not shown

NA
<GAR>
 : GB:AE001382; GB:AE001362; NID:g3845130; PIDN:AAC71839.1; PID:g384513
rce: clone 3D7

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EDED 343
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EDED 586

a-70 factor [imported] - Salmonella enterica subsp. enterica serovar
la enterica subsp. enterica serovar Typhi
es has also been called Salmonella typhi

l #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

agan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
'Gaora, P.
2, 2001

3 Qual, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
genome sequence of a multiple drug resistant Salmonella enterica serov
 : AB0502; MUID:21534947; PMID:11677608

3
ary
NA
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 : GB:AL513382; PIDN:CAD07736.1; PID:g16504288; GSPDB:GN00176

nscription initiation factor sigma 70; transcription initiation factor
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 333 DDEDEDED 342
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DB 238 DDEDEDED 247
|||||

RESULT 16
A54514
glutamic acid-rich protein precursor - malaria parasite (Plasmodium ffa
N; Alternate names: GARP
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 21-Jul
C:Accession: A54514
R;Triglia, T.; Stahl, H.D.; Crewther, P.E.; Silva, A.; Anders, R.F.; K
Mol. Biochem. Parasitol. 31, 199-202, 1988
A;Title: Structure of a Plasmodium falciparum gene that encodes a glut
A;Reference number: A54514; MUID:89040048; PMID:2903445
A;Accession: A54514
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-678 <TRI>
A;Cross-References: GB:J03998; NID:gl60298; PIDN:AAA29605.1; PID:gl6160
C;Genetics:
A;Introns: 25/3
C;Superfamily: histone H1
C;Keywords: tandem repeat

Query Match 1.9%; Score 10; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 331 EDDDEDEDE 340
|||||
DB 640 EDDDEDEDE 649
|||||

RESULT 17
H87302
chemotaxis protein CheA [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May
C:Accession: H87302
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen,
B.; Laub, M.T.; DeBooy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.;
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.B.; Shapiro, L.; Venter,
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-762 <STO>
A;Cross-References: GB:AE005673; NID:gi3421600; PIDN:AAK22420.1; GSPDB
C;Genetics:
A;Gene: CC0433
C;Superfamily: chemotaxis protein cheA

Query Match 1.9%; Score 10; DB 2; Length 762;
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Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 118 APAAAAAAP 127
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DB 338 APAAAAAAP 347
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RESULT 18
AG1221
probable calcium transporter rdgB - fruit fly (Drosophila melanogaster
C:Species: Drosophila melanogaster
C>Date: 03-May-1994 #sequence_revision 09-Sep-1994 #text_change 21-Jul

21 Hyde, D.R.; O'Tousa, J.E.
-768, 1991
1 and characterization of the Drosophila retinal degeneration B (rdgB)
c: A61221; MUID:91231170; PMID:1903119
21 mRNA
4 <VIH>
s: GB:X57978; NID:g510883; PIDN:CAA41044.1; PID:g510884
3: FlyBase:FBgn0003218
um binding; calcium transport; glycoprotein; transmembrane protein
calcium binding #status predicted <CAL>
, 852,928/Binding site: carbohydrate (Asn) (covalent) #status predicted
1.9%; Score 10; DB 2; Length 1054;
larity 100.0%; Pred. No. 4;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
EDDDEDE 338
|||||||
EDDDEDE 333
ivator SRG3 - mouse
sculus (house mouse)
99 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
57
Z. M.G.; Kim, Y.H.; Lee, C.; Park, S.D.; Seong, R.H.
EMBL Data Library, January 1997
new mouse gene, SRG3, related to the SWI3 of Saccharomyces cerevisiae.
r: Z20948
57
nary; translated from GB/EMBL/DBJ
mRNA
0 <JO>
s: EMBL:U85614; NID:gl816634; PID:gl816635; PIDN:AAB42085.1
olved in glucocorticoid-induced apoptosis in the thymoma cell line; ma
1.9%; Score 10; DB 2; Length 1100;
larity 100.0%; Pred. No. 4.1;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QQQPPPP 229
|||||||
QQQPPPP 1082
se (EC 2.3.1.85) alpha chain - yeast (Saccharomyces cerevisiae)
: protein P1409; protein YPL231w
romyces cerevisiae
96 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
03; S65256; S65250; A31107
A.
EMBL Data Library, December 1995
r: S61699
03
DNA
7 <URR>
s: EMBL:X94561; NID:gl181252; PIDN:CAA64256.1; PID:gl181257
A.; Vissers, S.
Protein Sequence Database, May 1996
r: S65251
56
DNA

A;Residues: 1-1887 <URW>
A;Cross-references: EMBL:Z73587; NID:gl370477; PIDN:CAA97948.1; PID:g
A;Experimental source: strain S288C (AB972)
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65202
A;Accession: S65250
A;Molecule type: DNA
A;Residues: 1567-1887 <RIE>
A;Cross-references: EMBL:Z73587; MIPS:YPL231w
A;Experimental source: strain S288C (AB972)
R;Mohamed, A.H.; Chirala, S.S.; Mody, N.H.; Huang, W.Y.; Wakil, S.J.
J. Biol. Chem. 263, 12315-12325, 1988
A;Title: Primary structure of the multifunctional alpha subunit prote
A;Reference number: A31107; MUID:88315020; PMID:2900835
A;Accession: A31107
A;Molecule type: DNA
A;Residues: 1-310,'TTGTGG',311-593,'I',595-940,'CINCVKSWLKLKLERPPSK
A;Cross-references: EMBL:J03936; NID:gl71501; PIDN:AAA34601.1; PID:gl
C;Genetics:
A;Gene: SGD:FAS2
A;Cross-references: SGD:S0006152; MIPS:YPL231w
A;Map position: 16L
C;Superfamily: yeast fatty-acid synthase
C;Keywords: acyltransferase; coenzyme A
Query Match 1.9%; Score 10; DB 2; Length 1887;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY 137 PAPVAAAAPA 146
Db 125 PAPVAAAAPA 134
RESULT 21
T17126
hypothetical protein T30A10.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct
C;Accession: T17126
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18708
A;Accession: T17126
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <BEV>
A;Cross-references: EMBL:AL117386
A;Experimental source: cultivar Columbia; BAC clone T30A10
C;Genetics:
A;Map position: 4
A;Introns: 30/3
A;Note: T30A10.30
Query Match 1.7%; Score 9; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 221 PQQQQPPPP 229
Db 65 PQQQQPPPP 73
RESULT 22
R6UTP1
acidic ribosomal protein P1 - Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Ju
C;Accession: S22644; S19924
R;Vazquez, M.P.; Schijman, A.G.; Levin, M.J.
Nucleic Acids Res. 20, 2599, 1992
A;Title: Nucleotide sequence of a cDNA encoding a Trypanosoma cruzi a

: S22644; MUID:92285148; PMID:1598221
 acid sequence not shown
 RNA
 <VAZ>
 : EMBL:X65025; NID:gl0629; PIDN:CAA46159.1; PID:gl0630
 acidic ribosomal protein P1
 protein; protein biosynthesis; ribosome
 1.7%; Score 9; DB 1; Length 109;
 identity 100.0%; Pred. No. 4.1;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 WAAA 126
 ||||
 WAAA 85
 protein P1 - maize
 ribosomal protein L12
 ; (maize)
 ; #sequence_revision 24-Mar-1999 #text_change 13-Aug-1999
 Murchish, M.P.; Bokhari-Riza, A.; Mascarenhas, J.P.
 MBL Data Library, November 1995
 Z14703
 ; translated from GB/EMBL/DBJ
 RNA
 :HAM>
 EMBL:U40147; NID:gl209700; PIDN:AAA91168.1; PID:gl209701
 ce: strain W-22
 acidic ribosomal protein P1
 ; biosynthesis; ribosome
 1.7%; Score 9; DB 2; Length 109;
 identity 100.0%; Pred. No. 4.1;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 JAAP 146
 ||||
 JAAP 77
 protein P1a - maize
 : (maize)
 ; #sequence_revision 26-Feb-1999 #text_change 13-Aug-1999
 ; Vangala, S.; Szick, K.; Lee, C.H.
 1293-1305, 1997
 aphoprotein complex of the 60S ribosomal subunit of maize seedling ro
 Z14507; MUID:97422884; PMID:9276949
 ; translated from GB/EMBL/DBJ
 RNA
 :BAL>
 EMBL:U62752; NID:g2431768; PIDN:AAB71079.1; PID:g2431769
 ce: strain B73
 acidic ribosomal protein P1
 ; biosynthesis; ribosome
 1.7%; Score 9; DB 2; Length 109;
 identity 100.0%; Pred. No. 4.1;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 JAAP 146
 ||||

Db 69 APVAAAAPA 77
 RESULT 25
 E86141
 protein T25K16.9 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar
 C;Accession: E86141
 R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Ma
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: E86141
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-112 <STO>
 A;Cross-references: GB:AE005172; NID:g6715644; PIDN:AAF26471.1; GSPDB:
 C;Genetics:
 A;Gene: T25K16.9
 A;Map position: 1
 C;Superfamily: rat acidic ribosomal protein P1
 Query Match 1.7%; Score 9; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 QY 138 APVAAAAPA 146
 |||||
 Db 71 APVAAAAPA 79
 RESULT 26
 F86176
 protein F19P19.9 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar
 C;Accession: F86176
 R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Ma
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F86176
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-172 <STO>
 A;Cross-references: GB:AE005172; NID:g2341030; PIDN:AAB70430.1; GSPDB:(
 C;Genetics:
 A;Gene: F19P19.9
 A;Map position: 1
 Query Match 1.7%; Score 9; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 QY 119 PAAAAAAP 127
 |||||
 Db 42 PAAAAAAP 50

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RE polymerase delta chain homolog lmo2560 [imported] - Listeria monocytogenes
AB a monocytogenes
AC #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
AD 34
AE aguel, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
AF al, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
AG Garst, U.
AH 352, 2001
AI J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
AJ : T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
AK live genomics of Listeria species.
AL : AB1077; MUID:21537279; PMID:11679669
AM 34
AN lary
AO DNA
AP <GLA>
AQ : GB:NC_003210; PIDN:CAD00638.1; PID:gi6412048; GSPDB:GN00177
AR rce: strain EGD-e
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A:Reference number: Z14889
 A:Accession: T04353
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-217 <HS>
 A:Cross-references: EMBL:U25283; NID:gi753084; PIDN:AAB39320.1; PID:g
 A:Experimental source: cv. Tainung 67, seed

Query Match 1.7%; Score 9; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAAPP 127
 DB 52 PAAAAAAPP 60

RESULT 30
 I51382
 I51382
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Ju
 C:Accession: I51382
 R:Jasoni, C.D.; Walker, M.B.; Morris, M.D.; Reh, T.A.
 Development 120, 769-783, 1994
 A:Title: A chicken achaete-scute homolog (CASH-1) is expressed in a t
 A:Reference number: I51382; MUID:95324365; PMID:7600956
 A:Accession: I51382
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-219 <JAS>
 A:Cross-references: EMBL:U01339; NID:g401726; PIDN:AAC59658.1; PID:g4

Query Match 1.7%; Score 9; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 120 AAAAAAAPP 128
 DB 28 AAAAAAAPP 36

RESULT 31
 WMAD51
 late 33K protein - human adenovirus 5
 C:Species: Mastadenovirus h5 (human adenovirus 5)
 A:Note: host Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 04-Ma
 C:Accession: F39449
 R:Chroboczek, J.; Bieher, F.; Jacrot, B.
 Virology 186, 280-285, 1992
 A:Title: The sequence of the genome of adenovirus type 5 and its comp
 A:Reference number: A39449; MUID:92087470; PMID:1727603
 A:Accession: F39449
 A:Molecule type: DNA
 A:Residues: 1-229 <CHR>
 A:Cross-references: GB:M73260
 C:Superfamily: adenovirus late 33K protein
 C:Keywords: late protein

Query Match 1.7%; Score 9; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 7.7; Mismatches 0; Indels 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 118 AAAAAAAPP 126
 DB 109 AAAAAAAPP 117

RESULT 32
 T31231
 traw protein homolog - Sphingomonas aromaticivorans plasmid pML1
 C:Species: Sphingomonas aromaticivorans

```

) #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
llwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
4BL Data Library, July 1998
plete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
: Z20992
ary; translated from GB/EMBL/DBJ
VA
: EMBL:AF079317; NID:g3378261; PID:g3378372; PIDN:AAD03955.1
DNL1
erichia coli plasmid F F-pilus assembly periplasmic protein traw
1.7%; Score 9; DB 2; Length 231;
arity 100.0%; Pred. No. 7.8;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
PARAP 149
|||||
PARAP 222
sin - Mycobacterium tuberculosis (strain H37RV)
erium tuberculosis
) #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
ch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
s, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
t, 1998
R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
g the biology of Mycobacterium tuberculosis from the complete genome
: A70500; MUID:9829598; PMID:9634230
ary; nucleic acid sequence not shown; translation not shown
VA
COL>
: GB:295554; GB:AL123456; NID:g3261771; PIDN:CAB08905.1; PID:g2113895
ce: strain H37RV
le-3-glycerol-phosphate synthase; trpC homology
C homology <TRC>
1.7%; Score 9; DB 2; Length 272;
arity 100.0%; Pred. No. 8.9;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
WAPP 129
|||||
WAPP 40
merase-related protein [imported] - Caulobacter crescentus
ter crescentus
) #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
ldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
Boy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
ici, U.S.A. 98, 4136-4141, 2001
genome Sequence of Caulobacter crescentus.
: A87249; MUID:2117369; PMID:11259647
ary
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A;Residues: 1-273 <STO>
A;Cross-references: GB:AE005673; NID:g13422678; PIDN:AAK23314.1; GSPDE
C;Genetics:
A;Gene: CCI333
Query Match 1.7%; Score 9; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 133 PPPPPAPVA 141
|||||
DB 47 PPPPPAPVA 55
RESULT 35
D86208
protein F22G5.34 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug
C;Accession: D86208
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Ma
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86208
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <STO>
A;Cross-references: GB:AE005172; NID:g8778555; PIDN:AAF79563.1; GSPDB:
C;Genetics:
A;Gene: F22G5.34
A;Map position: 1
C;Superfamily: Escherichia coli ribosomal protein L4
Query Match 1.7%; Score 9; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 330 EEEEDDEDE 338
|||||
DB 267 EEEEDDEDE 275
RESULT 36
A61047
ectodermal (ect) - fruit fly (Drosophila melanogaster) (strain Oregon-
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Feb
C;Accession: A61047
R;Raha, D.; Nguyen, Q.D.; Garen, A.
Dev. Genet. 11, 310-317, 1990
A;Title: Molecular and developmental analyses of the protein encoded b;
A;Reference number: A61047; MUID:91215866; PMID:2090376
A;Accession: A61047
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-280 <RAH>
A;Note: in the nucleotide sequence codons for residues 25-28 are not s;
A;Note: the authors' translation is shown for the codon GAG at residue
C;Genetics:
A;Gene: FlyBase:ect
A;Cross-references: FlyBase:FBgn0000451
Query Match 1.7%; Score 9; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
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DDDEDE 338
|||||
DDDEDE 87

sin F57C7.3 - Caenorhabditis elegans
habditis elegans
9 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
16

EMBL Data Library, February 1996

c: Z19625

16

ary; translated from GB/EMBL/DBJ

DNA

<WIL>

3: EMBL:Z69646; PIDN:CAA93474.1; GSPDB:GN00028; CESP:F57C7.3

orce: clone F57C7

7.3

37/1; 120/3; 191/2; 231/1

1.7%; Score 9; DB 2; Length 288;

larity 100.0%; Pred.No. 9.4;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDEDE 340

|||||

DEDEDE 153

ly protein 1 - soybean

max (soybean)

36

92 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000

M.C.; Lee, S.Y.; Hwang, I.; Bahk, J.D.; Hong, J.C.; Ishimi, Y.; Cho,

249, 465-473, 1995

cloning and functional characterization of a cDNA encoding nucleosome

3: S60892; MUID:96133687; PMID:8544812

32

ary

nRNA

<YOO>

3: EMBL:L38856; NID:g1161251; PIDN:AAA89792.1; PID:g1161252

1.7%; Score 9; DB 2; Length 358;

larity 100.0%; Pred.No. 11;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3DEEDD 343

|||||

3DEEDD 321

sin eve - fruit fly (Drosophila melanogaster)

nila melanogaster

97 #sequence_revision 25-Oct-1987 #text_change 24-Sep-1999

66; B26066; A26636

Ingham, P.; Struhl, G.

1986

n, structure, and expression of even-skipped: a second pair-rule gene

r: A26066; MUID:97051744; PMID:2877745

56

DNA

<MAC>

A;Cross-references: GB:M14767; NID:g157386; PIDN:AAA28522.1; PID:g157

A;Accession: B26066

A;Molecule type: mRNA

A;Residues: 32-268;279-376 <MA2>

A;Cross-references: GB:M14767

R;Fraser, M.; Hoey, T.; Rushlow, C.; Doyle, H.; Levine, M.

EMBO J. 6, 749-759, 1987

A;Title: Characterization and localization of the even-skipped protei

A;Reference number: A26636; MUID:87218536; PMID:2884106

A;Accession: A26636

A;Molecule type: mRNA

A;Residues: 1-299,'L',301-376 <FRA>

A;Cross-references: GB:X05138; NID:g7957; PIDN:CAA28784.1; PID:g7958

C;Genetics:

A;Gene: eve (even-skipped)

A;Cross-references: FlyBase:FBgn0000606

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;71-127/Domain: homeobox homology <HOX>

Query Match 1.7%; Score 9; DB 2; Length 376;

Best Local Similarity 100.0%; Pred.No. 12;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 118 APAAAAAAA 126

|||||

Db 165 APAAAAAAA 173

RESULT 40

H75457

hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Ma

C;Accession: H75457

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: H75457

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <WHI>

A;Cross-references: GB:AE001946; GB:AE000513; NID:g6458655; PIDN:AAF1

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0938

A;Map position: 1

Query Match 1.7%; Score 9; DB 2; Length 395;

Best Local Similarity 100.0%; Pred.No. 12;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 181 PPAPAAPPA 189

|||||

Db 95 PPAPAAPPA 103

RESULT 41

E70675

probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct

C;Accession: E70675

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Ha

i; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Haml

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Sq

Nature 393, 537-544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barr

A;Title: Deciphering the biology of Mycobacterium tuberculosis from th

A;Reference number: A70500; MUID:98295987; PMID:9634230

```

RY; nucleic acid sequence not shown; translation not shown
IA
COL>
GB:Z82098; GB:AL123456; NID:g3261664; PIDN:CAB05065.1; PID:e1299861;
ce: strain H37RV

1.7%; Score 9; DB 2; Length 406;
urity 100.0%; Pred. No. 13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAPP 129
|||||
AAPP 295

n T23D8.3 - Caenorhabditis elegans
bditis elegans
#sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

TBL Data Library, October 1996
Z19989

RY; translated from GB/EMBL/DBJ
IA
WIL>
EMBL:Z81128; PIDN:CAB03401.1; GSPDB:GN00019; CESP:T23D8.3
ce: clone T23D8

3
8/3; 247/3; 396/3

1.7%; Score 9; DB 2; Length 410;
urity 100.0%; Pred. No. 13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DDED 337
|||||
DDED 161

n E01B7.1 - Caenorhabditis elegans
bdtis elegans
#sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

TBL Data Library, December 1996
Z19267

RY; translated from GB/EMBL/DBJ
IA
WIL>
EMBL:Z83222; PIDN:CAB05712.1; GSPDB:GN00023; CESP:E01B7.1
ce: clone E01B7

1
1/3; 110/3; 174/2; 202/2; 259/3

1.7%; Score 9; DB 2; Length 410;
urity 100.0%; Pred. No. 13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAPP 189
|||||

```

```

Db 338 PPAPAPPA 346

RESULT 44
S12541
evxi protein - murine sarcoma virus
C;Species: murine sarcoma virus
C;Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 24-Sep
C;Accession: S12541
R;Bastian, H.; Gruss, P.
EMBO J. 9, 1839-1852, 1990
A;Title: A murine even-skipped homologue, Evx 1, is expressed during e
A;Reference number: S12541; MUID:90269218; PMID:1971786
A;Accession: S12541
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <BAS>
A;Cross-references: GB:X54239; NID:G50875; PIDN:CAA38145.1; PID:G50876
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;184-240/Domain: homeobox homology <HOX>

Query Match 1.7%; Score 9; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 148 APRAAAAAA 156
|||||
Db 366 APRAAAAAA 374
|||||

RESULT 45
T15142
hypothetical protein T28F2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan
C;Accession: T15142
R;Madsen, C.; Fronick, B.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid T28F2.
A;Reference number: Z18300
A;Accession: T15142
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-418 <MAD>
A;Cross-references: EMBL:AF000198; NID:g2047345; PID:g2047346; PIDN:AA
A;Experimental source: strain Bristol N2; clone T28F2
C;Genetics:
A;Gene: CESP:T28F2.6
A;Map position: 1
A;Introns: 49/3
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match 1.7%; Score 9; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 178 AAPPPAPAA 186
|||||
Db 368 AAPPPAPAA 376
|||||

RESULT 46
T03293
probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (I
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Aug
C;Accession: T03293
R;Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
submitted to the EMBL Data Library, April 1995
A;Description: Rice early embryogenesis gene.
A;Reference number: Z14889
A;Accession: T03293

```

```
ed from GB/EMBL/DBJ
RNA
<HSI>
: EMBL:U25430; NID:G818848; PID:G818849
: source: strain Tainung 67

an phosphodiesterase I / nucleotide pyrophosphatase 4
me A; metalloprotein; phosphoric diester hydrolase

1.7%; Score 9; DB 2; Length 479;
arity 100.0%; Pred. No. 14;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPP 128
|||||
AAAPP 10

helix protein, DEC2 - human
piens (man)
l1 #sssequence_revision 30-Jun-2001 #text_change 30-Jun-2001
33
ien, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E.
Res. Commun. 280, 164-171, 2001
: cloning and characterization of DEC2, a new member of basic helix-loop-
: JG7583; MUID:21092582; PMID:11162494
33
RNA
<PUJ>
: DDBJ:AB044088
rotein, a novel member of the DEC subfamily of basic helix-loop-helix R
p11.23-p12.1
:ription factor
:gly conserved #status predicted
Orange #status predicted <ORA>
alanine and glycine-rich #status predicted

1.7%; Score 9; DB 2; Length 482;
arity 100.0%; Pred. No. 14;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 402

HLX1 - human
piens (man)
15 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
10; 154180
ayner, J.C.; Morris, C.M.
355, 1994
: structure, promoter sequence, and revised translation of human homeobox
: A55180; MUID:95104845; PMID:7806220
10
ary; not compared with conceptual translation
DNA
<KEN>
: Purchio, A.F.; Murray, J.C.
364, 1993
localization of TGF2 and the human homeobox gene HLX1 to chromosome 1q
: 154180; MUID:93194183; PMID:8095486
30
ary; translated from GB/EMBL/DBJ
DNA
39 <RES>

A;Cross-references: GB:S56767; NID:G298601; PIDN:AAD13883.1; PID:G426;
C:Genetics:
A:Gene: GDB:HLX1
A;Cross-references: GDB:128988; OMIM:142995
A:Map position: 1q41-1q42.1
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:277-333/Domain: homeobox homology <HOX>

Query Match 1.7%; Score 9; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 221 PQQQQPPPP 229
|||||
DB 133 PQQQQPPPP 141

RESULT 49
S52830
HMS1 protein - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YM9916.09; protein YMR070w
C:Species: Saccharomyces cerevisiae
C:Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 29-Oct
C:Accession: S52830; S59820
R:Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995
A:Reference number: S52814
A:Accession: S52830
A:Molecule type: DNA
A:Residues: 1-490 <PEA>
A:Cross-references: EMBL:Z48952; NID:G763008; PIDN:CAA88795.1; PID:G76
A:Experimental source: strain AB972
R:Madison, J.; Winston, F.
submitted to the EMBL Data Library, April 1995
A:Reference number: S59820
A:Accession: S59820
A:Molecule type: DNA
A:Residues: 1-490 <MAD>
A:Cross-references: EMBL:U25279; NID:G805129; PIDN:AAC49982.1; PID:G80
C:Genetics:
A:Gene: SGD:MOT3; HMS1
A:Cross-references: MIPS:YMR070w; SGD:S0004674
A:Map position: 13R

Query Match 1.7%; Score 9; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAAATAP 159
|||||
DB 443 AAAAAATAP 451

RESULT 50
C85435
Hypothetical protein AT4G36860 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb
C:Accession: C85435
R:anonymous, The European Union Arabidopsis Genome Sequencing Consorti
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsi
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: C85435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-542 <STO>
A:Cross-references: GB:NC_001268; NID:G720635; PIDN:CAB80352.1; GSPDI
C:Genetics:
A:Gene: AT4G36860
A:Map position: 4
```

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1.7%; Score 9; DB 2; Length 542;
urity 100.0%; Pred. No. 16;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDE 341
|||||
DEDE 114

st (Saccharomyces cerevisiae)
protein YKR072c
#sequence_revision 03-May-1994 #text_change 21-Jul-2000
#S4982; S43078
F.M.
rotein Sequence Database, March 1994
S37897

IA
:POH>
EMBL:Z28297; NID:g486544; PID:g486545; MIPS:YKR072c
ce: strain S288C
se, R.; Arndt, K.T.
17, 1995
ision of S152, which contains an extremely acidic region, increases th
S54982; MUID:95220693; PMID:7705654

IA
:DIW>
EMBL:U01878; NID:g430983; PIDN:AAA80000.1; PID:g430984

SGD:S0001780; MIPS:YKR072c

1.7%; Score 9; DB 2; Length 562;
urity 100.0%; Pred. No. 16;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDE 338
|||||
DEDE 504

n KIAA0616 - human (fragment)
iens (man)
#sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
ase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
, 1998
i of the coding sequences of unidentified human genes. X. The complete
214142; MUID:98403880; PMID:9734811
ary; translated from GB/EMBL/DBJ
RNA
:ISH>
ce: EMBL:AB014516; NID:g3327045; PIDN:BAA31591.1; PID:g3327046
ce: brain

1.7%; Score 9; DB 2; Length 634;
urity 100.0%; Pred. No. 18;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

PQPPP 235
|||||
PQPPP 371

```

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RESULT 53
T22002
hypothetical protein F39H11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct
C;Accession: T22002
R;White, S.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19500
A;Accession: T22002
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-650 <WIL>
A;Cross-references: EMBL:Z81079; PIDN:CAB03084.1; GSPDB:GN00019; CBSP:1
A;Experimental source: clone F39H11
C;Genetics:
A;Gene: CESP:F39H11.4
A;Map position: 1
A;Introns: 109/3; 154/1; 357/1; 420/3; 464/3; 566/2; 594/1; 628/3

Query Match 1.7%; Score 9; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 128 PPTPAPPPP 136
|||||
DB 136 PPTPAPPPP 144

RESULT 54
E86358
F12K8.13 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov
C;Accession: E86358
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86358
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-683 <STO>
A;Cross-references: GB:AE005172; NID:g6587836; PIDN:AAF18525.1; GSPDB:
C;Genetics:
A;Map position: 1

Query Match 1.7%; Score 9; DB 2; Length 683;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 132 APPPPAPV 140
|||||
DB 116 APPPPAPV 124

RESULT 55
T40168
hypothetical protein SPBC30B4.02c - fission yeast (Schizosaccharomyces
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec
C;Accession: T40168
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft
submitted to the EMBL Data Library, August 1998

```


1: Z21909
2: 8
3: ary; translated from GB/EMBL/DBJ
4: NA
5: <LYN>
6: A: EMBL:AL031262; PIDN:CRAA20315.1; GSPDB:GN00067; SPDB:SPBC30B4.02c
7: rce: strain 972h-; cosmid c30B4
8: OB4.02c
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A: GB:ML6801; NID:G187460; PIDN:AAA59571.1; PID:G307166
 A:Map position: 12R
 GDB:120188; OMIM:264350
 31-4q31
 assigned erba-related proteins; erba transforming protein homology
 binding; transcription regulation; zinc finger
 erba transforming protein homology <ERBA>
 zinc finger
 zinc finger
 1.7%; Score 9; DB 2; Length 984;
 arity 100.0%; Pred.No. 26;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QPPPP 229
 QPPPP 697
 in F25E4.40 - Arabidopsis thaliana
 psis thaliana (mouse-ear cross)
 9 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 2
 rd, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
 rotein Sequence Database, June 1999
 : Z16533
 2
 NA
 <BEV>
 : EMBL:AL050399; GSPDB:GNO0062; ATSP:F25E4.40
 rce: cultivar Columbia; BAC clone F25E4
 .40
 76/3; 248/3; 371/3; 381/3; 457/3; 511/3; 585/3; 654/3; 723/3; 750/3; 8
 1.7%; Score 9; DB 2; Length 987;
 arity 100.0%; Pred.No. 27;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAA 126
 AAAAA 899
 st (Saccharomyces cerevisiae)
 protein L8083.9; protein YLR223c; RRP3 protein
 omies cerevisiae
 5 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
 2; S51446; S47477
 laux, P.
 1995
 gene product interacts with a fork head protein in Saccharomyces cerev
 : S55352; MUID:95304839; PMID:7785326
 2
 acid sequence not shown
 NA
 : <CHE>
 : EMBL:Z29488; NID:G531491; PIDN:CAA82624.1; PID:G531492
 R
 EMBL Data Library, December 1994
 : sequence of S. cerevisiae cosmid 8083.
 : S51443
 16
 NA
 : <HAL>
 : EMBL:U19027; NID:G609363; PID:G609372; MIPS:YLR223C

A:Gene: SGD:IFH1; RRP3
 A:Cross-references: SGD:S0004213; MIPS:YLR223C
 A:Map position: 12R
 Query Match 1.7%; Score 9; DB 2; Length 1085;
 Best Local Similarity 100.0%; Pred.No. 29;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 329 EEEEDDED 337
 Db 133 EEEEDDED 141
 RESULT 66
 A33507
 hypothetical protein DUC-1 - human
 C:Species: Homo sapiens (man)
 C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 05-Nov
 C:Accession: A33507
 R:Fujii, H.; Shimada, T.
 J. Biol. Chem. 264, 10057-10064, 1989
 A:Title: Isolation and characterization of cDNA clones derived from t
 A:Reference number: A33507; MUID:89255490; PMID:2722860
 A:Accession: A33507
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1137 <FUJ>
 A:Cross-references: GB:J04810; NID:G181841; PIDN:AA847281.1; PID:G1818
 Query Match 1.7%; Score 9; DB 2; Length 1137;
 Best Local Similarity 100.0%; Pred.No. 30;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 120 AAAAAAPP 128
 Db 56 AAAAAAPP 64
 RESULT 67
 EDIEIF
 immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Fu
 C:Species: suid herpesvirus 1
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Fel
 C:Accession: S04713
 R:Cheung, A.K.
 Nucleic Acids Res. 17, 4637-4646, 1989
 A:Title: DNA nucleotide sequence analysis of the immediate-early gene
 A:Reference number: S04713; MUID:89315207; PMID:2546124
 A:Accession: S04713
 A:Molecule type: DNA
 A:Residues: 1-1460 <CHE>
 C:Superfamily: herpesvirus immediate-early protein regulation
 C:Keywords: DNA binding; early protein; transcription regulation
 Query Match 1.7%; Score 9; DB 1; Length 1460;
 Best Local Similarity 100.0%; Pred.No. 37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 118 APAAAAAAA 126
 Db 377 APAAAAAAA 385
 RESULT 68
 T30250
 Gtl protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul
 C:Accession: T30250
 R:Imai, Y.; Suzuki, Y.; Matsui, T.; Tohyama, M.; Wanaka, A.; Takagi, J
 Brain Res. Mol. Brain Res. 31, 1-9, 1995
 A:Title: Cloning of a retinoic acid-induced gene, Gtl, in the embryonal
 A:Reference number: Z20788; MUID:96078271; PMID:7476016

ry; translated from GB/EMBL/DBJ
NA
<IMA>
EMBL:D29801; NID:g475015; PIDN:BAA06184.1; PID:g475016
was specifically localized in neurons but not in glial cells
ity 1.7%; Score 9; DB 2; Length 1840;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
QPQP 233
|||||
QPQP 126

3 - winter flounder
euronectes americanus (winter flounder)
#sequence_revision 01-Sep-1981 #text_change 23-Aug-1996
n, Y.
Cta 495, 388-392, 1977
of a peptide antifreeze and mechanism of adsorption to ice.
A03192; MUID:78060969; PMID:588591

otein
EV>
freeze protein
eze
ity 1.5%; Score 8; DB 1; Length 37;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||||
ATA 36

enase (EC 1.14.16.2) type 1 and 2 - orangutan (fragment)
xygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
gmaeus (orangutan)
#sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
e, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
es. Commun. 195, 158-165, 1993
heterogeneity of tyrosine hydroxylase in humans.
PN0575; MUID:93371398; PMID:7689834

inomic RNA
ICH>
GB:114800
ce: lymphocytes of peripheral blood
yme catalyzes the first and rate-limiting step of catecholamine biosy
ylalanine 4-monooxygenase
lin; monooxygenase; oxidoreductase
ity 1.5%; Score 8; DB 2; Length 45;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAP 127
|||||
AAP 31

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - common gibbon (f
N; Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine
C; Species: Hylobates lar (common gibbon, white-handed gibbon)
C; Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-
C; Accession: PN0592
R; Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A; Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A; Reference number: PN0575; MUID:93371398; PMID:7689834
A; Accession: PN0592
A; Molecule type: Genomic RNA
A; Residues: 1-45 <ICH>
A; Cross-references: GB:114794
A; Experimental source: lymph nodes
C; Comment: This enzyme catalyzes the first and rate-limiting step of c
C; Superfamily: phenylalanine 4-monooxygenase
C; Keywords: biopterin; monooxygenase; oxidoreductase

Query Match 1.5%; Score 8; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 120 AAAAAAAP 127
|||||
DB 24 AAAAAAAP 31

RESULT 72

PN0593
tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - Japanese macaque
N; Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine
C; Species: Macaca fuscata (Japanese macaque)
C; Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-
C; Accession: PN0593
R; Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A; Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A; Reference number: PN0575; MUID:93371398; PMID:7689834
A; Accession: PN0593
A; Molecule type: genomic RNA
A; Residues: 1-45 <ICH>
A; Experimental source: kidney
C; Comment: This enzyme catalyzes the first and rate-limiting step of c
C; Superfamily: phenylalanine 4-monooxygenase
C; Keywords: biopterin; monooxygenase; oxidoreductase

Query Match 1.5%; Score 8; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 120 AAAAAAAP 127
|||||
DB 24 AAAAAAAP 31

RESULT 73

FDLAW
antifreeze protein A precursor - winter flounder
C; Species: Pseudopleuronectes americanus (winter flounder)
C; Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 22-Jun
C; Accession: JS0704; A03194
R; Davies, P.L.
Gene 112, 163-170, 1992
A; Title: Conservation of antifreeze protein-encoding genes in tandem r
A; Reference number: JH0627; MUID:92209995; PMID:1555765
A; Accession: JS0704
A; Molecule type: DNA
A; Residues: 1-82 <DAI>
A; Cross-references: GB:M62412; GB:M62416; NID:g213592; PIDN:AAA49471.1
R; Davies, P.L.; Roach, A.H.; Hew, C.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 335-339, 1982
A; Title: DNA sequence coding for an antifreeze protein precursor from
A; Reference number: A03194; MUID:82197490; PMID:6952188

A: RNA
A: DA2>
A: rce: clones 4-2b and 2A-7c
A: s translated the codon AGC for residue 24 as Arg
C: ifreeze protein
C: eeze; plasma; tandem repeat
C: nal sequence #status predicted <SIG>
C: eptide #status predicted <PRO>
C: antifreeze protein A #status predicted <MAT>
Query Match 1.5%; Score 8; DB 1; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 0; Mismatches 0; Indels 0;
QY AATA 158
Db AATA 80
RESULT 76
A05161
antifreeze protein B precursor - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 24-Oct-2000
C:Accession: A05161
R: Davies, P.L.; Hough, C.; Scott, G.K.; Ng, N.; White, B.N.; Hew, C.L.
J. Biol. Chem. 259, 9241-9247, 1984
A:Reference number: A05161; MUID:84264559; PMID:6086629
A:Accession: A05161
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:L00138; GB:J00929; NID:g343126; PIDN:AA859964;
C:Genetics:
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Keywords: antifreeze
Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
Db 73 AAAAAATA 80
RESULT 77
JS0705
antifreeze protein (clones 1A-la and 3-3a) - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
C:Accession: JS0705
R: Davies, P.L.
Gene 112, 163-170, 1992
A:Title: Conservation of antifreeze protein-encoding genes in tandem
A:Reference number: JH0627; MUID:92209995; PMID:1555765
A:Accession: JS0705
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M62413; NID:g213586; PIDN:AAA49468.1; PID:g213;
C:Genetics:
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Keywords: antifreeze
Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
Db 73 AAAAAATA 80
RESULT 78
IS1125
antifreeze protein - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
A: rce: clones 4-2b and 2A-7c
A: s translated the codon AGC for residue 24 as Arg
C: ifreeze protein
C: eeze; plasma; tandem repeat
C: nal sequence #status predicted <SIG>
C: eptide #status predicted <PRO>
C: antifreeze protein A #status predicted <MAT>
Query Match 1.5%; Score 8; DB 1; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 0; Mismatches 0; Indels 0;
QY AATA 158
Db AATA 80
RESULT 76
A05161
antifreeze protein B precursor - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 24-Oct-2000
C:Accession: A05161
R: Davies, P.L.; Hough, C.; Scott, G.K.; Ng, N.; White, B.N.; Hew, C.L.
J. Biol. Chem. 259, 9241-9247, 1984
A:Reference number: A05161; MUID:84264559; PMID:6086629
A:Accession: A05161
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:L00138; GB:J00929; NID:g343126; PIDN:AA859964;
C:Genetics:
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Keywords: antifreeze
Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
Db 73 AAAAAATA 80
RESULT 77
JS0705
antifreeze protein (clones 1A-la and 3-3a) - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
C:Accession: JS0705
R: Davies, P.L.
Gene 112, 163-170, 1992
A:Title: Conservation of antifreeze protein-encoding genes in tandem
A:Reference number: JH0627; MUID:92209995; PMID:1555765
A:Accession: JS0705
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M62413; NID:g213586; PIDN:AAA49468.1; PID:g213;
C:Genetics:
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Keywords: antifreeze
Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
Db 73 AAAAAATA 80
RESULT 78
IS1125
antifreeze protein - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
A: rce: clones 4-2b and 2A-7c
A: s translated the codon AGC for residue 24 as Arg
C: ifreeze protein
C: eeze; plasma; tandem repeat
C: nal sequence #status predicted <SIG>
C: eptide #status predicted <PRO>
C: antifreeze protein A #status predicted <MAT>
Query Match 1.5%; Score 8; DB 1; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 0; Mismatches 0; Indels 0;
QY AATA 158
Db AATA 80
RESULT 76
A05161
antifreeze protein B precursor - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 24-Oct-2000
C:Accession: A05161
R: Davies, P.L.; Hough, C.; Scott, G.K.; Ng, N.; White, B.N.; Hew, C.L.
J. Biol. Chem. 259, 9241-9247, 1984
A:Reference number: A05161; MUID:84264559; PMID:6086629
A:Accession: A05161
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:L00138; GB:J00929; NID:g343126; PIDN:AA859964;
C:Genetics:
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Keywords: antifreeze
Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
Db 73 AAAAAATA 80
RESULT 77
JS0705
antifreeze protein (clones 1A-la and 3-3a) - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
C:Accession: JS0705
R: Davies, P.L.
Gene 112, 163-170, 1992
A:Title: Conservation of antifreeze protein-encoding genes in tandem
A:Reference number: JH0627; MUID:92209995; PMID:1555765
A:Accession: JS0705
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M62413; NID:g213586; PIDN:AAA49468.1; PID:g213;
C:Genetics:
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Keywords: antifreeze
Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
Db 73 AAAAAATA 80
RESULT 78
IS1125
antifreeze protein - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)

```

1  #sequence_revision 13-Sep-1996 #text_change 24-Oct-2000
2  C;Genetics:
3  C;Introns: 19/2
4  C;Superfamily: antifreeze protein
5  C;Keywords: antifreeze; tandem repeat
6  F;1-21/Domain: signal sequence #status predicted <SIG>
7  F;22-91/Product: antifreeze protein IIA7 #status predicted <MAT>
8  Query Match 1.5%; Score 8; DB 2; Length 91;
9  Best Local Similarity 100.0%; Pred. No. 25;
10 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
11
12 QY 151 AAAAATA 158
13 Db 45 AAAAATA 52
14
15 RESULT 81
16 S58341
17 cystatin - Trypanosoma cruzi
18 C;Species: Trypanosoma cruzi
19 C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Sep
20 C;Accession: S58341
21 R;Stock, R.P.; Moro, A.; Ruiz-Cabello, F.; Gonzalez, A.
22 submitted to the EMBL Data Library, January 1995
23 A;Description: Cloning and sequence of a cystatin-like gene from Trypa
24 A;Reference number: S58341
25 A;Accession: S58341
26 A;Status: preliminary
27 A;Molecule type: DNA
28 A;Residues: 1-91 <STO>
29 A;Cross-references: EMBL:Z47798; NID:g940939; PID:g940940
30
31 Query Match 1.5%; Score 8; DB 2; Length 91;
32 Best Local Similarity 100.0%; Pred. No. 25;
33 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
34
35 QY 10 PETAAAAAT 17
36 Db 27 PETAAAAAT 34
37
38 RESULT 82
39 S02376
40 antifreeze protein precursor - yellowtail flounder
41 C;Species: Limanda ferruginea (yellowtail flounder)
42 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 24-Oct
43 C;Accession: S02376
44 R;Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L.
45 Eur. J. Biochem. 168, 629-633, 1987
46 A;Title: Structural variations in the alanine-rich antifreeze proteins
47 A;Reference number: S02376; MUID:88029483; PMID:3665937
48 A;Accession: S02376
49 A;Molecule type: mRNA
50 A;Residues: 1-97 <SCO>
51 A;Cross-references: EMBL:X06356; NID:g64041; PIDN:CAA29655.1; PID:g640
52 A;Note: part of this sequence, including the amino end of the mature p
53 C;Superfamily: antifreeze protein
54 C;Keywords: antifreeze
55 F;1-23/Domain: signal sequence #status predicted <SIG>
56 F;24-48/Domain: propeptide #status predicted <PRO>
57 F;49-96/Product: antifreeze protein #status predicted <MAT>
58
59 Query Match 1.5%; Score 8; DB 2; Length 97;
60 Best Local Similarity 100.0%; Pred. No. 26;
61 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
62
63 QY 119 PAAAAAAA 126
64 Db 39 PAAAAAAA 46
65
66 RESULT 83
67 7,65-91 <GAU>
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1  #sequence_revision 13-Sep-1996 #text_change 24-Oct-2000
2  C;Genetics:
3  C;Introns: 19/2
4  C;Superfamily: antifreeze protein
5  C;Keywords: antifreeze; tandem repeat
6  F;1-21/Domain: signal sequence #status predicted <SIG>
7  F;22-91/Product: antifreeze protein IIA7 #status predicted <MAT>
8  Query Match 1.5%; Score 8; DB 2; Length 91;
9  Best Local Similarity 100.0%; Pred. No. 25;
10 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
11
12 QY 151 AAAAATA 158
13 Db 45 AAAAATA 52
14
15 RESULT 81
16 S58341
17 cystatin - Trypanosoma cruzi
18 C;Species: Trypanosoma cruzi
19 C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Sep
20 C;Accession: S58341
21 R;Stock, R.P.; Moro, A.; Ruiz-Cabello, F.; Gonzalez, A.
22 submitted to the EMBL Data Library, January 1995
23 A;Description: Cloning and sequence of a cystatin-like gene from Trypa
24 A;Reference number: S58341
25 A;Accession: S58341
26 A;Status: preliminary
27 A;Molecule type: DNA
28 A;Residues: 1-91 <STO>
29 A;Cross-references: EMBL:Z47798; NID:g940939; PID:g940940
30
31 Query Match 1.5%; Score 8; DB 2; Length 91;
32 Best Local Similarity 100.0%; Pred. No. 25;
33 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
34
35 QY 10 PETAAAAAT 17
36 Db 27 PETAAAAAT 34
37
38 RESULT 82
39 S02376
40 antifreeze protein precursor - yellowtail flounder
41 C;Species: Limanda ferruginea (yellowtail flounder)
42 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 24-Oct
43 C;Accession: S02376
44 R;Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L.
45 Eur. J. Biochem. 168, 629-633, 1987
46 A;Title: Structural variations in the alanine-rich antifreeze proteins
47 A;Reference number: S02376; MUID:88029483; PMID:3665937
48 A;Accession: S02376
49 A;Molecule type: mRNA
50 A;Residues: 1-97 <SCO>
51 A;Cross-references: EMBL:X06356; NID:g64041; PIDN:CAA29655.1; PID:g640
52 A;Note: part of this sequence, including the amino end of the mature p
53 C;Superfamily: antifreeze protein
54 C;Keywords: antifreeze
55 F;1-23/Domain: signal sequence #status predicted <SIG>
56 F;24-48/Domain: propeptide #status predicted <PRO>
57 F;49-96/Product: antifreeze protein #status predicted <MAT>
58
59 Query Match 1.5%; Score 8; DB 2; Length 97;
60 Best Local Similarity 100.0%; Pred. No. 26;
61 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
62
63 QY 119 PAAAAAAA 126
64 Db 39 PAAAAAAA 46
65
66 RESULT 83
67 7,65-91 <GAU>
68
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A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: C69436
A:Status: preliminary; nucleic acid sequence not shown; translation n
A:Molecule type: DNA
A:Residues: 1-106 <KLE>
A:Cross-references: GB:AE000999; GB:AE000782; NID:G2689322; PIDN:AA8B8
C:Superfamily: rat acidic ribosomal protein P1

Query Match 1.5%; Score 8; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 118 APAAAAAA 125
|||||
Db 66 APAAAAAA 73

RESULT 86
S20693
hypothetical protein, 12.3K (early region E3) - human adenovirus 41
C:Species: Mastadenovirus h41 (human adenovirus 41)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-A-Ja
C:Accession: S20693
R:Pienaziek, N.J.; Slemenda, S.B.; Pienazek, D.; Velarde Jr., J.; Luf
submitted to the EMBL Data Library, March 1990
A:Description: Characterisation of the early region E3 of the human e
A:Reference number: S20688
A:Accession: S20693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <PIE>
A:Cross-references: EMBL:X52198; NID:G58660; PIDN:CAA36448.1; PID:G58
C:Superfamily: adenovirus early E3B 14.5K protein

Query Match 1.5%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 133 PPPPPAPV 140
|||||
Db 83 PPPPPAPV 90

RESULT 87
T38936
non-histone chromosomal protein high mobility group - fission yeast ("

C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Ja
C:Accession: T38936
R:Radcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z21818
A:Accession: T38936
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-108 <BAD>
A:Cross-references: EMBL:Z94864; PIDN:CAP08172.1; GSPDB:GN000066; SPDB:
A:Experimental source: strain 972h-; cosmid c57A10
C:Genetics:
A:Gene: SPDB:SPAC57A10.09c
A:Map position: 1
A:Introns: 44/1; 63/3
C:Superfamily: unassigned HMG box proteins; HMG box homology

Query Match 1.5%; Score 8; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 118 APAAAAAA 125
|||||
Db 98 APAAAAAA 105

rotein P1 - fruit fly (*Drosophila melanogaster*)
ribosomal protein A; ribosomal protein DL12EII; ribosomal protein rp2
ila melanogaster
#sequence_revision 31-Dec-1990 #text_change 22-Jun-1999

15, 10064, 1987
duced amino acid sequence of *Drosophila* rp21C, another 'A'-type ribo
: S00659; MUID:88096510; PMID:3122177

RNA
<WT>
: EMBL:Y00504; NID:g8475; PIDN:CAA68557.1; PID:g8476

2) 21C
: FlyBase:FBgn0002593
acidic ribosomal protein P1
protein; protein biosynthesis; ribosome

1.5%; Score 8; DB 1; Length 112;
arity 100.0%; Pred. No. 30;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 125
|||||
AAA 83

tein - common sunflower
us annuus (common sunflower)
#sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

J.L.; Pillay, D.T.N.; Steinmetz, A.
9, 238-244, 1991
ntron separates the signal peptide coding sequence of an anther-speci
S17718; MUID:92017657; PMID:1921973

RY
A
DOM>

1.5%; Score 8; DB 2; Length 121;
rity 100.0%; Pred. No. 32;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

PPP 137
|||
PPP 89

tein SP2 precursor - common sunflower
proline-rich protein
us annuus (common sunflower)
#sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
S13373
J.L.; Herdenberger, F.; Pillay, D.T.N.; Steinmetz, A.
, 643-646, 1990
sequence of two anther-specific cDNAs from sunflower (*Helianthus ann*
S12245; MUID:91338702; PMID:2102380

NA
DOM>
EMBL:X53374; NID:g18814; PIDN:CAA37454.1; PID:g18815
o, C.; Saint-Guilly, A.; Weil, J.H.; Kuntz, M.
, 271-281, 1991
cific, developmentally regulated expression of genes encoding a new d

A;Reference number: S13373; MUID:91370869; PMID:1716499
A;Accession: S13373
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-121 <EVR>
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-121/Product: anther-specific protein SP2 #status predicted <MAT>

Query Match 1.5%; Score 8; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 130 TPAPPPPP 137
|||
Db 82 TPAPPPPP 89

RESULT 91
T03603
another specific protein - rice
C;Species: *Oryza sativa* (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul
C;Accession: T03603
R;Tsuchiya, T.; Toriyama, K.; Ejiri, S.; Hinata, K.
Plant Mol. Biol. 26, 1737-1746, 1994
A;Title: Molecular characterization of rice genes specifically express
A;Reference number: Z14972; MUID:95161699; PMID:7858214
A;Accession: T03603
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-128 <TSU>
A;Cross-references: EMBL:D21160; NID:g736717; PIDN:BAA04696.1; PID:g16
A;Experimental source: subsp. Japonica
C;Genetics:
A;Introns: 110/3; 125/3
A;Note: g68

Query Match 1.5%; Score 8; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 18 TAAASSS 25
|||
Db 7 TAAASSS 14

RESULT 92
SEPG
secretin precursor - pig
C;Species: *Sus scrofa domestica* (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-
C;Accession: B35094; A01544; A36052
R;Kopin, A.S.; Wheeler, M.B.; Leiter, A.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 2299-2303, 1990
A;Title: Secretin: structure of the precursor and tissue distribution
A;Reference number: A35094; MUID:90192795; PMID:2315322
A;Accession: B35094
A;Molecule type: mRNA
A;Residues: 1-131 <KOP>
A;Cross-references: GB:M31496; NID:gl64670; PIDN:AAA31121.1; PID:gl6467
R;Mutt, V.; Jorpes, J.E.; Magnusson, S.
Eur. J. Biochem. 15, 513-519, 1970
A;Title: Structure of porcine secretin. The amino acid sequence.
A;Reference number: A91147; MUID:70282334; PMID:5465996
A;Accession: A01544
A;Molecule type: protein
A;Residues: 30-56 <MUT>
A;Note: tryptic peptides were sequenced
R;Gafvelin, G.; Joernvall, H.; Mutt, V.
Proc. Natl. Acad. Sci. U.S.A. 87, 6781-6785, 1990
A;Title: Processing of prosecretin: isolation of a secretin precursor f
A;Reference number: A36052; MUID:90370867; PMID:2395872
A;Accession: A36052


```

C:Superfamily: Escherichia coli ribosomal protein S16

Query Match      1.5%; Score 8; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 35;
Matches      8; Conservative      0; Mismatches      0; Indels      0;

QY      120 AAAAAAAP 127
      |||||
DB      120 AAAAAAAP 127

RESULT 95
A56062
Alu RNA-binding protein - human
C:Species: Homo sapiens (man)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 07-May-1995
C:Accession: A56062
R:Chang, D.Y.; Nelson, B.; Bilyeu, T.; Hsu, K.; Darlington, G.J.; Marzella, Jr.; Mol. Cell. Biol. 14, 3949-3959, 1994
A:Title: A human Alu RNA-binding protein whose expression is associated with the 5' long terminal repeat of the Alu element
A:Reference number: A56062; MUID:94254852; PMID:8196634
A:Accession: A56062
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CHA>
A:Cross-references: GB:U07857; NID:5469048; PID:g468209
C:Keywords: RNA binding

Query Match      1.5%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 35;
Matches      8; Conservative      0; Mismatches      0; Indels      0;

QY      120 AAAAAAAP 127
      |||||
DB      110 AAAAAAAP 117

RESULT 96
S34196
signal recognition particle 14K chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: S34196
R:Leffers, H.
submitted to the EMBL Data Library, June 1993
A:Description: The human signal recognition particle subunit (SRP14) n
A:Reference number: S34196
A:Accession: S34196
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <LEFF>
A:Cross-references: EMBL:X73459; NID:g313660; PIDN:CAA51838.1; PID:g313660

Query Match      1.5%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 35;
Matches      8; Conservative      0; Mismatches      0; Indels      0;

QY      120 AAAAAAAP 127
      |||||
DB      110 AAAAAAAP 117

RESULT 97
S34D97
hexon-associated protein - human adenovirus 7
N:Alternate names: polypeptide IX
C:Species: Mastadenovirus h7 (human adenovirus 7)
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 05-Jun-1981
C:Accession: A03954
R:DiJKema, R.; Maat, J.; Dekker, B.M.M.; van Ormondt, H.; Boyer, H.W.
Gene 13, 375-385, 1981
A:Title: The gene for polypeptide IX of human adenovirus type 7.
A:Reference number: A91480; MUID:81261948; PMID:6266923

```

ribonuclease Sa (EC 3.1.27.-) precursor - Streptomyces aureofaciens (s
N;Alternate names: guanyloribonuclease; ribonuclease Sa3
C;Species: Streptomyces aureofaciens
C;Date: 30-Sep-1993 #sequence_revision 02-Dec-1994 #text_change 06-Dec
C;Accession: JCI1287
R;Homeroova, D.; Hollaenderova, Z.; Kormanec, J.; Sevcik, J.
Gene 119, 147-148, 1992
A;Title: Cloning and sequencing of the gene encoding a ribonuclease fr
A;Reference number: JCI1287; MUID:93012968; PMID:1398084
A;Accession: JCI1287
A;Molecule type: DNA
A;Residues: 1-141 <ROM>
A;Cross-references: GB:M82920
A;Experimental source: strain CCM3239
C;Superfamily: ribonuclease Sa
C;Keywords: extracellular protein; hydrolase
F;1-28/Domain: (or 1-34) signal sequence #status predicted <SIG>
F;29-141/Product: (or 35-141) ribonuclease #status predicted <MAT>

Query Match 1.5%; Score 8; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 139 PVAAAAPA 146
Db 24 PVAAAAPA 31

RESULT 101
T06485
barwin homolog wheatwin1 precursor - wheat
N;Alternate names: barwin homolog PR4a
C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C;Accession: T06485
R;Caruso, C.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z15711
A;Accession: T06485
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-146 <CAR>
A;Cross-references: EMBL:AJ006098; PIDN:CAA06856.1
A;Experimental source: cv. S. Pastore, endosperm
C;Genetics:
A;Gene: PR4a
C;Superfamily: pathogenesis-related protein 4a; barwin homolog
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-146/Product: barwin homolog wheatwin1 #status predicted <MAT>
F;22-146/Domain: barwin homolog <BAR>

Query Match 1.5%; Score 8; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158
Db 14 AAAAAATA 21

RESULT 102
T06486
barwin homolog wheatwin2 precursor - wheat
N;Alternate names: barwin homolog PR4b
C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C;Accession: T06486
R;Caruso, C.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z15711
A;Accession: T06486
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA

ribonuclease Sa (EC 3.1.27.-) precursor - Streptomyces aureofaciens (s
N;Alternate names: guanyloribonuclease; ribonuclease Sa3
C;Species: Streptomyces aureofaciens
C;Date: 30-Sep-1993 #sequence_revision 02-Dec-1994 #text_change 06-Dec
C;Accession: JCI1287
R;Homeroova, D.; Hollaenderova, Z.; Kormanec, J.; Sevcik, J.
Gene 119, 147-148, 1992
A;Title: Cloning and sequencing of the gene encoding a ribonuclease fr
A;Reference number: JCI1287; MUID:93012968; PMID:1398084
A;Accession: JCI1287
A;Molecule type: DNA
A;Residues: 1-141 <ROM>
A;Cross-references: GB:M82920
A;Experimental source: strain CCM3239
C;Superfamily: ribonuclease Sa
C;Keywords: extracellular protein; hydrolase
F;1-28/Domain: (or 1-34) signal sequence #status predicted <SIG>
F;29-141/Product: (or 35-141) ribonuclease #status predicted <MAT>

Query Match 1.5%; Score 8; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 139 PVAAAAPA 146
Db 24 PVAAAAPA 31

RESULT 101
T06485
barwin homolog wheatwin1 precursor - wheat
N;Alternate names: barwin homolog PR4a
C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C;Accession: T06485
R;Caruso, C.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z15711
A;Accession: T06485
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-146 <CAR>
A;Cross-references: EMBL:AJ006098; PIDN:CAA06856.1
A;Experimental source: cv. S. Pastore, endosperm
C;Genetics:
A;Gene: PR4a
C;Superfamily: pathogenesis-related protein 4a; barwin homolog
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-146/Product: barwin homolog wheatwin1 #status predicted <MAT>
F;22-146/Domain: barwin homolog <BAR>

Query Match 1.5%; Score 8; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158
Db 14 AAAAAATA 21

RESULT 102
T06486
barwin homolog wheatwin2 precursor - wheat
N;Alternate names: barwin homolog PR4b
C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C;Accession: T06486
R;Caruso, C.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z15711
A;Accession: T06486
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA

11:33:41 2004

us-09-976-740-43.olog.rpr

```
<CAR>
: EMBL:AJ006099; PIDN:CAA06857.1
: cv: S. Pastore, endosperm

: hogenesis-related protein 4A; barwin homology
: inal sequence #status predicted <SIG>
: barwin homology wheatwin2 #status predicted <MAT>
: barwin homology <BAR>

1.5%; Score 8; DB 2; Length 148;
arity 100.0%; Pred. No. 38;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AATA 158
|||||
AATA 23

P protein HMG - fava bean
aba (fava bean)
4 #sequence_revision 03-Aug-1995 #text_change 21-May-1999
6
Ohlfarth, T.; Baumlein, H.; Feix, G.
3, 619-625, 1993
ve analysis of chromosomal HMG proteins from monocotyledons and dicoty
: S39556; MUID:94033341; PMID:8219095
6
ary
RNA
<GRA>
assigned HMG box proteins; HMG box homology
nding; nucleus
MG box homology <HMG1>

1.5%; Score 8; DB 2; Length 149;
arity 100.0%; Pred. No. 38;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

DEED 342
|||||
DEED 142

S16 [imported] - Caulobacter crescentus
cter crescentus
1 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
2
eldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
eBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Sci. U.S.A. 98, 4136-4141, 2001
Genome Sequence of Caulobacter crescentus.
: A87249; MUID:21173698; PMID:11259647
2
ary
NA
<STO>
: GB:AE005673; NID:gl3425408; PIDN:AAK25614.1; GSPDB:GN00148

1.5%; Score 8; DB 2; Length 165;
arity 100.0%; Pred. No. 41;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAP 127
|||||
AAP 142
```

```
RESULT 105
S35568
sex-determining protein Sry - multimammate rat (Mastomys hildebrandtii,
C:Species: Mastomys hildebrandtii
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Sep
C:Accession: S35568
R:Tucker, P.K.; Lundrigan, B.L.
Nature 364, 715-717, 1993
A:Title: Rapid evolution of the sex determining locus in Old World mi
A:Reference number: S35565; MUID:93361118; PMID:8355784
A:Accession: S35568
A:Molecule type: DNA
A:Residues: 1-172 <TUC>
A:Cross-references: GB:L29542; NID:g496161; PIDN:AAA40587.1; PID:g4961
C:Genetics:
A:Gene: Sry
A:Map position: Y
A:Superfamily: unassigned HMG box proteins; HMG box homology
C:Keywords: DNA binding
F:2-77/Domain: HMG box homology <HMG1>

Query Match 1.5%; Score 8; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 120 AAAAAAAP 127
Db 151 AAAAAAAP 158

RESULT 106
I48752
gene RXRbeta protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct
C:Accession: I48752
R:Nagata, T.; Kanno, Y.; Ozato, K.; Taketo, M.
Gene 142, 183-189, 1994
A:Title: The mouse Rxb gene encoding RXR beta: genomic organization a
A:Reference number: I48752; MUID:94252565; PMID:8194750
A:Accession: I48752
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-176 <RES>
A:Cross-references: EMBL:X72017; NID:g510152; PIDN:CAA50896.1; PID:g51
C:Genetics:
A:Gene: RXRbeta
A:Introns: 76/1; 137/2
C:Superfamily: mouse gene RXRbeta protein

Query Match 1.5%; Score 8; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 119 PAAAAAAA 126
Db 45 PAAAAAAA 52

RESULT 107
AB3269
outer membrane lipoprotein [imported] - Brucella melitensis (strain 16
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb
C:Accession: AB3269
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.;
; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Cal
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3269
```

```

ary
NA
<KUR>
: GB:AE008917; PIDN:AA151317.1; PID:g17982013; GSPDB:GN00190
rce: strain 16M

1.5%; Score 8; DB 2; Length 177;
arity 100.0%; Pred.No. 44;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PAPV 140
|||||
PAPV 41

tein, 57K - mouse
culus (house mouse)
5 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
1
Patrick, D.
MBL Data Library, September 1990
Accural analysis of mouse placental 57-KD Calcium-binding protein.
: S26491
1
ary
RNA
<TUA>
: EMBL:X56603; NID:g53597; PIDN:CAA39940.1; PID:g53598
n binding

1.5%; Score 8; DB 2; Length 178;
arity 100.0%; Pred.No. 44;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

DEED 342
|||||
DEED 24

In knirps - house fly (fragment)
mestica (house fly)
: #sequence_revision 06-Jan-1995 #text_change 07-May-1999
), D.
: 9-430, 1991
on gene expression in the housefly Musca domestica.
A61600; MUID:92146255; PMID:1685986
),
ary; not compared with conceptual translation
IA
: SOM>

1.5%; Score 8; DB 2; Length 180;
arity 100.0%; Pred.No. 44;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 126
|||||
AAA 173

HACPI88 - American lobster (fragment)
mericanus (American lobster)
: #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997

```

```

C;Accession: S77928
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the Ameri
A;Reference number: S77925
A;Accession: S77928
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-184 <NOU>
C;Keywords: blocked amino end; pyroglutamic acid
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimer

Query Match 1.5%; Score 8; DB 2; Length 184;
Best Local Similarity 100.0%; Pred.No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 120 AAAAAAAP 127
|||||
Db 175 AAAAAAAP 182

RESULT 111
JQ2247
Photosystem I chain D precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 28-May
C;Accession: JQ2247
R;Kjarulff, S.; Okkels, J.S.
Plant Physiol. 101, 335-336, 1993
A;Title: Cloning and sequencing of a full-length cDNA clone encoding t
A;Reference number: JQ2247; MUID:94105296; PMID:8278501
A;Accession: JQ2247
A;Molecule type: mRNA
A;Residues: 1-205 <KJA>
A;Cross-references: GB:M98254; NID:g167084; PIDN:AAA18567.1; PID:g1670
C;Superfamily: photosystem I chain II
C;Keywords: chloroplast; photosystem I
P;1-43/Domain: transit peptide (chloroplast) #status predicted <TNP>
P;44-205/Product: photosystem I chain D #status predicted <MAT>

Query Match 1.5%; Score 8; DB 2; Length 205;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 182 PAPAAPPA 189
|||||
Db 50 PAPAAPPA 57

RESULT 112
S41002
Hypothetical protein T05G5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep
C;Accession: S41002
R;Thomas, K.
submitted to the EMBL Data Library, October 1993
A;Reference number: S41001
A;Accession: S41002
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <THO>
A;Cross-references: EMBL:Z27079; NID:g414641; PID:g414643
C;Genetics:
A;Introns: 21/3

Query Match 1.5%; Score 8; DB 2; Length 205;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 132 APPPPAP 139
|||||
Db 176 APPPPAP 183

```

```

ein F2K13_270 - Arabidopsis thaliana
opsis thaliana (mouse-ear cross)
00 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
67
ura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
Protein Sequence Database, August 2000
r: Z25394
67
nary
DNA
<SAT>
s: EMBL:AL391141
irce: cultivar Columbia; BAC clone F2K13

141/3

1.5%; Score 8; DB 2; Length 207;
larity 100.0%; Pred. No. 50;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

EDDDE 336
|||||
EDDDE 38

in T29A15.30 - Arabidopsis thaliana
opsis thaliana (mouse-ear cross)
19 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
19
er Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; HC
Protein Sequence Database, March 1999
1: Z15455
19
NA
<BEV>
1: EMBL:AL035602
urce: cultivar Columbia; BAC clone T29A15

bidopsis thaliana hypothetical protein T29A15.30

1.5%; Score 8; DB 2; Length 208;
arity 100.0%; Pred. No. 50;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SSSA 26
|||||
SSSA 45

tein - dog
HSP27 protein
opus familiaris (dog)
5 #sequence_revision 08-Feb-1996 #text_change 13-Aug-1999
4
rthoffer, W.T.; Hickey, E.; Weber, L.A.
1995
nd sequencing of a cDNA encoding the canine HSP27 protein.
4: J4244; MUID:93394379; PMID:7665102
4
RNA

```

A;Residues: 1-209 <IAR>
A;Cross-references: GB:U19368; NID:G624684; PIDN:AAA87172.1; PID:G624
A;Experimental source: smooth muscle
C;Comment: This protein is synthesized in a wide range of tissues in
entiation, modulation of actin microfilament dynamics and smooth musc
C;Superfamily: alpha-crystallin
C;Keywords: heat shock; phosphoprotein; stress-induced protein
F;66-75/Region: alanine-rich
F;15,82,86/Binding site: phosphate (Ser) (covalent) (by MAP kinase II

Query Match 1.5%; Score 8; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 119 PAAAAAAA 126
|||||
DB 66 PAAAAAAA 73

RESULT 116
A86455
hypothetical protein F9L11.19 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-De
C;Accession: A86455
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creas
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; K
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; M
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidops
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86455
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 <STO>
A;Cross-references: GB:AB005172; NID:G6910577; PIDN:AAF31282.1; GSPDB
C;Genetics:
A;Map position: 1

Query Match 1.5%; Score 8; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 330 EEEDEDED 337
|||||
DB 37 EEEDEDED 44

RESULT 117
B89716
protein F45B8.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov
C;Accession: B89716
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for in
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac
A;Note: published errata appeared in Science 283, 35, 1999; Science 28
A;Accession: B89716
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: GB:chr_X; PIDN:CAB05726.1; PID:G3877144; GSPDB:GNO
C;Genetics:
A;Gene: F45B8.3
A;Map position: X

1.5%; Score 8; DB 2; Length 211;
 arity 100.0%; Pred. No. 51;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

PAAP 187
 ||||
 PAAP 119

a PFL - rice
 ativa (rice)
 9 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 l
 ; Ichida, A.; Quail, P.H.
 301, 1994
 -T hook containing DNA binding protein from rice that interacts with a
 : Z15142; MUID:94198599; PMID:8148649
 l
 ry; translated from GB/EMBL/DBDJ
 RNA
 <NIE>
 : EMBL:L24390; NID:g453691; PIDN:AAA33914.1; PID:g453692
 ce: cv. Nipponbare, shoot

one H1
 iding

1.5%; Score 8; DB 2; Length 213;
 ivity 100.0%; Pred. No. 51;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAP 127
 ||||
 AAAP 117

nucleoprotein-associated protein Sm11, cardiac - rat (fragment)
 orvegicus (Norway rat)
 #sequence_revision 22-Jun-1990 #text_change 26-May-2000
 S.; Russo, A.F.; Simmons, D.M.; Rosenfeld, M.G.
 ci. U.S.A. 86, 9778-9782, 1989
 of cDNA clones encoding small nuclear ribonucleoparticle-associated H
 A34503; MUID:90093348; PMID:2532363

ry
 NA
 LIS>
 GB:M29295; NID:g207009; PIDN:AAA42159.1; PID:g207010
 ine-rich protein
 muscle; heart

1.5%; Score 8; DB 2; Length 214;
 rity 100.0%; Pred. No. 51;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158
 ||||
 ATA 142

- rainbow trout
 chus mykiss (rainbow trout)
 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

R;Stros, M.; Retief, J.D.; Dixon, G.H.
 Gene 158, 181-187, 1995
 A:Title: cDNA sequence and structure of a trout HMG-2 gene. Evidence f
 A:Reference number: 151067; MUID:95331614; PMID:7607539
 A:Accession: 151067
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-215 <STR>
 A:Cross-references: GB:L32954; NID:g609552; PIDN:AAA74556.1; PID:g6095
 C:Genetics:
 A:Gene: HMG-T2
 A:Introns: 50/3; 101/2; 159/3
 C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
 F;6-83/Domain: HMG box homology <HMG1>
 F;94-168/Domain: HMG box homology <HMG2>

Query Match 1.5%; Score 8; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 330 EEEEDDED 337
 |||||
 Db 206 EEEEDDED 213

RESULT 121
 RDNCUF
 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) Rieske iron-sulfur prot
 C:Species: Neurospora crassa
 C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 03-Jun
 C:Accession: A24612
 R;Harnisch, U.; Weiss, H.; Sebal, W.
 Eur. J. Biochem. 149, 95-99, 1985
 A:Title: The primary structure of the iron-sulfur subunit of ubiquinol
 A:Reference number: A24612; MUID:85203899; PMID:2986972
 A:Accession: A24612
 A:Molecule type: DNA
 A:Residues: 1-231 <HAR>
 A:Cross-references: GB:X02472; NID:g3001; PIDN:CAA26308.1; PID:g3002
 C:Genetics:
 A:Introns: 92/1; 121/3; 172/1
 C:Superfamily: ubiquinol-cytochrome-c reductase iron-sulfur protein; R
 C:Keywords: 2Fe-2S; electron transfer; membrane-associated complex; me
 F;164-211/Domain: Rieske [2Fe-2S] homology <RSK>
 F;174-176,193,196/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (c
 F;179-195/Disulfide bonds: #status predicted
 F;196/Active site: His #status predicted

Query Match 1.5%; Score 8; DB 1; Length 231;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 141 AAAAPARA 148
 |||||
 Db 14 AAAAPARA 21

RESULT 122
 IS3659
 Sm-B protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-
 C:Accession: IS3659
 R;Griffith, A.J.; Schmauss, C.; Craft, J.E.
 Gene 114, 195-201, 1992
 A:Title: The murine gene encoding the highly conserved Sm B protein cor
 A:Reference number: IS3659; MUID:92290275; PMID:1376292
 A:Accession: IS3659
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-231 <RES>
 A:Cross-references: GB:M58761; NID:g200991; PIDN:AAA40119.1; PID:g20099
 C:Superfamily: proline-rich protein

1.5%; Score 8; DB 2; Length 231;
 Identity 100.0%; Pred. No. 55;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATA 158
 |||||
 AAATA 159

tion regulator protein [imported] - Sinorhizobium meliloti (strain 102
 izobium meliloti
 11 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 30
 nder, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Sci. U.S.A. 98, 9889-9894, 2001
 late sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
 : A95842; MUID:21396508; PMID:11481431
 30
 1ary
 DNA
 <KUR>
 : GB:AL591985; PIDN:CAC48548.1; PID:gl15140020; GSPDB:GN00167
 :ce: strain 1021, megaplasmid pSymb
 :nan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
 :; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 Jones, T.
 72, 2001
); Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 mbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 site genome of the legume symbiont Sinorhizobium meliloti.
 : A96039; MUID:21368234; PMID:11474104
 ition

1.5%; Score 8; DB 2; Length 233;
 Identity 100.0%; Pred. No. 55;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
 |||||
 AAAA 114

lulator, GntR family pdhR [imported] - Agrobacterium tumefaciens (strain
 erium tumefaciens
 12 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 18
 bal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 P.; Zhang, S.
 2323, 2001
); Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 e of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 : AB2577; MUID:21608550; PMID:11743193
 18
 1ary
 DNA
 <KUR>
 : GB:AE008687; PIDN:AAL45767.1; PID:gl7743501; GSPDB:GN00188
 :ce: strain C58 (Dupont)

1.5%; Score 8; DB 2; Length 234;
 Identity 100.0%; Pred. No. 55;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 55;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAA 126
 |||||
 DB 107 PAAAAAA 114

RESULT 125
 PQ0806
 glycinin A3B4 - soybean (cv. Mandarin) (fragment)
 N:Alternate names: 11S globulin; basic and acidic chains
 C:Species: Glycine max (soybean)
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 C:Accession: PQ0806
 R:Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
 A:Title: An attempt to elucidate the origin of cultivated soybean via
 genitor, Glycine soja.
 A:Reference number: PQ0806
 A:Accession: PQ0806
 A:Molecule type: mRNA
 A:Residues: 1-236 <ZAK>
 C:Superfamily: glycinin
 C:Keywords: seed; storage protein
 F:84-236/Product: glycinin, B4 chain #status predicted <GB4>

Query Match 1.5%; Score 8; DB 2; Length 236;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 334 DDEDEEE 341
 |||||
 DB 26 DDEDEEE 33

RESULT 126
 PQ0809
 glycinin A3B4 (plasmid pSGLI) - Glycine soja (strain 123) (fragment)
 N:Alternate names: 11S globulin; basic and acidic chains
 C:Species: Glycine soja
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 C:Accession: PQ0809
 R:Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
 A:Title: An attempt to elucidate the origin of cultivated soybean via
 genitor, Glycine soja.
 A:Reference number: PQ0809
 A:Accession: PQ0809
 A:Molecule type: mRNA
 A:Residues: 1-238 <ZAK>
 C:Superfamily: glycinin
 C:Keywords: seed; storage protein
 F:99-238/Product: glycinin B4 chain #status predicted <GLB>

Query Match 1.5%; Score 8; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 334 DDEDEEE 341
 |||||
 DB 41 DDEDEEE 48

RESULT 127
 AG3553
 transcription regulator, gntR family BMEI10352 [imported] - Brucella m
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Jul
 C:Accession: AG3553
 R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.;
 ; Mazur, M.; Coltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Cal

Sci. U.S.A. 99, 443-448, 2002
 A: Sequence of the facultative intracellular pathogen *Brucella melitens*
 : AD3252; PMID:11756688
 3
 A: Translation not shown
 A: Molecule type: mRNA
 A: Residues: 1-229, 'LL' <SCH>
 A: Cross-references: EMBL:X15893; NID:g29409; PIDN:CAA33902.1; PID:g294
 A: Note: This is a revision to the sequence from reference S07641
 R: Schmauss, C.; McAllister, G.; Ohosone, Y.; Hardin, J.A.; Lerner, M.F.
 Nucleic Acids Res. 17, 1733-1743, 1989
 A: Title: A comparison of snRNP-associated Sm-autoantigens: human N, ra
 A: Reference number: S07641; MUID:89160326; PMID:2522186
 A: Contents: annotation
 A: Note: translation of nucleotide sequence is not given
 A: Note: the nucleotide sequence contains several frameshift errors tha
 R: Ohosone, Y.; Mimori, T.; Griffith, A.; Akizuki, M.; Homma, M.; Craft
 Proc. Natl. Acad. Sci. U.S.A. 86, 4249-4253, 1989
 A: Title: Molecular cloning of cDNA encoding Sm autoantigen: derivation
 A: Reference number: A32909; MUID:89264596; PMID:2524838
 A: Accession: A32909
 A: Molecule type: mRNA
 A: Residues: 1-171, 'L', 173, 175-201, 203-216, 'S', 219-226, 'CEAFFDPWPQSMVEVA
 A: Cross-references: GB:J04564; NID:g190246; PIDN:AAA60151.1; PID:g1902
 A: Note: this sequence has been corrected in reference A36189
 R: Ohosone, Y.; Mimori, T.; Griffith, A.; Akizuki, M.; Homma, M.; Craft
 Proc. Natl. Acad. Sci. U.S.A. 86, 8982, 1989
 A: Reference number: A36189
 A: Accession: A36189
 A: Molecule type: mRNA
 A: Residues: 170-229, 'LL' <OH2>
 A: Note: this is a revision to reference A32909
 C: Comment: snRNP proteins B and B' result from alternative splicing of
 C: Genetix:
 A: Gene: GDB:SNRNP; SNRNP1
 A: Cross-references: GDB:118877; OMIM:182282
 A: Map position: 20pter-20qter
 A: Introns: 229/1
 A: Note: the list of introns may be incomplete
 C: Superfamily: proline-rich protein
 C: Keywords: alternative splicing; nucleus; splicing protein
 Query Match 1.5%; Score 8; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 Qy 151 AAAAAATA 158
 Db 152 AAAAAATA 159
 RESULT 129
 H69932
 hypothetical protein ypbE - *Bacillus subtilis*
 C: Species: *Bacillus subtilis*
 C: Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct
 C: Accession: H69932
 R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; A
 C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.;
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret
 Nature 390, 249-256, 1997
 A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; G
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hoson
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapid
 A: Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.;
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.;
 A: Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; St
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Ya
 A: Title: The complete genome sequence of the Gram-positive bacterium B
 A: Reference number: A69580; MUID:98044033; PMID:9384377
 A: Accession: H69932
 A: Status: preliminary; nucleic acid sequence not shown; translation not

Sci. U.S.A. 99, 443-448, 2002
 A: Sequence of the facultative intracellular pathogen *Brucella melitens*
 : AD3252; PMID:11756688
 3
 A: Translation not shown
 A: Molecule type: mRNA
 A: Residues: 1-229, 'LL' <SCH>
 A: Cross-references: EMBL:X15893; NID:g29409; PIDN:CAA33902.1; PID:g294
 A: Note: This is a revision to the sequence from reference S07641
 R: Schmauss, C.; McAllister, G.; Ohosone, Y.; Hardin, J.A.; Lerner, M.F.
 Nucleic Acids Res. 17, 1733-1743, 1989
 A: Title: A comparison of snRNP-associated Sm-autoantigens: human N, ra
 A: Reference number: S07641; MUID:89160326; PMID:2522186
 A: Contents: annotation
 A: Note: translation of nucleotide sequence is not given
 A: Note: the nucleotide sequence contains several frameshift errors tha
 R: Ohosone, Y.; Mimori, T.; Griffith, A.; Akizuki, M.; Homma, M.; Craft
 Proc. Natl. Acad. Sci. U.S.A. 86, 4249-4253, 1989
 A: Title: Molecular cloning of cDNA encoding Sm autoantigen: derivation
 A: Reference number: A32909; MUID:89264596; PMID:2524838
 A: Accession: A32909
 A: Molecule type: mRNA
 A: Residues: 1-171, 'L', 173, 175-201, 203-216, 'S', 219-226, 'CEAFFDPWPQSMVEVA
 A: Cross-references: GB:J04564; NID:g190246; PIDN:AAA60151.1; PID:g1902
 A: Note: this sequence has been corrected in reference A36189
 R: Ohosone, Y.; Mimori, T.; Griffith, A.; Akizuki, M.; Homma, M.; Craft
 Proc. Natl. Acad. Sci. U.S.A. 86, 8982, 1989
 A: Reference number: A36189
 A: Accession: A36189
 A: Molecule type: mRNA
 A: Residues: 170-229, 'LL' <OH2>
 A: Note: this is a revision to reference A32909
 C: Comment: snRNP proteins B and B' result from alternative splicing of
 C: Genetix:
 A: Gene: GDB:SNRNP; SNRNP1
 A: Cross-references: GDB:118877; OMIM:182282
 A: Map position: 20pter-20qter
 A: Introns: 229/1
 A: Note: the list of introns may be incomplete
 C: Superfamily: proline-rich protein
 C: Keywords: alternative splicing; nucleus; splicing protein
 Query Match 1.5%; Score 8; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 Qy 151 AAAAAATA 158
 Db 152 AAAAAATA 159
 RESULT 129
 H69932
 hypothetical protein ypbE - *Bacillus subtilis*
 C: Species: *Bacillus subtilis*
 C: Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct
 C: Accession: H69932
 R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; A
 C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.;
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret
 Nature 390, 249-256, 1997
 A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; G
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hoson
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapid
 A: Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.;
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.;
 A: Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; St
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Ya
 A: Title: The complete genome sequence of the Gram-positive bacterium B
 A: Reference number: A69580; MUID:98044033; PMID:9384377
 A: Accession: H69932
 A: Status: preliminary; nucleic acid sequence not shown; translation not


```

DNA
<XUN>
s: GB:Z99115; GB:Z99116; GB:ALC00126; NID:G2634723; PIDN:CAB14232.1; PID:
rce: strain 168

1.5%; Score 8; DB 2; Length 240;
arity 100.0%; Pred. No. 57;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AASSS 25
|||||
AASSS 167

sin F45B8.3 - Caenorhabditis elegans
habditis elegans
#9 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
16

EMBL Data Library, December 1996
Z19531
6
ary; translated from GB/EMBL/DDBJ
DNA
<WIL>
s: EMBL:Z83227; PIDN:CAB05726.2; GSPDB:GN00028; CESP:F45B8.3
rce: clone F45B8
1.3
8/3; 211/2
1.5%; Score 8; DB 2; Length 241;
arity 100.0%; Pred. No. 57;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PAAP 187
|||||
PAAP 119

ybean (cv. Mukden) (fragment)
11S globulin; basic and acidic chains
max (soybean)
#4 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
17
Epishin, S.M.; Vinetski, Y.P.
78, 852-856, 1989
t to elucidate the origin of cultivated soybean via comparison of nucl
coja.
PQ0806
17
RNA
<ZAK>
cinin
storage protein
1.5%; Score 8; DB 2; Length 243;
arity 100.0%; Pred. No. 57;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEEE 341
|||||
DEEE 48


```

```

A28993
auxin-induced protein aux28 - soybean
C:Species: Glycine max (soybean)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Au
C:Accession: A28993
R:Ainley, W.M.; Walker, J.C.; Nagao, R.T.; Key, J.L.
J. Biol. Chem. 263, 10658-10666, 1988
A:Title: Sequence and characterization of two auxin-regulated genes f
A:Reference number: A92658; MUID:88273183; PMID:2899079
A:Accession: A28993
A:Molecule type: mRNA
A:Residues: 1-243 <AIN>
A:Cross-references: GB:J03919; NID:gl69920; PIDN:AAA33945.1; PID:gl69
C:Genetics:
A:Gene: aux28
C:Superfamily: auxin-induced protein aux28
C:Keywords: nucleus

Query Match 1.5%; Score 8; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 15 AATTAAAA 22
|||||
DB 54 AATTAAAA 61

RESULT 133
A98330
sporulation transcription factor (AF096293) [imported] - Agrobacteriu
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov
C:Accession: A98330
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qu
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappa
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A98330
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-244 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90163.1; PID:gl5160164; GSPDI
C:Genetics:
A:Gene: AGR_L_3177
A:Map position: linear chromosome
C:Superfamily: transcription regulator, GntR family

Query Match 1.5%; Score 8; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAAA 126
|||||
DB 118 PAAAAAAA 125

RESULT 134
AD2953
transcription regulator, GntR family Atu3226 [imported] - Agrobacteriu
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov
C:Accession: AD2953
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, F
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Rao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tume
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2953
A:Status: preliminary


```

NA
 <KUR>
 : GB:AF008689; PIDN:AA144042.1; PID:gl7741604; GSPDB:GN00187
 rce: strain C58 (Dupont)

near chromosome
 nscription regulator, GntR family

1.5%; Score 8; DB 2; Length 244;
 arity 100.0%; Pred. No. 57;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
 |||||
 AAAA 125

rB9 homolog [imported] - Brucella melitensis (strain 16M)
 a melitensis
 2 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 3
 ; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 sman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Sci. U.S.A. 99, 443-448, 2002
 e sequence of the facultative intracellular pathogen Brucella melitensis
 : AD3252; PMID:11756688
 3
 axY
 NA
 <KUR>
 : GB:AF008918; PIDN:AAU53274.1; PID:gl7984156; GSPDB:GN00191
 rce: strain 16M

or-inducing plasmid pTic58 virB9 protein

1.5%; Score 8; DB 2; Length 247;
 arity 100.0%; Pred. No. 58;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
 |||||
 AAAA 110

integral membrane protein - Streptomyces coelicolor
 myces coelicolor
 ; #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
 i
 is, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 4BL Data Library, January 1998
 : Z21548
 i
 irY; translated from GB/EMBL/DBDJ
 NA
 <MUR>
 : EMBL:AL021411; PIDN:CAA16216.1; GSPDB:GN00070; SCOEDB:SC7H1.29C
 rce: strain A3(2)

DB:SC7H1.29C
 ult transport protein Q homolog

1.5%; Score 8; DB 2; Length 249;
 arity 100.0%; Pred. No. 58;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

QAGG 244

DB 97 GGAVRAGG 104
 |||||
 RESULT 137
 A37280
 C/EBP-related protein CRP1 - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 13-Sep
 C/Accession: A37280
 R.Williams, S.C.; Cantwell, C.A.; Johnson, P.F.
 Genes Dev. 5, 1553-1567, 1991
 A/Title: A family of C/EBP-related proteins capable of forming covalent
 A/Reference number: A37280; MUID:91357471; PMID:1884998
 A/Accession: A37280
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-249 <WIL>
 A/Cross-references: GB:M85143
 C/Superfamily: CCAAT/enhancer-binding protein alpha

Query Match 1.5%; Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 138 APVAAAAP 145
 |||||
 Db 139 APVAAAAP 146

RESULT 138
 S59404
 hypothetical protein YLR435w - Yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein L9753.3
 C/Species: Saccharomyces cerevisiae
 C/Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr
 C/Accession: S59404
 R/Du, Z.
 submitted to the EMBL Data Library, February 1995
 A/Description: The sequence of S. cerevisiae cosmid 9753.
 A/Reference number: S59401
 A/Accession: S59404
 A/Molecule type: DNA
 A/Residues: 1-249 <DUZ>
 A/Cross-references: EMBL:U21094; NID:q665967; PIDN:AA567515.1; PID:q66
 A/Experimental source: strain S288C (AB972)
 C/Genetics:
 A/Gene: MIPS:YLR435w
 A/Cross-references: SGD:S0004427
 A/Map position: 12R

Query Match 1.5%; Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 334 DDEDEEE 341
 |||||
 Db 209 DDEDEEE 216

RESULT 139
 A41497
 36K antigen pra - Mycobacterium leprae
 C/Species: Mycobacterium leprae
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jun-
 C/Accession: A41497
 R/hole, J.E.R.; Stabel, L.F.B.M.; Suykerbuyk, M.B.G.; de Wit, M.Y.L.;
 Infect. Immun. 58, 80-87, 1990
 A/Title: A major immunogenic 36,000-molecular-weight antigen from Mycol
 A/Reference number: A41497; MUID:90093489; PMID:1688422
 A/Accession: A41497
 A/Molecule type: DNA
 A/Residues: 1-249 <THO>

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A: 1: GB:X65546
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    100.0%; Pred. No. 58;
    0; Mismatches 0; Indels 0; Gaps 0;
    APPPP 136
    |||||
    APPPP 19

polymerase (EC 2.7.7.6) III chain C31 - yeast (Saccharomyces cerevisiae)
: DNA-directed RNA polymerase C chain C31; DNA-directed RNA polymerase
: myces cerevisiae
: 1 #sequence revision 31-Dec-1991 #text change 21-Jul-2000
: 5; A33811; A33656; S42275; S60976; S63103; S63823; S12321
: M.; Beltrame M.; Cassar, E.; Sentenac, A.; Thuriaux, P.
: 10, 4737-4743, 1990
: 1 gene of Saccharomyces cerevisiae encodes a subunit of RNA polymerase
: A36465; MUID:90355990; PMID:2201900
: 5
: acid sequence not shown
: NA
: <MOS>
: 1: EMBL:X51498; NID:G4376; PIDN:CAA35866.1; PID:G4377
: 1
: protein
: 58-63 <MOS2>
: odrubetz, D.
: 1, 1282-1289, 1988
: aromyces cerevisiae ACP2 gene encodes an essential HMGI-like protein.
: A33656; MUID:88216604; PMID:2835668
: 6
: NA
: <HAG>
: 1: EMBL:M20315
: odrubetz, D.
: MBL Data Library, February 1989
: 1: S42275
: 5
: NA
: R' 13-204, 'H' 206-251 <HA2>
: 1: EMBL:M20315; NID:G170983; PIDN:AAA34390.1; PID:G170984
: A.M.; Herbert, C.J.
: MBL Data Library, October 1995
: sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 co
: nase.
: 1: S60958
: 6
: NA
: <NAS>
: 1: EMBL:X92517; NID:G1050783; PIDN:CAA63288.1; PID:G1050801
: A.M.; Herbert, C.
: rotein Sequence Database, April 1996
: 1: S62967
: 3
: NA
: <NAW>
: 1: EMBL:Z71427; NID:G1302107; PIDN:CAA96038.1; PID:G1302108; GSPDB:GN00
: ice: strain S288C
: A.M.; Herbert, C.J.
: 1996
: nce of 36.8 kb from the left arm of chromosome XIV reveals 24 complete
: 1: S63805; MUID:96287653; PMID:8686380
: 3
: acid sequence not shown; translation not shown
: NA
: <NAF>
: 1: EMBL:X92517; NID:G1050783; PIDN:CAA63288.1; PID:G1050801
: tide sequence was submitted to the EMBL Data Library, October 1995

C:Genetics:
A:Gene: SGD:RPC31; APC2; RPC8; MIPS:YNL151C
A:Cross-references: SGD:S0005095; MIPS:YNL151C
A:Map position: 14L
C:Superfamily: DNA-directed RNA polymerase III chain C31
C:Keywords: DNA binding; nucleotidyltransferase; transcription
F:202-248/Region: acidic

Query Match 1.5%; Score 8; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 336 EDEDEDD 343
DB 215 EDEDEDD 222

RESULT 141
PQ0808
Glycinin A3B4 (plasmid pSG204) - soybean (cv. Rannaya-10) (fragment)
N:Alternate names: 11S globulin; basic and acidic chains
N:Contains: glycinin B4 chain
C:Species: Glycine max (soybean)
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-
C:Accession: PQ0808
R:Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
Theor. Appl. Genet. 78, 852-856, 1989
A:Title: An attempt to elucidate the origin of cultivated soybean via
genitor, Glycine soja
A:Reference number: PQ0806
A:Accession: PQ0808
A:Molecule type: mRNA
A:Residues: 1-251 <ZAK>
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:99-251/Product: glycinin B4 chain #status predicted <GB4>

Query Match 1.5%; Score 8; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 334 DDEDEDE 341
DB 41 DDEDEDE 48

RESULT 142
TI9129
hypothetical protein C09F9.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct
C:Accession: TI9129
R:Smve, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19078
A:Accession: TI9129
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-253 <WIL>
A:Cross-references: EMBL:Z81465; PIDN:CA03860.1; GSPDB:GN000020; CESP:
A:Experimental source: clone C09F9
C:Genetics:
A:Gene: CESP:C09F9.4
A:Map position: 2
A:Introns: 111/3; 128/1; 189/3

Query Match 1.5%; Score 8; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 220 PPQQQQPP 227
DB 203 PPQQQQPP 210

```

in Rv1995 - Mycobacterium tuberculosis (strain H37RV)
terium tuberculosis
8 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
8
ch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
es, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
4, 1998
R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
ng the biology of Mycobacterium tuberculosis from the complete genome
8 : A70500; MUID:98295987; PMID:9634230
ary; nucleic acid sequence not shown; translation not shown
NA
<COL>
: GB:274025; GB:AL123456; NID:g3261586; PIDN:CAA98391.1; PID:e248805;
rce: strain H37RV
bacterium tuberculosis hypothetical protein Rv1995
1.5%; Score 8; DB 2; Length 255;
arity 100.0%; Pred. No. 60;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 22
|||||
AAAA 166
} - rice
ativa (rice)
; #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
MBL Data Library, February 1997
: Z15103
; r; translated from GB/EMBL/DBJ
RNA
;COR>
EMBL:Y11414; PIDN:CAA72217.1
ce: cv. Arborio, coleoptile
idopsis 28K leaf-specific myb-related protein; myb DNA-binding repeat
DNA-binding repeat homology <MYB1>
b DNA-binding repeat homology <MYB>
1.5%; Score 8; DB 2; Length 257;
arity 100.0%; Pred. No. 60;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
APP 128
|||
APP 150
r protein - alfalfa (fragment)
sativa (alfalfa)
; #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
681-682, 1993
ing putative zinc finger motifs from salt-tolerant alfalfa (Medicago

A;Reference number: Z16794; MUID:94151444; PMID:8108516
A;Accession: T09646
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-257 <WIN>
A;Cross-references: EMBL:L07291; NID:gl66409; PID:gl66410
A;Experimental source: strain HG2; callus
C;Keywords: zinc finger
Query Match 1.5%; Score 8; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 329 EEEEDDDE 336
Db 191 EEEEDDDE 198
|||
|||
RESULT 146
H88130
protein F10G7.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May
C;Accession: H88130
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for in
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac
A;Note: published errata appeared in Science 283, 35, 1999; Science 28
A;Accession: H88130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <STO>
A;Cross-references: GB:chr_II; PIDN:AA81128.1; PID:g1055159; GSPDB:GNO
C;Genetics:
A;Gene: F10G7.3
A;Map position: 2
Query Match 1.5%; Score 8; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 329 EEEEDDDE 336
Db 173 EEEEDDDE 180
|||
|||
RESULT 147
S63604
homeobox protein Gsh-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 17-Nov
C;Accession: S63604; S66126; A37290; A38809
R;Li, H.; Zeitler, F.S.; Valerius, M.T.; Small, K.; Potter, S.S.
EMBO J. 15, 714-724, 1996
A;Title: Gsh-1, an orphan hox gene, is required for normal pituitary d
A;Reference number: S63604; MUID:96181350; PMID:8631293
A;Accession: S63604
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-261 <LHA>
R;Valerius, M.T.; Li, H.; Stock, J.L.; Weinstein, M.; Kaur, S.; Singh,
Dev. Dyn. 203, 337-351, 1995
A;Title: Gsh-1: A novel murine homeobox gene expressed in the central i
A;Reference number: S66126; MUID:96172995; PMID:8589431
A;Accession: S66126
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <VAL>
A;Cross-references: EMBL:U21224; NID:g936957; PIDN:AAA96814.1; PID:g936
R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copel
Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991

11:33:41 2004

us-09-976-740-43.Orig.rpr

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A: cation of 10 murine homeobox genes.
A: r: A37290; MUID:92073356; PMID:1683707
A: 90
A: nary
A: DNA
A: 05 <SIN>
A: assigned homeobox proteins; homeobox homology
A: inding; homeobox; nucleus; transcription regulation
A: homeobox homology <HOX>
A: 1.5%; Score 8; DB 2; Length 261;
A: larity 100.0%; Pred. No. 61;
A: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A: AAAAA 126
A: |||||
A: AAAAA 116
A:
A: sin - common tobacco
A: ina tabacum (common tobacco)
A: 95 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
A: 56
A: illi, A.G.; Albersheim, P.
A: EMBL Data Library, July 1993
A: ivation of a tobacco glycine-rich protein gene by a fungal glucan prep
A: : S34666
A: 56
A: nary
A: DNA
A: <BRA>
A: : EMBL:X74106; NID:G395146; PIDN:CAA52208.1; PID:G395147
A: iseculus glycine-rich protein 1.0
A: 1.5%; Score 8; DB 2; Length 271;
A: arity 100.0%; Pred. No. 63;
A: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A:
A: KGAGG 266
A: |||||
A: KGAGG 261
A:
A: or hoxa-9 - mouse
A: culus (house mouse)
A: 8 #sequence_revision 05-Dec-1998 #text_change 15-Oct-1999
A: 3
A: aki, K.; Chisaka, O.; Araki, M.; Takagi, K.; Yamamura, K.
A: 998
A: of the murine Hoxa-9 cDNA: An alternatively spliced transcript encodes
A: : JC6553; MUID:98192518; PMID:9524228
A: 3
A: RNA
A: <FUJ>
A: : DDBJ:AB008914
A:
A: assigned homeobox proteins; homeobox homology
A: nding; homeobox; metal binding; nucleus; transcription regulation
A: homeobox homology <HOX>
A: 1.5%; Score 8; DB 2; Length 271;
A: arity 100.0%; Pred. No. 63;
A: conservative 0; Mismatches 0; Indels 0; Gaps 0;
A:
A: AAP 145
A: |||||
A: AAP 102

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RESULT 150
T52103
GATA-binding transcription factor homolog 1 [imported] - Arabidopsis
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Ma
C;Accession: T52103
R;Teakle, G.R.; Gilmartin, P.M.
submitted to the EMBL Data Library, June 1997
A;Description: Two types of GATA factor are found in fungi but are un
A;Reference number: Z25956
A;Accession: T52103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-274 <TEA>
A;Cross-references: EMBL:Y13648; PIDN:CAA73999.1
A;Experimental source: ecotype Columbia
C;Genetics:
C;Gene: GATA-1
C;Superfamily: Arabidopsis thaliana GATA transcription factor 4
Query Match 1.5%; Score 8; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 329 EEEEDDDE 336
Db 17 EEEEDDDE 24

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Search completed: March 30, 2004, 15:02:39
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
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(without alignments)
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-09-976-740-43
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IGO
pop 60.0 , Gapext 60.0

65169 seqs, 261661801 residues

ts satisfying chosen parameters: 1065169

gth: 0

gth: 2000000000

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t than or equal to the score of the result being printed,
id by analysis of the total score distribution.

SUMMARIES

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1.0	538	12	US-10-671-242-43	Sequence 43, Appl
1.0	538	13	US-10-023-529-43	Sequence 43, Appl
1.0	538	13	US-10-023-523-43	Sequence 43, Appl
1.0	538	15	US-10-616-187-43	Sequence 43, Appl
1.3	217	9	US-09-962-055-7	Sequence 7, Appl
1.3	217	9	US-09-976-740-7	Sequence 7, Appl
1.3	217	12	US-10-671-242-7	Sequence 7, Appl
1.3	217	13	US-10-023-529-7	Sequence 7, Appl
1.3	217	13	US-10-023-523-7	Sequence 7, Appl
1.3	217	15	US-10-616-187-7	Sequence 7, Appl
1.8	241	14	US-10-102-806-665	Sequence 665, App
1.4	550	9	US-09-976-740-47	Sequence 47, Appl
1.4	550	12	US-10-671-242-47	Sequence 47, Appl
1.4	550	13	US-10-023-529-47	Sequence 47, Appl

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17	99	18.4	550	15	US-10-616-187-47	Sequence
18	76	14.1	232	9	US-09-962-055-3	Sequence
19	76	14.1	232	9	US-09-976-740-3	Sequence
20	76	14.1	232	12	US-10-671-242-3	Sequence
21	76	14.1	232	13	US-10-023-529-3	Sequence
22	76	14.1	232	13	US-10-023-523-3	Sequence
23	76	14.1	232	15	US-10-616-187-3	Sequence
24	76	14.1	252	9	US-09-962-055-4	Sequence
25	76	14.1	252	9	US-09-976-740-4	Sequence
26	76	14.1	252	12	US-10-671-242-4	Sequence
27	76	14.1	252	13	US-10-023-529-4	Sequence
28	76	14.1	252	13	US-10-023-523-4	Sequence
29	76	14.1	252	15	US-10-616-187-4	Sequence
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31	76	14.1	317	9	US-09-976-740-2	Sequence
32	76	14.1	317	12	US-10-671-242-2	Sequence
33	76	14.1	317	13	US-10-023-529-2	Sequence
34	76	14.1	317	13	US-10-023-523-2	Sequence
35	76	14.1	317	15	US-10-616-187-2	Sequence
36	26	4.8	26	9	US-09-962-055-20	Sequence
37	26	4.8	26	9	US-09-976-740-20	Sequence
38	26	4.8	26	12	US-10-671-242-20	Sequence
39	26	4.8	26	13	US-10-023-529-20	Sequence
40	26	4.8	26	13	US-10-023-523-20	Sequence
41	26	4.8	26	15	US-10-616-187-20	Sequence
42	15	2.8	15	9	US-09-962-055-19	Sequence
43	15	2.8	15	9	US-09-976-740-19	Sequence
44	15	2.8	15	12	US-10-671-242-19	Sequence
45	15	2.8	15	13	US-10-023-529-19	Sequence
46	15	2.8	15	13	US-10-023-523-19	Sequence
47	15	2.8	15	15	US-10-616-187-19	Sequence
48	15	2.8	102	12	US-10-221-625-66	Sequence
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51	11	2.0	11	9	US-09-976-740-21	Sequence
52	11	2.0	11	12	US-10-671-242-21	Sequence
53	11	2.0	11	13	US-10-023-529-21	Sequence
54	11	2.0	11	13	US-10-023-523-21	Sequence
55	11	2.0	11	15	US-10-616-187-21	Sequence
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57	11	2.0	12	9	US-09-976-740-27	Sequence
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60	11	2.0	12	13	US-10-023-523-27	Sequence
61	11	2.0	12	15	US-10-616-187-27	Sequence
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63	11	2.0	28	9	US-09-976-740-26	Sequence
64	11	2.0	28	12	US-10-671-242-26	Sequence
65	11	2.0	28	13	US-10-023-529-26	Sequence
66	11	2.0	28	13	US-10-023-523-26	Sequence
67	11	2.0	28	15	US-10-616-187-26	Sequence
68	11	2.0	129	14	US-10-357-322-12	Sequence
69	11	2.0	135	12	US-10-425-114-42252	Sequence
70	11	2.0	189	9	US-09-810-264-20	Sequence
71	11	2.0	334	15	US-10-108-260A-4241	Sequence
72	11	2.0	2103	14	US-10-184-644-319	Sequence
73	11	2.0	2103	14	US-10-184-634-319	Sequence
74	11	2.0	2103	14	US-10-063-685-105	Sequence
75	11	2.0	2340	14	US-10-184-644-333	Sequence
76	11	2.0	2340	14	US-10-184-634-333	Sequence
77	10	1.9	10	9	US-09-962-055-22	Sequence
78	10	1.9	10	9	US-09-962-055-28	Sequence
79	10	1.9	10	9	US-09-976-740-22	Sequence
80	10	1.9	10	9	US-09-976-740-28	Sequence
81	10	1.9	10	12	US-10-671-242-22	Sequence
82	10	1.9	10	12	US-10-671-242-28	Sequence
83	10	1.9	10	13	US-10-023-529-22	Sequence
84	10	1.9	10	13	US-10-023-523-22	Sequence
85	10	1.9	10	13	US-10-023-529-28	Sequence
86	10	1.9	10	13	US-10-023-523-28	Sequence
87	10	1.9	10	15	US-10-616-187-28	Sequence
88	10	1.9	10	15	US-10-616-187-28	Sequence

[illegible]
$$\frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} f(\tau) d\tau = \mathcal{I}^\alpha f(t)$$

RESULT 2
US-10-671-242-43
; Sequence 43, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.

Simon W.
 onal, Anibal A.
 ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 ON: ATHEROSCLEROSIS
 10797-004001
 ION NUMBER: US/10/671,242
 DATE: 2003-09-24
 N NUMBER: US/09/616,289
 E: 2000-07-14
 N NUMBER: US 09/517,849
 CE: 2000-03-02
 N NUMBER: US 08/979,608
 CE: 1997-11-26
 N NUMBER: US 60/031,930
 CE: 1996-11-27
 N NUMBER: US 60/048,547
 E: 1997-06-03
 NOS: 53
 Q for Windows Version 4.0

sapiens

100.0%; Score 538; DB 12; Length 538;
 100.0%; Pred. No. 0;
 0; Mismatches 0; Indels 0; Gaps 0;
 'ALPPETAATAAATAAASSAASPHYQWILDTIDSLRSRKARPDLEICRMVRR 60
 'ALPPETAATAAATAAASSAASPHYQWILDTIDSLRSRKARPDLEICRMVRR 60
 'PERTAELEKLIQORAVLRVSVKSGISYRNAARVQPPRRGATPPAPPAPGAPA 120
 'PERTAELEKLIQORAVLRVSVKSGISYRNAARVQPPRRGATPPAPPAPGAPA 120
 'APPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPAQRAAPLAAP 180
 'APPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPAQRAAPLAAP 180
 'APPAVAPPAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPQPPPPGGAV 240
 'APPAVAPPAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPQPPPPGGAV 240
 'ARVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALPRG 300
 'ARVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALPRG 300
 'APPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 360
 'APPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 360
 'GERGQSAKERVKWTGCGPHQODGGRGPAQSGTRQVFSMAANKKEGGTASVA 420
 'GERGQSAKERVKWTGCGPHQODGGRGPAQSGTRQVFSMAANKKEGGTASVA 420
 'PSPVPLPGKALPCADGTPGCPGPKRKESDPVMTVMDVVEYFTFAGFPEQA 480
 'PSPVPLPGKALPCADGTPGCPGPKRKESDPVMTVMDVVEYFTFAGFPEQA 480
 'QEIDGKSILLMORTDLVLTGLSIRLGPALKIYEHHIKVLQOQHFDDEDDPDGFLG 538
 'QEIDGKSILLMORTDLVLTGLSIRLGPALKIYEHHIKVLQOQHFDDEDDPDGFLG 538

ication US/10023529
 S20020129368A1
 ON:

Ann M.

APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 TITLE OF INVENTION: ATHEROSCLEROSIS
 FILE REFERENCE: 10797-004001
 CURRENT APPLICATION NUMBER: US/10/023,529
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 09/517,849
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US 08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US 60/031,930
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 60/048,547
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 43
 LENGTH: 538
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-023-529-43

Query Match 100.0%; Score 538; DB 13; Length 538;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; G

QY 1 MAGPPALPPETATAAATAAASSAASPHYQWILDTIDSLRSRKARPDLEICRI
 DB 1 MAGPPALPPETATAAATAAASSAASPHYQWILDTIDSLRSRKARPDLEICRI
 QY 61 RHGPEPERTRAELEKLIQORAVLRVSVKSGISYRNAARVQPPRRGATPPAPPAPRI
 DB 61 RHGPEPERTRAELEKLIQORAVLRVSVKSGISYRNAARVQPPRRGATPPAPPAPRI
 QY 121 AAAAAAPPPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPAQRAAPAI
 DB 121 AAAAAAPPPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPAQRAAPAI
 QY 181 PPAPAPPAVAPPAAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPGGAV
 DB 181 PPAPAPPAVAPPAAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPGGAV
 QY 241 RAGGAARPVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALAI
 DB 241 RAGGAARPVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALAI
 QY 301 DRPGAPPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 360
 DB 301 DRPGAPPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 360
 QY 361 HHQNGERGQSAKERVKWTGCGPHQODGGRGPAQSGTRQVFSMAANKKEGGTASVA
 DB 361 HHQNGERGQSAKERVKWTGCGPHQODGGRGPAQSGTRQVFSMAANKKEGGTASVA
 QY 421 TGPDSFSPVPLPGKALPCADGTPGCPGPKRKESDPVMTVMDVVEYFTFAGFPEQA
 DB 421 TGPDSFSPVPLPGKALPCADGTPGCPGPKRKESDPVMTVMDVVEYFTFAGFPEQA
 QY 481 TAFQOEIDGKSILLMORTDLVLTGLSIRLGPALKIYEHHIKVLQOQHFDDEDDPDGFLG
 DB 481 TAFQOEIDGKSILLMORTDLVLTGLSIRLGPALKIYEHHIKVLQOQHFDDEDDPDGFLG

RESULT 4

US-10-023-523-43
 ; Sequence 43, Application US/10023523
 ; Publication No. US20020152485A1
 ; GENERAL INFORMATION:

S, Ann M.
 es, Robert S.
 w, Simon W.
 jona, Anibal A.
 TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 TION: ATHEROSCLEROSIS
 : 10797-004001
 ATION NUMBER: US/10/023,523
 DATE: 2001-12-17
 ION NUMBER: US/09/616,289
 ATE: 2000-07-14
 ION NUMBER: US 09/517,849
 ATE: 2000-03-02
 ION NUMBER: US 08/979,608
 ATE: 1997-11-26
 ION NUMBER: US 60/031,930
 ATE: 1996-11-27
 ION NUMBER: US 60/048,547
 ATE: 1997-06-03
 ID NOS: 53
 SEQ for Windows Version 4.0

c sapiens

100.0%; Score 538; DB 13; Length 538;
 larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PALPPETAAATTAASSAASPHYQEWILDTISLSRKARPDLEICRMVRR 60
 PALPPETAAATTAASSAASPHYQEWILDTISLSRKARPDLEICRMVRR 60
 PERTRAELKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRAPGAPA 120
 PERTRAELKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRAPGAPA 120
 AAPPTTAPPPPPVAAAPAPRAAAAAATAPPSPGPAQPGPRAAPLAAP 180
 AAPPTTAPPPPPVAAAPAPRAAAAAATAPPSPGPAQPGPRAAPLAAP 180
 AAPPAVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPPPPPPPGGAV 240
 AAPPAVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPPPPPPPGGAV 240
 AAPRVSLREVVRVYLGSGGAGGLTRGVQGLLEEEAAARGLERLRLGALALPRG 300
 AAPRVSLREVVRVYLGSGGAGGLTRGVQGLLEEEAAARGLERLRLGALALPRG 300
 AAPPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDRPAGAQ 360
 AAPPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDRPAGAQ 360
 NGERGPOSARVKEWTPCGPHQODEGRGPAQSGTRQVFSMAAMNKEGTSVA 420
 NGERGPOSARVKEWTPCGPHQODEGRGPAQSGTRQVFSMAAMNKEGTSVA 420
 SPSPVPLPPGKPALPGADGTPPGCPGKKEKPSDPVETVMDVVVEYFTEAGF 480
 SPSPVPLPPGKPALPGADGTPPGCPGKKEKPSDPVETVMDVVVEYFTEAGF 480
 EQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHHIKVLQOGHFEDDDPDGFLG 538
 EQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHHIKVLQOGHFEDDDPDGFLG 538

lication US/10616187
 US20040013668A1

GENERAL INFORMATION:
 APPLICANT: Lees, Ann M.
 APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
 TITLE OF INVENTION: ATHEROSCLEROSIS
 FILE REFERENCE: 10797-004001
 CURRENT APPLICATION NUMBER: US/10/616,187
 CURRENT FILING DATE: 2003-07-09
 PRIOR APPLICATION NUMBER: US/09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 09/517,849
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US 08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US 60/031,930
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 60/048,547
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 43
 LENGTH: 538
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-616-187-43

Query Match 100.0%; Score 538; DB 15; Length 538;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MAGPALPPETAAATTAASSAASPHYQEWILDTISLSRKARPDLEIC
 Db 1 MAGPALPPETAAATTAASSAASPHYQEWILDTISLSRKARPDLEIC
 QY 61 RHGPPEPTRAELEKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRA
 Db 61 RHGPPEPTRAELEKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRA
 QY 121 AAAAAAPPTTAPPPPPAPVAAAAAPARAAAAAATAPPSPGPAQPGPRAAA
 Db 121 AAAAAAPPTTAPPPPPAPVAAAAAPARAAAAAATAPPSPGPAQPGPRAAA
 QY 181 PPAPAAVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPPPPPPPPP
 Db 181 PPAPAAVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPPPPPPPPP
 QY 241 RAGGAARVSVLRVYLGSGGAGGLTRGVQGLLEEEAAARGLERLRLGAL
 Db 241 RAGGAARVSVLRVYLGSGGAGGLTRGVQGLLEEEAAARGLERLRLGAL
 QY 301 DRGRAPPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDR
 Db 301 DRGRAPPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDR
 QY 361 HHQNGERGPOSARVKEWTPCGPHQODEGRGPAQSGTRQVFSMAAMNKEGT
 Db 361 HHQNGERGPOSARVKEWTPCGPHQODEGRGPAQSGTRQVFSMAAMNKEGT
 QY 421 TGPDSPSVPPLPPGKPALPGADGTPPGCPGKKEKPSDPVETVMDVVVEYFTEAGF
 Db 421 TGPDSPSVPPLPPGKPALPGADGTPPGCPGKKEKPSDPVETVMDVVVEYFTEAGF
 QY 481 TAFEQEIIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHHIKVLQOGHFEDDDPDG
 Db 481 TAFEQEIIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHHIKVLQOGHFEDDDPDG

RESULT 6
 US-09-962-055-7
 ; Sequence 7, Application US/09962055

20052033A1
 ACTION:
 : Lees, Ann M.
 : Lees, Robert S.
 : Law, Simon W.
 : Arjona, Anibal A.
 INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
 BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
 TREATING ATHEROSCLEROSIS
 SEQUENCES: 42
 DENCE ADDRESS:
 ESSEE: Fish & Richardson P.C.
 ST: 225 Franklin Street
 : Boston
 3: MA
 IRY: USA
 02110-2804
 READABLE FORM:
 JM TYPE: Diskette
 JTER: IBM Compatible
 ATING SYSTEM: DOS
 VARE: FastSEQ for Windows Version 2.0
 PPLICATION DATA:
 : CATION NUMBER: US/09/962,055
 IG DATE: 24-Sep-2001
 : CATION DATA:
 : CATION NUMBER: 08/979,608
 IG DATE: 26-NOV-1997
 : CATION NUMBER: US 60/031,930
 IG DATE: 27-NOV-1996
 : GENT INFORMATION:
 : Myers, Louis
 : TRATION NUMBER: 35,965
 : ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
 : CATION INFORMATION:
 : PHONE: 617/542-5070
 : FAX: 617/542-8906
 : SEQ ID NO: 7:
 : CHARACTERISTICS:
 : H: 217 amino acids
 : amino acid
 : OG: linear
 : YPE: protein
 : ESCRIPTION: SEQ ID NO: 7:
 40.3%; Score 217; DB 9; Length 217;
 rity 100.0%; Pred. No. 1.6e-161;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 EKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHQLNGERGQSAKERVKWT 381
 EKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHQLNGERGQSAKERVKWT 60
 QQDEGRGPAGSGTQVFSMAAMNKEGGTASVATGDPSPVPLPGKALPCA 441
 QQDEGRGPAGSGTQVFSMAAMNKEGGTASVATGDPSPVPLPGKALPCA 120
 GCPGRKEKPSDPVWVMTVDVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDV 501
 GCPGRKEKPSDPVWVMTVDVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDV 180
 IRLGPALKIYEHKIKVLQQGHFEDDDPDGFLG 538
 IRLGPALKIYEHKIKVLQQGHFEDDDPDGFLG 217
 cation US/09976740
 S20020194633A1
 ON:
 Ann M.

APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 TITLE OF INVENTION: ATHEROSCLEROSIS
 FILE REFERENCE: 10797-004001
 CURRENT APPLICATION NUMBER: US/09/976,740
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US 60/031,930
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 60/048,547
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 217
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-976-740-7
 Query Match 40.3%; Score 217; DB 9; Length 217;
 Best Local Similarity 100.0%; Pred. No. 1.6e-161;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; G
 QY 322 EERVLEKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHQLNGERGQSAKERV
 DB 1 EERVLEKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHQLNGERGQSAKERV
 QY 382 PCGPHQCGDEGRGPAGSGTQVFSMAAMNKEGGTASVATGDPSPVPLPGKPA
 DB 61 PCGPHQCGDEGRGPAGSGTQVFSMAAMNKEGGTASVATGDPSPVPLPGKPA
 QY 442 DGTFFGCPGRKEKPSDPVWVMTVDVVEYFTAGPPEQATAFQEQEIDGKSLLMQ
 DB 121 DGTFFGCPGRKEKPSDPVWVMTVDVVEYFTAGPPEQATAFQEQEIDGKSLLMQ
 QY 502 LTGLSIRLGPALKIYEHKIKVLQQGHFEDDDPDGFLG 538
 DB 181 LTGLSIRLGPALKIYEHKIKVLQQGHFEDDDPDGFLG 217
 RESULT 8
 US-10-671-242-7
 ; Sequence 7, Application US/10671242
 ; Publication No. US20040040049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/10/671,242
 ; CURRENT FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US/09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSEQ for Windows Version 4.0

```
> sapiens
      40.3%; Score 217; DB 12; Length 217;
      larity 100.0%; Pred. No. 1.6e-161;
      conservative 0; Mismatches 0; Indels 0; Gaps 0;
      LEKEEEDDDDEDEDDVSEGEVPSVPSMAANKGGTASVATGDPSPVPLPPGKPAK 381
      LEKEEEDDDDEDEDDVSEGEVPSVPSMAANKGGTASVATGDPSPVPLPPGKPAK 60
      HQQDEGRGAPGSGTRQVFSMAANKGGTASVATGDPSPVPLPPGKPAK 441
      HQQDEGRGAPGSGTRQVFSMAANKGGTASVATGDPSPVPLPPGKPAK 120
      FCGPPGRKEKPSDPVETWMDVVEYFTAGFPEQATAFQEQEIDGKSLLLM 501
      FCGPPGRKEKPSDPVETWMDVVEYFTAGFPEQATAFQEQEIDGKSLLLM 180
      SIRLGPALKIYEHHIKVLQOQHFFEDDDPDGFLG 538
      SIRLGPALKIYEHHIKVLQOQHFFEDDDPDGFLG 217
      .ication US/10023529
      US20020129388A1
      ION:
      s, Ann M.
      s, Robert S.
      , Simon W.
      ona, Anibal A.
      ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
      ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
      ION: ATHEROSCLEROSIS
      10797-004001
      ION NUMBER: US/10/023,529
      DATE: 2001-12-17
      CN NUMBER: 09/616,289
      TE: 2000-07-14
      CN NUMBER: US 09/517,849
      TE: 2000-03-02
      CN NUMBER: US 08/979,608
      TE: 1997-11-26
      CN NUMBER: US 60/031,930
      TE: 1996-11-27
      CN NUMBER: US 60/048,547
      TE: 1997-06-03
      D NOS: 53
      EQ for Windows Version 4.0
      sapiens
      40.3%; Score 217; DB 13; Length 217;
      arity 100.0%; Pred. No. 1.6e-161;
      conservative 0; Mismatches 0; Indels 0; Gaps 0;
      LEKEEEDDDDEDEDDVSEGEVPSVPSMAANKGGTASVATGDPSPVPLPPGKPAK 381
      LEKEEEDDDDEDEDDVSEGEVPSVPSMAANKGGTASVATGDPSPVPLPPGKPAK 60
      HQQDEGRGAPGSGTRQVFSMAANKGGTASVATGDPSPVPLPPGKPAK 441
      HQQDEGRGAPGSGTRQVFSMAANKGGTASVATGDPSPVPLPPGKPAK 120
      FCGPPGRKEKPSDPVETWMDVVEYFTAGFPEQATAFQEQEIDGKSLLLM 501
      FCGPPGRKEKPSDPVETWMDVVEYFTAGFPEQATAFQEQEIDGKSLLLM 180
      SIRLGPALKIYEHHIKVLQOQHFFEDDDPDGFLG 538
      SIRLGPALKIYEHHIKVLQOQHFFEDDDPDGFLG 217
      .ication US/10023523
      US20020152485A1
      ION:
      s, Ann M.
      s, Robert S.
      , Simon W.
      ona, Anibal A.
      ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
      ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
      ION: ATHEROSCLEROSIS
      10797-004001
      ION NUMBER: US/10/023,523
      DATE: 2001-12-17
      CN NUMBER: 09/616,289
      TE: 2000-07-14
      CN NUMBER: US 09/517,849
      TE: 2000-03-02
      CN NUMBER: US 08/979,608
      TE: 1997-11-26
      CN NUMBER: US 60/031,930
      TE: 1996-11-27
      CN NUMBER: US 60/048,547
      TE: 1997-06-03
      D NOS: 53
      EQ for Windows Version 4.0
      sapiens
      40.3%; Score 217; DB 13; Length 217;
      Best Local Similarity 100.0%; Pred. No. 1.6e-161;
      Matches 217; Conservative 0; Mismatches 0; Indels 0;
      QY 322 EERVLEKEEEDDDDEDEDDVSEGEVPSVPSMAANKGGTASVATGDPSPVPLPPGKPAK 381
      DB 1 EERVLEKEEEDDDDEDEDDVSEGEVPSVPSMAANKGGTASVATGDPSPVPLPPGKPAK 60
      QY 382 PCGPHQGDGGRGAPGSGTRQVFSMAANKGGTASVATGDPSPVPLPPGKPAK 441
      DB 61 PCGPHQGDGGRGAPGSGTRQVFSMAANKGGTASVATGDPSPVPLPPGKPAK 120
      QY 442 DGTGPGCPGGRKEKPSDPVETWMDVVEYFTAGFPEQATAFQEQEIDGKSLLLM 501
      DB 121 DGTGPGCPGGRKEKPSDPVETWMDVVEYFTAGFPEQATAFQEQEIDGKSLLLM 180
      QY 502 LTGLSIRLGPALKIYEHHIKVLQOQHFFEDDDPDGFLG 538
      DB 181 LTGLSIRLGPALKIYEHHIKVLQOQHFFEDDDPDGFLG 217
      RESULT 11
      US-10-616-187-7
      ; Sequence 7, Application US/10616187
      ; Publication No. US20040013668A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Lees, Ann M.
      ; APPLICANT: Lees, Robert S.
      ; APPLICANT: Law, Simon W.
      ; APPLICANT: Arjona, Anibal A.
      ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
      ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
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ON: ATHEROSCLEROSIS
10797-004001
ION NUMBER: US/10/616,187
ATE: 2003-07-09
N NUMBER: US/09/616,289
E: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
E: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

sapiens

40.3%; Score 217; DB 15; Length 217;
rity 100.0%; Pred. No. 1.6e-161; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
EKEEEDEDEDEDDVSEGEVPESDRPAQAQHHQLNGRGPQSAKERVKEWT 381
EKEEEDEDEDEDDVSEGEVPESDRPAQAQHHQLNGRGPQSAKERVKEWT 60
QQQDEGRGPAQSGTRQVFSMAAMNKEGGTASVATGPDSPVPLPGKPALPGA 441
QQQDEGRGPAQSGTRQVFSMAAMNKEGGTASVATGPDSPVPLPGKPALPGA 120
GCPGRKEKPSDPVWETVMDVVEYFTEAGFPEQATAFQEQIDGKSLLMORTDV 501
GCPGRKEKPSDPVWETVMDVVEYFTEAGFPEQATAFQEQIDGKSLLMORTDV 180
IRLGPALKIYEHKIKVLOQGHFEDDDPDGFLG 538
IRLGPALKIYEHKIKVLOQGHFEDDDPDGFLG 217

lication US/10102806
S20030054421A1
ON:
et al.
ON: Nucleic Acids, Proteins and Antibodies
PA103P1C1
ION NUMBER: US/10/102,806
ATE: 2002-03-22
N NUMBER: 09/925,298
E: 2001-08-10
N NUMBER: PCT/US00/05881
E: 2000-03-08
N NUMBER: 60/124,270
E: 1999-03-12
NOS: 846
In Ver. 2.0

sapiens

ON: Xaa equals any of the naturally occurring L-amino acids
ON: Xaa equals any of the naturally occurring L-amino acids

Query Match 20.8%; Score 112; DB 14; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.1e-79;
Matches 112; Conservative 0; Mismatches 0; Indels 0; G
QY 307 PPAASARPSRSGGEERVLEKEEEDDEDEDDVSEGEVPESDRPAQAQHH(418
DB 10 PPAASARPSRSGGEERVLEKEEEDDEDEDDVSEGEVPESDRPAQAQHH(418
QY 367 ERGPQSAKERVKEWTPCGPHQGDGRGPAGSGTRQVFSMAAMNKEGGTAS 418
DB 70 ERGPQSAKERVKEWTPCGPHQGDGRGPAGSGTRQVFSMAAMNKEGGTAS 121

RESULT 13
US-09-976-740-47
; Sequence 47, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-976-740-47

Query Match 18.4%; Score 99; DB 9; Length 550;
Best Local Similarity 100.0%; Pred. No. 6e-69;
Matches 99; Conservative 0; Mismatches 0; Indels 0; G
QY 19 AAAASSAASPHYQEWILDTIDSLRSRKARPDLERICMVRRRHGHPEPTRAELH
DB 20 AAAASSAASPHYQEWILDTIDSLRSRKARPDLERICMVRRRHGHPEPTRAELH
QY 79 QRAVLRSYKGSISYRNAARVQPPRGATPPRAPRG 117
DB 80 QRAVLRSYKGSISYRNAARVQPPRGATPPRAPRG 118

RESULT 14
US-10-671-242-47
; Sequence 47, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24

ION NUMBER: US/09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

:ctolagus cuniculus

18.4%; Score 99; DB 12; Length 550;
arity 100.0%; Pred. No. 6e-69; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 78
|||||
ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 79

LRVSVKGSISYRNAARVQPPRGATPPAPPRAG 117
|||||
LRVSVKGSISYRNAARVQPPRGATPPAPPRAG 118

lication US/10023529
US20020129388A1

TION:

s, Ann M.

s, Robert S.

v, Simon W.

ona, Anibal A.

TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TION: ATHEROSCLEROSIS

10797-004001
ATION NUMBER: US/10/023,529

DATE: 2001-12-17

ION NUMBER: 09/616,289

ATE: 2000-07-14

ION NUMBER: US 09/517,849

ION NUMBER: US 08/979,608
ATE: 1997-11-26

ION NUMBER: US 60/031,930
ATE: 1996-11-27

ION NUMBER: US 60/048,547
ATE: 1997-06-03

ID NOS: 53

SEQ for Windows Version 4.0

:ctolagus cuniculus

18.4%; Score 99; DB 13; Length 550;
arity 100.0%; Pred. No. 6e-69; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 78
|||||
ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 79

LRVSVKGSISYRNAARVQPPRGATPPAPPRAG 117

Db 80 QRAVLRSYKGSISYRNAARVQPPRGATPPAPPRAG 118
|||||

RESULT 16

US-10-023-523-47

; Sequence 47, Application US/10023523

; Publication No. US20020152485A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/023,523

; CURRENT FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 47

; LENGTH: 550

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-10-023-523-47

Query Match

Best Local Similarity 18.4%; Score 99; DB 13; Length 550;

Matches 99; Conservative 0; Mismatches 0; Indels 0;

QY 19 AAAASSAASHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAEL
|||||

Db 20 AAAASSAASHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAEL
|||||

QY 79 QRAVLRSYKGSISYRNAARVQPPRGATPPAPPRAG 117
|||||

Db 80 QRAVLRSYKGSISYRNAARVQPPRGATPPAPPRAG 118
|||||

RESULT 17

US-10-616-187-47

; Sequence 47, Application US/10616187

; Publication No. US20040013668A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/616,187

; CURRENT FILING DATE: 2003-07-09

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

1.33:40 2004

us-09-976-740-43.olig.rapb

Y NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

olagus cuniculus

18.4%; Score 99; DB 15; Length 550;
rity 100.0%; Pred.No. 6e-69; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

SSAASPHYQEWILDTIDSLRSRKARPDLEICRMVRRHGHGPEPRTAELEKLIQ 78
SSAASPHYQEWILDTIDSLRSRKARPDLEICRMVRRHGHGPEPRTAELEKLIQ 79

RVSYKGSISYNAARVOPPRRGATPPAPRPG 117
RVSYKGSISYNAARVOPPRRGATPPAPRPG 118

cation US/09962055
0052033A1
TION:

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

SSSE: Fish & Richardson P.C.

T: 225 Franklin Street

Boston

: MA

RY: USA

02110-2804

EADABLE FORM:

M TYPE: Diskette

TER: IBM Compatible

TING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

CATION NUMBER: US/09/962,055

G DATE: 24-Sep-2001

ICATION DATA:

CATION NUMBER: 08/979,608

G DATE: 26-NOV-1997

CATION NUMBER: US 60/031,930

G DATE: 27-NOV-1996

GENT INFORMATION:

MYERS, Louis

TRATION NUMBER: 35,965

ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

: SEQ ID NO: 3:

HARACTERISTICS:

H: 232 amino acids

amino acid

LOGY: linear

YPE: protein

DESCRIPTION: SEQ ID NO: 3:

14.1%; Score 76; DB 9; Length 232;

Best Local Similarity 100.0%; Pred.No. 2.8e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVETVMDVVEYFTFAGPPEQATAFQOEIDGKSLLMORTDVLTLGSLRGLPALH
DB 152 DPVETVMDVVEYFTFAGPPEQATAFQOEIDGKSLLMORTDVLTLGSLRGLPALH

QY 518 HHKVLQOQHFEEDDP 533
DB 212 HHKVLQOQHFEEDDP 227

RESULT 19

US-09-976-740-3

; Sequence 3, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/976,740

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-976-740-3

Query Match

Best Local Similarity 14.1%; Score 76; DB 9; Length 232;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVETVMDVVEYFTFAGPPEQATAFQOEIDGKSLLMORTDVLTLGSLRGLPALH
DB 152 DPVETVMDVVEYFTFAGPPEQATAFQOEIDGKSLLMORTDVLTLGSLRGLPALH

QY 518 HHKVLQOQHFEEDDP 533
DB 212 HHKVLQOQHFEEDDP 227

RESULT 20

US-10-671-242-3

; Sequence 3, Application US/10671242

; Publication No. US2004004049A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/671,242

; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

11:33:40 2004

us-09-976-740-43.olg.rapb

ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 12; Length 232;
arity 100.0%; Pred. No. 2.8e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTVMVVEYFEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
WTVMVVEYFEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 211

VLOQGHFEDDDP 533
VLOQGHFEDDDP 227

ication US/10023529
US20020129388A1
TON:

, Ann M.
, Simon W.
ona, Anibal A.
TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TON: ATHEROSCLEROSIS
10797-004001
TION NUMBER: US/10/023,529
DATE: 2001-12-17
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 13; Length 232;
arity 100.0%; Pred. No. 2.8e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTVMVVEYFEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
WTVMVVEYFEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 211

VLOQGHFEDDDP 533
VLOQGHFEDDDP 227

RESULT 22

US-10-023-523-3
; Sequence 3, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-3

Query Match 14.1%; Score 76; DB 13; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0; C

QY 458 DPVETWMDVVEYFEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
DB 152 DPVETWMDVVEYFEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQGHFEDDDP 533
DB 212 HHKVLQGHFEDDDP 227

RESULT 23

US-10-616-187-3
; Sequence 3, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03

NOS: 53
Q for Windows Version 4.0

olagus cuniculus

14.1%; Score 76; DB 15; Length 232;
urity 100.0%; Pred. No. 2.8e-51;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

TVMQVVEYFTAGPEQATAFQEQIDGKSLLMQRTDVLGLSIRLGPAL
TVMQVVEYFTAGPEQATAFQEQIDGKSLLMQRTDVLGLSIRLGPAL
TVMQVVEYFTAGPEQATAFQEQIDGKSLLMQRTDVLGLSIRLGPAL

TQQGHFEDDDP 533

TQQGHFEDDDP 227

cation US/09962055
0052033A1

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

ESSEE: Fish & Richardson P.C.

ET: 225 Franklin Street

Boston

MA

RY: USA

02110-2804

READABLE FORM:

IM TYPE: Diskette

ITER: IBM Compatible

ATING SYSTEM: DOS

WARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/09/962,055

IG DATE: 24-Sep-2001

ICATION DATA:

ICATION NUMBER: 08/979,608

IG DATE: 26-NOV-1997

ICATION NUMBER: US 60/031,930

IG DATE: 27-NOV-1996

AGENT INFORMATION:

: Myers, Louis

ISTRATION NUMBER: 35,965

RENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

FAX: 617/542-8906

SEQ ID NO: 4

CHARACTERISTICS:

TH: 252 amino acids

: amino acid

LOGY: linear

TYPE: protein

DESCRIPTION: SEQ ID NO: 4:

14.1%; Score 76; DB 9; Length 252;
arity 100.0%; Pred. No. 3e-51;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVETVMDVVEYFTAGPEQATAFQEQIDGKSLLMQRTDVLGLSIRLGPAL
Db 172 DPVETVMDVVEYFTAGPEQATAFQEQIDGKSLLMQRTDVLGLSIRLGPAL

QY 518 HHKVLQOQHFEEDDDP 533
Db 232 HHKVLQOQHFEEDDDP 247

RESULT 25

US-09-976-740-4

; Sequence 4, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/976,740

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 252

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-976-740-4

Query Match 14.1%; Score 76; DB 9; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0; G

QY 458 DPVETVMDVVEYFTAGPEQATAFQEQIDGKSLLMQRTDVLGLSIRLGPAL
Db 172 DPVETVMDVVEYFTAGPEQATAFQEQIDGKSLLMQRTDVLGLSIRLGPAL

QY 518 HHKVLQOQHFEEDDDP 533
Db 232 HHKVLQOQHFEEDDDP 247

RESULT 26

US-10-671-242-4

; Sequence 4, Application US/10671242

; Publication No. US20040040049A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/671,242

; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 12; Length 252;
arity 100.0%; Pred. No. 3e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
|||||
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 231
VLQOGHFEDDDP 533
VLQOGHFEDDDP 247

ication US/10023529
US20020129388A1
ION:

, Ann M.
s, Robert S.
ona, Anibal A.
ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ION: ATHEROSCLEROSIS
10797-004001

TION NUMBER: US/10/023,529
DATE: 2001-12-17
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 13; Length 252;
arity 100.0%; Pred. No. 3e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
|||||
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 231
VLQOGHFEDDDP 533
VLQOGHFEDDDP 247

VLQOGHFEDDDP 533
VLQOGHFEDDDP 247

RESULT 28
US-10-023-523-4
; Sequence 4, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-4

Query Match 14.1%; Score 76; DB 13; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0;
QY 458 DPVWTVMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
DB 172 DPVWTVMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQOGHFEDDDP 533
DB 232 HHKVLQOGHFEDDDP 247

RESULT 29
US-10-616-187-4
; Sequence 4, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0

plagus cuniculus

14.1%; Score 76; DB 15; Length 252;
city 100.0%; Pred. No. 3e-51;
inservative 0; Mismatches 0; Indels 0; Gaps 0;

TVMDVVEYFTEAGPPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
TVMDVVEYFTEAGPPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 231

LQOGHFEDDDP 533
LQOGHFEDDDP 247

cation US/09962055
0052033A1

ITION:

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

SSEE: Fish & Richardson P.C.

T: 225 Franklin Street

Boston

: MA

RY: USA

02110-2804

EADABLE FORM:

M TYPE: Diskette

TER: IBM Compatible

TING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

CATION NUMBER: US/09/962,055

G DATE: 24-Sep-2001

ICATION DATA:

CATION NUMBER: 08/979,608

G DATE: 26-NOV-1997

CATION NUMBER: US 60/031,930

G DATE: 27-NOV-1996

GENT INFORMATION:

Myers, Louis

TRATION NUMBER: 35,965

ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 2:

CHARACTERISTICS:

H: 317 amino acids

amino acid

OGY: linear

YPE: protein

DESCRIPTION: SEQ ID NO: 2:

14.1%; Score 76; DB 9; Length 317;
arity 100.0%; Pred. No. 3.6e-51;
inservative 0; Mismatches 0; Indels 0; Gaps 0;

TVMDVVEYFTEAGPPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517

Db 237 DPVETVMDVVEYFTEAGPPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALK

QY 518 HHKVLQOGHFEDDDP 533

Db 297 HHKVLQOGHFEDDDP 312

RESULT 31

US-09-976-740-2

; Sequence 2, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/976,740

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 317

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(317)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-976-740-2

Query Match

Best Local Similarity 14.1%; Score 76; DB 9; Length 317;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 458 DPVETVMDVVEYFTEAGPPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALK

Db 237 DPVETVMDVVEYFTEAGPPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALK

QY 518 HHKVLQOGHFEDDDP 533

Db 297 HHKVLQOGHFEDDDP 312

RESULT 32

US-10-671-242-2

; Sequence 2, Application US/10671242

; Publication No. US20040040049A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/671,242

; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

IN NUMBER: US 09/517,849
 TE: 2000-03-02
 IN NUMBER: US 08/979,608
 TE: 1997-11-26
 IN NUMBER: US 60/031,930
 TE: 1996-11-27
 IN NUMBER: US 60/048,547
 TE: 1997-06-03
 NOS: 53
 SEQ for Windows Version 4.0

tolagus cuniculus

ANT
 ..(317)
 ION: Xaa = Any Amino Acid

arity 14.1%; Score 76; DB 12; Length 317;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

WTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
 WTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL

VLOQGHFEDDDP 533
 VLOQGHFEDDDP 312

ication US/10023529
 US20020129388A1
 ION:

s, Robert S.
 .. Simon W.
 ona, Anibal A.
 ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 ION: ATHEROSCLEROSIS

10797-004001
 TION NUMBER: US/10/023,529
 DATE: 2001-12-17
 ON NUMBER: 09/616,289
 TE: 2000-07-14
 ON NUMBER: US 09/517,849
 TE: 2000-03-02
 ON NUMBER: US 08/979,608
 TE: 1997-11-26
 ON NUMBER: US 60/031,930
 TE: 1996-11-27
 ON NUMBER: US 60/048,547
 TE: 1997-06-03
 NOS: 53
 SEQ for Windows Version 4.0

tolagus cuniculus

IANT
 ... (317)
 ION: Xaa = Any Amino Acid

arity 14.1%; Score 76; DB 13; Length 317;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
 Db 237 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
 QY 518 HHKVLQOQHFEEDDDP 533
 Db 297 HHKVLQOQHFEEDDDP 312

RESULT 34

US-10-023-523-2
 ; Sequence 2, Application US/10023523
 ; Publication NO. US20020129388A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/10/023,523
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: US/09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)..(317)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-10-023-523-2

Query Match 14.1%; Score 76; DB 13; Length 317;
 Best Local Similarity 100.0%; Pred. No. 3.6e-51;
 Matches 76; Conservative 0; Mismatches 0; Indels 0;

QY 458 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
 Db 237 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
 QY 518 HHKVLQOQHFEEDDDP 533
 Db 297 HHKVLQOQHFEEDDDP 312

RESULT 35

US-10-616-187-2
 ; Sequence 2, Application US/10616187
 ; Publication NO. US20040013668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREA
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001

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P:

ON NUMBER: US/10/616,187
TE: 2003-07-09
I NUMBER: US/09/616,289
I: 2000-07-14
I NUMBER: US 09/517,849
I: 2000-03-02
I NUMBER: US 08/979,608
I: 1997-11-26
I NUMBER: US 60/031,930
I: 1996-11-27
I NUMBER: US 60/048,547
I: 1997-06-03
NOS: 53
for Windows Version 4.0

lagus cuniculus

VT
(317)
DN: Xaa = Any Amino Acid

14.1%; Score 76; DB 15; Length 317;
rity 100.0%; Pred. No. 3.6e-51;
servative 0; Mismatches 0; Indels 0; Gaps 0;
TMDVVEYFTAGPPEQATFQEQEIDGKSLLMQRTDVLTLGSLRGLPKIYE 517
TMDVVEYFTAGPPEQATFQEQEIDGKSLLMQRTDVLTLGSLRGLPKIYE 296

LOQHFFEDDDP 533
LOQHFFEDDDP 312

ication US/09962055
0052033A1

TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.

Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA

RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
TING SYSTEM: DOS
IARE: FastSEQ for Windows Version 2.0
PLICATION DATA:
ICATION NUMBER: US/09/962,055
IG DATE: 24-Sep-2001
ICATION DATA:
ICATION NUMBER: 08/979,608
IG DATE: 26-NOV-1997
ICATION NUMBER: US 60/031,930
IG DATE: 27-NOV-1996
AGENT INFORMATION:
Myers, Louis
STRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5981.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-962-055-20

Query Match 4.8%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 EEEEDDEDEDEDDVSGSEVPESD 354
DB 1 EEEEDDEDEDEDDVSGSEVPESD 26

RESULT 37

US-09-976-740-20
Sequence 20, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
US-09-976-740-20

Query Match 4.8%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 EEEEDDEDEDEDDVSGSEVPESD 354
DB 1 EEEEDDEDEDEDDVSGSEVPESD 26

RESULT 38

US-10-671-242-20
Sequence 20, Application US/10671242
Publication No. US20040040049A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI

11:33:40 2004

us-09-976-740-43.olig.rapb

ION: ATHEROSCLEROSIS
10797-004001
TION NUMBER: US/10/671,242
DATE: 2003-09-24
ON NUMBER: US/09/616,289
TE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

> sapiens

4.8%; Score 26; DB 12; Length 26;
arity 100.0%; Pred. No. 5.6e-13;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3DDDEDEDDVSGSEVPESD 354
|||||
3DDDEDEDDVSGSEVPESD 26

Application US/10023529
US20020129388A1
TION:
s, Ann M.
as, Robert S.
ona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS
: 10797-004001
TION NUMBER: US/10/023,529
DATE: 2001-12-17
ION NUMBER: 09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

> sapiens

4.8%; Score 26; DB 13; Length 26;
arity 100.0%; Pred. No. 5.6e-13;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3DDDEDEDDVSGSEVPESD 354
|||||
3DDDEDEDDVSGSEVPESD 26

RESULT 40
US-10-023-523-20
; Sequence 20, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-523-20

Query Match 4.8%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

CY 329 EEEEDDEDEDDVSGSEVPESD 354
|||||
Db 1 EEEEDDEDEDDVSGSEVPESD 26

RESULT 41
US-10-616-187-20
; Sequence 20, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens

4.8%; Score 26; DB 15; Length 26;
rity 100.0%; Pred. No. 5.6e-13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDEDEDDVSEGVPEPESD 354
DDEDEDDVSEGVPEPESD 26
ication US/09962055
0052033A1
TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
ENCE ADDRESS:
SSER: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
: MA
RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
TING SYSTEM: DOS
ARE: FastSEQ for Windows Version 2.0
PLICATION DATA: US/09/962,055
CATION NUMBER: US/09/962,055
G DATE: 24-Sep-2001
ICATION DATA:
CATION NUMBER: 08/979,608
G DATE: 26-NOV-1997
CATION NUMBER: US 60/031,930
G DATE: 27-NOV-1996
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 19;
HARACTERISTICS:
H: 15 amino acids
amino acid
OGY: linear
YPE: protein
ESCRPTION: SEQ ID NO: 19;
2.8%; Score 15; DB 9; Length 15;
rity 100.0%; Pred. No. 0.00014;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDEDEDD 343
DDEDEDD 15
ication US/09976740
S20020194633A1

GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-740-19
Query Match 2.8%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 329 EEEEDDEDEDD 343
DB 1 EEEEDDEDEDD 15
RESULT 44
US-10-671-242-19
; Sequence 19, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-242-19
Query Match 2.8%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DDDEDEDD 343
|||||
DDDEDEDD 15

lication US/10023529

US20020129388A1

ION:

, Ann M.

s, Robert S.

, Simon W.

ona, Anibal A.

ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

TION NUMBER: US/10/023,529

DATE: 2001-12-17

ON NUMBER: 09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

D NOS: 53

EQ for Windows Version 4.0

sapiens

2.8%; Score 15; DB 13; Length 15;

arity 100.0%; Pred. No. 0.00014;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

DDDEDEDD 343

|||||

DDDEDEDD 15

lication US/10023523

US20020152485A1

ION:

, Ann M.

s, Robert S.

, Simon W.

ona, Anibal A.

ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

TION NUMBER: US/10/023,523

DATE: 2001-12-17

ON NUMBER: US/09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

D NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-023-523-19

Query Match

2.8%; Score 15; DB 13; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 15; Conservative 0; Mismatches 0; Indels 0; G

Qy 329 EEEEDDEDEDD 343

|||||

Db 1 EEEEDDEDEDD 15

RESULT 47

US-10-616-187-19

; Sequence 19, Application US/10616187

; Publication No. US20040013668A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/616,187

; CURRENT FILING DATE: 2003-07-09

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-616-187-19

Query Match

2.8%; Score 15; DB 15; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 15; Conservative 0; Mismatches 0; Indels 0; G

Qy 329 EEEEDDEDEDD 343

|||||

Db 1 EEEEDDEDEDD 15

RESULT 48

US-10-221-625-66

; Sequence 66, Application US/10221625

; Publication No. US20040033942A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: HILLMAN, Jennifer L.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: YUE, Henry

; APPLICANT: LAL, Preeti

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: PATTERSON, Chandra

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: BANDMAN, Olga

; APPLICANT: TANG, Y. Tom

```
UR, Preete
, Purvi
OUNG, Janice
Y, Roopa
ON: TRANSCRIPTION FACTORS
PF-0761 PCT
ION NUMBER: US/10/221,625
ATE: 2001-03-13
) NOS: 214
rogram

sapiens
feature
ON: Incyte ID No. US20040033942A1 2672566CD1
ity 2.8%; Score 15; DB 12; Length 102;
rity 100.0%; Pred.No. 0.00069;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DEIDGKSLILM 496
|||||
DEIDGKSLILM 65

plication US/10094749
IS20030219741A1
ON:
AI, TAKAO
YAMA, TOMOYASU
IKI, TETSUJI
AMATSU, AI
), HIROYUKI
), SHIZUKO
AMOTO, JUN-ICHI
NO, YUUKO
YURI
JKA, KAORU
AI, KEIICHI
E, RYOTARO
ECHIKA, ICHIRO
I, NAOHICO
IKAWA, TSUTOMU
JKA, MOTOYUKI
AHARI, KENJI
JHO, YASUHIKO
ON: NOVEL FULL-LENGTH CDNA
084335/0160
ION NUMBER: US/10/094,749
DATE: 2002-03-12
ON NUMBER: 60/350,435
E: 2002-01-24
ON NUMBER: JP 2001-328381
E: 2001-09-14
) NOS: 3381
in ver. 2.1

sapiens
2.8%; Score 15; DB 15; Length 116;
arity 100.0%; Pred.No. 0.00077;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DEIDGKSLILM 496
|||||
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Db 65 AFQEQIDGKSLILM 79

RESULT 50
US-09-962-055-21
; Sequence 21, Application US/09962055
; Patent No. US20020052033A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNO
; TREATING ATHEROSCLEROSIS
;
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,055
; FILING DATE: 24-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/598)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-962-055-21

Query Match 2.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 344 VSEGSVEVPESD 354
|||||
Db 1 VSEGSVEVPESD 11

RESULT 51
US-09-976-740-21
; Sequence 21, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
```


11:33:40 2004

us-09-976-740-43.olig.rapb

10797-004001
Publication US/09/976,740
DATE: 2001-10-12
CON NUMBER: 09/616,289
ATE: 2000-07-14
CON NUMBER: US 08/979,608
ATE: 1997-11-26
CON NUMBER: US 60/031,930
ATE: 1996-11-27
CON NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

sapiens

2.0%; Score 11; DB 9; Length 11;
arity 100.0%; Pred. No. 0.14;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 11

Publication US/10671242
US2004004049A1
TON:

s, Robert S.
, Simon W.

ona, Anibal A.
TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TON: ATHEROSCLEROSIS

10797-004001
Publication US/10/671,242
DATE: 2003-09-24
CON NUMBER: US/09/616,289
ATE: 2000-07-14
CON NUMBER: US 09/517,849
ATE: 2000-03-02
CON NUMBER: US 08/979,608
ATE: 1997-11-26
CON NUMBER: US 60/031,930
ATE: 1996-11-27
CON NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

sapiens

2.0%; Score 11; DB 12; Length 11;
arity 100.0%; Pred. No. 0.14;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 11

Publication US/10023529

Publication No. US20020129388A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-529-21

Query Match 2.0%; Score 11; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 344 VSEGEVPESED 354
Db 1 VSEGEVPESED 11

RESULT 54

US-10-023-523-21
Sequence 21, Application US/10023523
Publication No. US20020152485A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-523-21

Query Match 2.0%; Score 11; DB 13; Length 11;

ity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
EVPSD 354
|||||
EVPSD 11

ication US/10616187
S20040013668A1
ON:
Ann M.
Robert S.
Simon W.
na, Anibal A.
ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ON: ATHEROSCLEROSIS
ION NUMBER: US/10/616,187
ATE: 2003-07-09
N NUMBER: US/09/616,289
E: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
E: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

sapiens

2.0%; Score 11; DB 15; Length 11;
ity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
EVPSD 354
|||||
EVPSD 11

ication US/09962055
0052033A1
TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA
RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/598)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-962-055-27

Query Match 2.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 344 VSEGSEVPESD 354
Db 2 VSEGSEVPESD 12

RESULT 57
US-09-976-740-27
Sequence 27, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 12
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-976-740-27

Query Match 2.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 344 VSEGSEVPESD 354
Db 2 VSEGSEVPESD 12

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; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-27

Query Match      2.0%; Score 11; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      344 VSEGSEVPESD 354
      |||||
Db      2 VSEGSEVPESD 12

RESULT 60
US-10-023-523-27
; Sequence 27, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; D NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-27

Query Match      2.0%; Score 11; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      354
      |||||
Db      2 VSEGSEVPESD 12

RESULT 61
US-10-023-529-27
; Sequence 27, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; D NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-27
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; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-27

Query Match      2.0%; Score 11; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      344 VSEGSEVPESD 354
      |||||
Db      2 VSEGSEVPESD 12

RESULT 60
US-10-023-523-27
; Sequence 27, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-27

Query Match      2.0%; Score 11; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      344 VSEGSEVPESD 354
      |||||
Db      2 VSEGSEVPESD 12

RESULT 61
US-10-023-529-27
; Sequence 27, Application US/10023529
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; D NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-27
```

E: 2000-03-02
 IN NUMBER: US 08/979,608
 E: 1997-11-26
 IN NUMBER: US 60/031,930
 E: 1996-11-27
 IN NUMBER: US 60/048,547
 E: 1997-06-03
 NOS: 53
 Q for Windows Version 4.0

olagus cuniculus

2.0%; Score 11; DB 15; Length 12;
 rity 100.0%; Pred. No. 0.16; 0; Indels 0; Gaps 0;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354
 |||||
 EVPSD 12

ication US/09962055
 0052033A1

ATION:
 Lees, Ann M.
 Lees, Robert S.
 Law, Simon W.

Arjona, Anibal A.

VENTION: NOVEL LOW DENSITY LIPOPROTEIN
 BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
 TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

SSER: Fish & Richardson P.C.

T: 225 Franklin Street

Boston

MA

RY: USA

02110-2804

EADABLE FORM:

M TYPE: Diskette

TER: IBM Compatible

TING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

CATION NUMBER: US/09/962,055

G DATE: 24-Sep-2001

ICATION DATA:

CATION NUMBER: 08/979,608

G DATE: 26-NOV-1997

CATION NUMBER: US 60/031,930

G DATE: 27-NOV-1996

AGENT INFORMATION:

Myers, Louis

TRATION NUMBER: 35,965

ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 26;

CHARACTERISTICS:

H: 28 amino acids

amino acid

OGY: linear

YPE: protein

SCRIPTION: SEQ ID NO: 26;

Query Match 2.0%; Score 11; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; G;

QY 344 VSEGSEVPESD 354
 |||||
 Db 18 VSEGSEVPESD 28

RESULT 63

US-09-976-740-26
 ; Sequence 26, Application US/09976740
 ; Publication No. US20020194633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/09/976,740
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; US-09-976-740-26

Query Match 2.0%; Score 11; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; G;

QY 344 VSEGSEVPESD 354
 |||||
 Db 18 VSEGSEVPESD 28

RESULT 64

US-10-671-242-26
 ; Sequence 26, Application US/10671242
 ; Publication No. US20040040049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/10/671,242
 ; CURRENT FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US/09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547

TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

US

2.0%; Score 11; DB 12; Length 28;
arity 100.0%; Pred. No. 0.31;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 28

CY
DE

lication US/10023529
US20020129388A1

TON:

, Ann M.

s, Robert S.

, Simon W.

ona, Anibal A.

TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

TION NUMBER: US/10/023,529

DATE: 2001-12-17

ON NUMBER: 09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

D NOS: 53

EQ for Windows Version 4.0

tolagus cuniculus

2.0%; Score 11; DB 13; Length 28;
arity 100.0%; Pred. No. 0.31;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 28

CY
DE

lication US/10023523
US20020152485A1

TON:

, Ann M.

s, Robert S.

, Simon W.

ona, Anibal A.

TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

10797-004001

; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-26

Query Match 2.0%; Score 11; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 11; Conservative 0; Mismatches 0; Indels 0; C

QY 344 VSEGSEVPESD 354

DB 18 VSEGSEVPESD 28

|||||||

RESULT 67

US-10-616-187-26

; Sequence 26, Application US/10616187

; Publication No. US20040013668A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/616,187

; CURRENT FILING DATE: 2003-07-09

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 26

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-10-616-187-26

Query Match 2.0%; Score 11; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 344 VSEGSEVPESD 354

DB 18 VSEGSEVPESD 28

|||||||

RESULT 68

US-10-357-322-12

```

; Application US/10357322
; IS20030180768A1
; ION:
; a et al.
; ION: SCAY GENE AND METHODS OF USE
; Regents of the University of Minnesota
; TION NUMBER: US/10/357,322
; DATE: 2003-02-03
; DN NUMBER: US/09/684,843
; CE: 2000-10-06
; DN NUMBER: 60/056,170
; CE: 1997-08-19
; DN NUMBER: 09/135,994
; CE: 1998-08-18
; NOS: 14
; In Ver. 2.0

sapiens
    2.0%; Score 11; DB 14; Length 129;
    100.0%; Pred. No. 1.1;
    0; Mismatches 0; Indels 0; Gaps 0;

pppppq 232
    2.0%; Score 11; DB 14; Length 129;
    100.0%; Pred. No. 1.1;
    0; Mismatches 0; Indels 0; Gaps 0;

pppppq 44
    2.0%; Score 11; DB 14; Length 129;
    100.0%; Pred. No. 1.1;
    0; Mismatches 0; Indels 0; Gaps 0;

; Application US/10425114
; IS20040034889A1
; ION:
; Jingdong
; Yihua
; ilic, David K.
; en, Steven E
; ska, Jack E
; Yongwei
; ION: Nucleic Acid Molecules and Other Molecules Associated with
; ION: Plants and Uses Thereof for Plant Improvement
; 38-21(53313)B
; TION NUMBER: US/10/425,114
; DATE: 2003-04-28
; NOS: 73128

ne max
    2.0%; Score 11; DB 12; Length 135;
    100.0%; Pred. No. 1.2;
    0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
    2.0%; Score 11; DB 12; Length 135;
    100.0%; Pred. No. 1.2;
    0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 101
    2.0%; Score 11; DB 12; Length 135;
    100.0%; Pred. No. 1.2;
    0; Mismatches 0; Indels 0; Gaps 0;

; Application US/09810264
; ION:
; du, Virginia C.
; Xu, Omolayo O.
; Xu

```

```

; APPLICANT: Lu, Guihua
; APPLICANT: Zhang, Lingyu
; TITLE OF INVENTION: WRKY Transcription Factors and Methods
; FILE REFERENCE: 1183
; CURRENT APPLICATION NUMBER: US/09/810,264
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,467
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-09-810-264-20

Query Match 2.0%; Score 11; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 133 PPPPPAPVAAA 143
DB 104 PPPPPAPVAAA 114

RESULT 71
US-10-108-260A-4241
; Sequence 4241, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4241
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-108-260A-4241

Query Match 2.0%; Score 11; DB 15; Length 334;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 225 QPPPPQPPPP 235
DB 230 QPPPPQPPPP 240

RESULT 72
US-10-184-644-319
; Sequence 319, Application US/10184644
; Publication No. US2003004930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCI
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC227
; CURRENT APPLICATION NUMBER: US/10/184,644

```

DATE: 2002-06-28
on removed - See File Wrapper or Palm
ID NOS: 612

Sapien

2.0%; Score 11; DB 14; Length 2103;
arity 100.0%; Pred. No. 11;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||||
ATTAAAA 521

Application US/10184634
US20030068684A1

ION:

Kevin P.

an, Jian

noyers, Luc

Idard, Audrey

owski, Paul J.

ney, Austin L.

James

th, Victoria

anabe, Colin K.

od, William I.

ing, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

P3430R1C217

ATION NUMBER: US/10/184,634

DATE: 2002-06-28

on removed - See File Wrapper or Palm
ID NOS: 612

Sapien

2.0%; Score 11; DB 14; Length 2103;
arity 100.0%; Pred. No. 11;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||||
ATTAAAA 521

Application US/10063685
US20030180909A1

ION:

an, Dan L.

lvaroff, Ellen

ritsen, Mary E.

Idard, Audrey

dowski, Paul J.

imaldi, Christopher J.

ney, Austin L.

tanabe, Colin K.

od, William I.

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

P3230R1C1

CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT FILING DATE: 2002-05-08

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 105

LENGTH: 2103

TYPE: DNA

ORGANISM: Homo Sapien

US-10-063-685-105

Query Match 2.0%; Score 11; DB 14; Length 2103;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 12 TAAAAATTAAAA 22
|||||||
DB 511 TAAAAATTAAAA 521

RESULT 75

US-10-184-644-333

Sequence 333, Application US/10184644

Publication No. US2003004930A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C227

CURRENT APPLICATION NUMBER: US/10/184,644

CURRENT FILING DATE: 2002-06-28

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 333

LENGTH: 2340

TYPE: DNA

ORGANISM: Homo Sapien

US-10-184-644-333

Query Match 2.0%; Score 11; DB 14; Length 2340;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 12 TAAAAATTAAAA 22
|||||||
DB 2329 TAAAAATTAAAA 2339

RESULT 76

US-10-184-634-333

Sequence 333, Application US/10184634

Publication No. US20030068684A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

11:33:40 2004

us-09-976-740-43.olig.rapb

I

ON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ON: ACIDS ENCODING THE SAME
P343OR1C217
ION NUMBER: US/10/184,634
ATE: 2002-06-28
n removed - See File Wrapper or Palm
NOS: 612

Sapien

2.0%; Score 11; DB 14; Length 2340;
urity 100.0%; Pred.No.13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

WTAAAA 22
|||||
WTAAAA 2339

ication US/09962055
0052033A1
ATION:

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

DENCE ADDRESS:

ESSEE: Fish & Richardson P.C.
ET: 225 Franklin Street
Boston
MA

RY: USA

02110-2804

READABLE FORM:

IM TYPE: Diskette

ITER: IBM Compatible

ATING SYSTEM: DOS

HARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/09/962,055

IG DATE: 24-Sep-2001

ICATION DATA:

ICATION NUMBER: 08/979,608

IG DATE: 26-NOV-1997

ICATION NUMBER: US 60/031,930

IG DATE: 27-NOV-1996

AGENT INFORMATION:

Myers, Louis

ISTRATION NUMBER: 35,965

ERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 22;

CHARACTERISTICS:

CH: 10 amino acids

: amino acid

OGY: linear

TYPE: protein

DESCRIPTION: SEQ ID NO: 22:

urity 1.9%; Score 10; DB 9; Length 10;
urity 100.0%; Pred.No.0.81;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY 529 EDDDPDGFGLG 538
Db |||||
1 EDDDPDGFGLG 10

RESULT 78

US-09-962-055-28

; Sequence 28, Application US/09962055

; Patent No. US20020052033A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; Lees, Robert S.

; Law, Simon W.

; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNO
TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/962,055

; FILING DATE: 24-Sep-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/979,608

; FILING DATE: 26-NOV-1997

; APPLICATION NUMBER: US 60/031,930

; FILING DATE: 27-NOV-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/598

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-962-055-28

Query Match

Best Local Similarity 1.9%; Score 10; DB 9; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 432 PPGKPALPGA 441

Db |||||

1 PPGKPALPGA 10

RESULT 79

US-09-976-740-22

; Sequence 22, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

ona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS

10797-004001
TION NUMBER: US/09/976,740
DATE: 2001-10-12
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 08/979,608
TE: 1997-11-26
TE: 1996-11-27
ON NUMBER: US 60/031,930
TE: 1997-06-03
ON NUMBER: US 60/048,547
D NOS: 53
EQ for Windows Version 4.0

, sapiens

1.9%; Score 10; DB 9; Length 10;
arity 100.0%; Pred.No. 0.81; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PDGFLG 538
|||||
PDGFLG 10

lication US/09976740
US20020194633A1
TION:

, Ann M.
s, Robert S.
, Simon W.

ona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS

10797-004001
TION NUMBER: US/09/976,740
DATE: 2001-10-12
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

1.9%; Score 10; DB 9; Length 10;
arity 100.0%; Pred.No. 0.81; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PALPGA 441
|||||
PALPGA 10

US-10-671-242-22
; Sequence 22, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-242-22

Query Match 1.9%; Score 10; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 529 EDDPDGFLG 538
Db 1 EDDPDGFLG 10

RESULT 82
US-10-671-242-28
; Sequence 28, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-671-242-28

1.9%; Score 10; DB 12; Length 10;
rity 100.0%; Pred. No. 0.81; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

ALPGA 441
|||||
ALPGA 10

ication US/10023529
S20020129388A1

ON:
Ann M.
, Robert S.
, Simon W.
na, Anibal A.
ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ON: ATHEROSCLEROSIS

10797-004001
ION NUMBER: US/10/023,529
ATE: 2001-12-17
N NUMBER: 09/616,289
E: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
E: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

sapiens

1.9%; Score 10; DB 13; Length 10;
rity 100.0%; Pred. No. 0.81; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DGFLG 538
|||||
DGFLG 10

ication US/10023529
S20020129388A1

ON:
Ann M.
, Robert S.
, Simon W.
na, Anibal A.
ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ON: ATHEROSCLEROSIS

10797-004001
ION NUMBER: US/10/023,529
ATE: 2001-12-17
N NUMBER: 09/616,289
E: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-28

Query Match 1.9%; Score 10; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 PPGKALPGA 441
Db 1 PPGKALPGA 10

RESULT 85

US-10-023-523-22
; Sequence 22, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-523-22

Query Match 1.9%; Score 10; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 EDDPDGFLG 538
Db 1 EDDPDGFLG 10

RESULT 86

US-10-023-523-28
; Sequence 28, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TON: ATHEROSCLEROSIS

10797-004001

ATION NUMBER: US/10/023,523

DATE: 2001-12-17

ON NUMBER: US/09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

ID NOS: 53

SEQ for Windows Version 4.0

tolagus cuniculus

1.9%; Score 10; DB 13; Length 10;

arity 100.0%; Pred. No. 0.81; 0; Indels 0; Gaps 0;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

PALPGA 441

|||||

TPALPGA 10

lication US/10616187

US20040013668A1

TON:

is, Ann M.

is, Robert S.

ona, Simon W.

ona, Anibal A.

TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TON: ATHEROSCLEROSIS

10797-004001

ATION NUMBER: US/10/616,187

DATE: 2003-07-09

ON NUMBER: US/09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

ID NOS: 53

SEQ for Windows Version 4.0

sapiens

1.9%; Score 10; DB 15; Length 10;

arity 100.0%; Pred. No. 0.81; 0; Indels 0; Gaps 0;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

PDGFLG 538

|||||

PDGFLG 10

RESULT 88

US-10-616-187-28

; Sequence 28, Application US/10616187

; Publication No. US20040013668A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/616,187

; CURRENT FILING DATE: 2003-07-09

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-10-616-187-28

Query Match

Best Local Similarity 100.0%; Score 10; DB 15; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; C

QY 432 PPGKPALPGA 441

|||||

Db 1 PPGKPALPGA 10

RESULT 89

US-10-424-599-175120

; Sequence 175120, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 175120

; LENGTH: 142

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(142)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_129151C.1.pep

US-10-424-599-175120

Query Match

Best Local Similarity 100.0%; Score 10; DB 12; Length 142;

Matches 10; Conservative 0; Mismatches 0; Indels 0; C

TAPPS 161
|||||
TAPPS 62

Application US/10425114
US20040034888A1

IN:

Jingdong

Yihua

Li, David K.

en, Steven E

uska, Jack E

Yongwei

ON: Nucleic Acid Molecules and Other Molecules Associated With

ON: Plants and Uses Thereof for Plant Improvement

38-21(53223)B

ION NUMBER: US/10/425,114

ATE: 2003-04-28

NOS: 73128

ays

ON: Clone ID: LIB3356-019-E1_FLI.pep

1.9%; Score 10; DB 12; Length 154;

urity 100.0%; Pred. No. 7.9;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAP 127

|||||

AAAAP 152

8

Application US/10424599

US20040031072A1

ON:

La Thomas J

lic David K

Yihua

Yongwei

ON: Soy Nucleic Acid Molecules and Other Molecules Associated With

ON: Plants and Uses Thereof for Plant Improvement

38-21(53223)B

ION NUMBER: US/10/424,599

ATE: 2003-04-28

NOS: 285684

ne max

ON: Clone ID: PAT_MRT3847_97045C.1.pep

8

1.9%; Score 10; DB 12; Length 181;

urity 100.0%; Pred. No. 9;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAP 127

|||||

AAAAAP 170

US-10-424-599-188876
; Sequence 188876, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 188876

; LENGTH: 187

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_14156C.1.pep

US-10-424-599-188876

Query Match 1.9%; Score 10; DB 12; Length 187;

Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDDEDEDED 342

|||||

Db 96 DDDEDEDED 105

RESULT 93

US-10-424-599-224491

; Sequence 224491, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 224491

; LENGTH: 188

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_44746C.1.pep

US-10-424-599-224491

Query Match 1.9%; Score 10; DB 12; Length 188;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDDEDEDED 342

|||||

Db 98 DDDEDEDED 107

RESULT 94

US-10-282-122A-45132

; Sequence 45132, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlser, Karl

11:33:40 2004

us-09-976-740-43.olog.rapb

kind, Judith
l, Daniel
wick, John
r, Grant
amoto, Robert
syth, R.
H.

TON: Identification of Essential Genes in Microorganisms

ELITRA.034A

ATION NUMBER: US/10/282,122A

DATE: 2003-02-20

ON NUMBER: 60/191,078

TE: 2000-03-21

ON NUMBER: 60/206,848

TE: 2000-05-23

ON NUMBER: 60/207,727

TE: 2000-05-26

ON NUMBER: 60/230,335

TE: 2000-09-06

ON NUMBER: 60/230,347

TE: 2000-09-09

ON NUMBER: 60/242,578

TE: 2000-10-23

ON NUMBER: 60/253,625

TE: 2000-11-27

ON NUMBER: 60/257,931

TE: 2000-12-22

ON NUMBER: 60/267,636

TE: 2001-02-09

ON NUMBER: 60/269,308

TE: 2001-02-16

Application data removed - See File Wrapper or PALM.

ID NOS: 78614

itIn version 3.1

etobacter baumannii

.32

1.9%; Score 10; DB 12; Length 238;

arity 100.0%; Pred. No. 11;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

'AAAAA 146

|||||

'AAAAA 141

14 Application US/10425114

US2004003488A1

TION:

Jingdong

u, Yihua

alic, David K.

reen, Steven E

aska, Jack E

), Yongwei

TION: Nucleic Acid Molecules and Other Molecules Associated With

TION: Plants and Uses Thereof for Plant Improvement

: 38-21(5313)B

ATION NUMBER: US/10/425,114

DATE: 2003-04-28

ID NOS: 73128

mays

TION: Clone ID: UC-ZMELMO17014A11_FLI pep

04

Query Match 1.9%; Score 10; DB 12; Length 253;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 118 APAAAAAAP 127

|||||

Db 244 APAAAAAAP 253

RESULT 96

US-10-425-114-50072

; Sequence 50072, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Assc

; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 50072

; LENGTH: 307

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3594-013-A4_FLI pep

US-10-425-114-50072

Query Match

1.9%; Score 10; DB 12; Length 307;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 120 AAAAAAAPPP 129

|||||

Db 239 AAAAAAAPPP 248

RESULT 97

US-10-425-114-64408

; Sequence 64408, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Assc

; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 64408

; LENGTH: 361

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3732-052-H7_FLI pep

US-10-425-114-64408

Query Match

1.9%; Score 10; DB 12; Length 361;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

SSSAA 27
|||||
SSSAA 88

9 Application US/10424599
(S20040031072A1
ON:

isa Thomas J
ilic David K
Yihua
Yongwei

ON: Soy Nucleic Acid Molecules and Other Molecules Associated With
ON: Plants and Uses Thereof for Plant Improvement
38-21(53223)B
ION NUMBER: US/10/424,599
ATE: 2003-04-28
NOS: 285684

ne max

ON: Clone ID: PAT_MRT3847_74372C.1.pap
9

1.9%; Score 10; DB 12; Length 368;
rity 100.0%; Pred. No. 16;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATAPP 160
|||||
ATAPP 37

Application US/10369493
(S20030233675A1
ON:

Yongwei
le, Gregory J.
er, Steven C.
man, Barry S.

ON: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ON: PLANTS WITH IMPROVED PROPERTIES
38-10(52052)B
ION NUMBER: US/10/369,493
ATE: 2003-02-28
N NUMBER: US 60/360,039
E: 2002-02-21
NOS: 47374

ionomas campestris

1.9%; Score 10; DB 15; Length 401;
rity 100.0%; Pred. No. 17;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 127
|||||
AAAAA 112

.ication US/10229345

; Publication No. US20040038220A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CWRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/229,345
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-229-345-18

Query Match 1.9%; Score 10; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 178 AAPPAPAAP 187
|||||
DB 236 AAPPAPAAP 245

RESULT 101

US-10-274-177-18
; Sequence 18, Application US/10274177
; Publication No. US20040038225A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CWRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/274,177
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/10/229,345
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-177-18

Query Match 1.9%; Score 10; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 178 AAPPAPAAP 187
|||||
DB 236 AAPPAPAAP 245

RESULT 102

US-10-087-080-32
; Sequence 32, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Ros Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of M
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-0008400S
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555

TE: 2001-04-17
D NOS: 41
tIn Ver. 2.1

sapiens

TON: winged helix/forkhead transcription factor (HFW1)

1.9%; Score 10; DB 15; Length 402;
arity 100.0%; Pred. No. 17;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PAPAAP 187

|||||

PAPAAP 245

Application US/10369493
US20030233675A1

TON:

Yongwei

kle, Gregory J.

ter, Steven C.

dman, Barry S.

et, Xianfeng

TON: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TON: PLANTS WITH IMPROVED PROPERTIES

38-10(52052)B

ATION NUMBER: US/10/369,493

DATE: 2003-02-28

ION NUMBER: US 60/360,039

ATE: 2002-02-21

D NOS: 47374

thomonas campestris

1.9%; Score 10; DB 15; Length 404;
arity 100.0%; Pred. No. 18;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAP 127

|||||

AAAAAP 115

Application US/10369493
US20030233675A1

TON:

Yongwei

kle, Gregory J.

ter, Steven C.

ldman, Barry S.

an, Xianfeng

TON: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TON: PLANTS WITH IMPROVED PROPERTIES

: 38-10(52052)B

ATION NUMBER: US/10/369,493

DATE: 2003-02-28

ION NUMBER: US 60/360,039

ATE: 2002-02-21

ID NOS: 47374

TYPE: PRT
ORGANISM: Xanthomonas campestris
US-10-369-493-16231

Query Match 1.9%; Score 10; DB 15; Length 404;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 118 APAAAAAAP 127

|||||

DB 106 APAAAAAAP 115

RESULT 105

US-10-282-122A-50659

Sequence 50659, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorga

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PAL

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50659

LENGTH: 588

TYPE: PRT

ORGANISM: Burkholderia mallei

US-10-282-122A-50659

Query Match 1.9%; Score 10; DB 12; Length 588;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 118 APAAAAAAP 127

|||||

DB 476 APAAAAAAP 485

RESULT 106

```

3 Application US/10282122A
IS20040029129A1
ION:
Liangsu
dio, Carlos
ne, Cheryl
elbeck, Robert
sen, Kari
ind, Judith
l, Daniel
vick, John
r, Grant
amoto, Robert
syth, R.
H.
[ON: Identification of Essential Genes in Microorganisms
ELITRA.034A
TION NUMBER: US/10/282,122A
DATE: 2003-02-20
N NUMBER: 60/191,078
TE: 2000-03-21
N NUMBER: 60/206,848
TE: 2000-05-23
N NUMBER: 60/207,727
TE: 2000-05-26
N NUMBER: 60/230,335
TE: 2000-09-06
N NUMBER: 60/230,347
TE: 2000-09-09
N NUMBER: 60/242,578
TE: 2000-10-23
N NUMBER: 60/253,625
TE: 2000-11-27
N NUMBER: 60/257,931
TE: 2000-12-22
N NUMBER: 60/267,636
TE: 2001-02-09
N NUMBER: 60/269,308
TE: 2001-02-16
Application data removed - See File Wrapper or PALM.
NOS: 78614
in version 3.1

```

```

erichia coli
33

```

```

arity 1.9%; Score 10; DB 12; Length 613;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DEDEED 342
|||||
DEDEED 200

```

```

39 Application US/10282122A
IS20040029129A1
ION:
Liangsu
dio, Carlos
ne, Cheryl
elbeck, Robert
sen, Kari
ind, Judith
l, Daniel
vick, John
r, Grant
amoto, Robert

```

```

; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorgan
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74989
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-74989

```

```

Query Match 1.9%; Score 10; DB 12; Length 660;
Best Local Similarity 100.0%; Pred. NO. 26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY 333 DDEDEDEED 342
|||||
Db 238 DDEDEDEED 247

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RESULT 108
US-10-282-122A-75492
; Sequence 75492, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorgan
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06

```


ION NUMBER: 60/230,347
ATE: 2000-09-09
ION NUMBER: 60/242,578
ATE: 2000-10-23
ION NUMBER: 60/253,625
ATE: 2000-11-27
ION NUMBER: 60/257,931
ATE: 2000-12-22
ION NUMBER: 60/267,636
ATE: 2001-02-09
ION NUMBER: 60/269,308
ATE: 2001-02-16
r Application data removed - See File Wrapper or PALM.
ID NOS: 78614
ntin version 3.1

monella typhi
492

1.9%; Score 10; DB 12; Length 660;
larity 100.0%; Pred. No. 26;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEDEED 342
|||||||
SEDEED 247

plication US/10627476
US20040030116A1

IIION:

pejus, Mark
gger, Burkhard
oder, Hartwig
lder, Oskar

berhauer, Gregor
TION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

IIION: TRANSPORT

: BGI-125CFCN
TION NUMBER: US/10/627,476
DATE: 2003-07-25

ION NUMBER: 09/602,787

ATE: 2000-06-23
ION NUMBER: USSN 60/141031

ATE: 1999-06-25

ION NUMBER: DE 19931454.3
ATE: 1999-07-08

ION NUMBER: DE 19931478.0

ATE: 1999-07-08

ION NUMBER: DE 19931563.9
ATE: 1999-07-08

ION NUMBER: DE 19932122.1
ATE: 1999-07-09

ION NUMBER: DE 19932124.8

ATE: 1999-07-09

ION NUMBER: DE 19932125.6
ATE: 1999-07-09

ION NUMBER: DE 19932128.0
ATE: 1999-07-09

ION NUMBER: DE 19932180.9
ATE: 1999-07-09

r Application data removed - See File Wrapper or PALM.
ID NOS: 678

ynebacterium glutamicum

Query Match 1.9%; Score 10; DB 12; Length 1277;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 137 PAFVAAAAPA 146

Db 984 PAFVAAAAPA 993

RESULT 110

US-10-092-900A-224

; Sequence 224, Application US/10092900A
; Publication No. US20040043382A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Taupier Jr., Raymond J.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Li, Ji

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: Gorman, Linda

; APPLICANT: Miller, Charles E.

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Patturajan, Meera

; APPLICANT: Gangolli, Baha A.

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Guo, Xiaojia Sasha

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Fernandes, Elma R.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Liu, Yi

; APPLICANT: Anderson, David W.

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Catterton, Elina

; APPLICANT: Leite, Mario W.

; APPLICANT: Zhong, Hailong

; APPLICANT: Alsobrook, John P.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Aci

; FILE REFERENCE: 21402-290C

; CURRENT APPLICATION NUMBER: US/10/092,900A

; CURRENT FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: USSN 60/274,322

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/283,675

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: USSN 60/338,092

; PRIOR FILING DATE: 2001-12-03

; PRIOR APPLICATION NUMBER: USSN 60/274,281

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/274,191

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/325,681

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: USSN 60/304,354

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: USSN 60/279,995

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: USSN 60/294,899

; PRIOR FILING DATE: 2001-05-31

; PRIOR APPLICATION NUMBER: USSN 60/287,424

; PRIOR FILING DATE: 2001-04-30

; Remaining Prior Application data removed - See File Wrapper or PALM

; NUMBER OF SEQ ID NOS: 768

; SEQ ID NO 224

```

sapiens
      1.9%; Score 10; DB 12; Length 1390;
      100.0%; Pred. No. 49;
      0; Mismatches 0; Indels 0; Gaps 0;

JQPPPP 235
|||||
JQPPPP 986

Application US/10032585
JS20030180953A1
CON: Roemer D.
Jiang
Jles, Boone
Jrd, Bussey
CON: Gene Disruption Methodologies for Drug Target Discovery
10182-005-999
TION NUMBER: US/10/032,585
DATE: 2001-12-20
NOS: 8000
In version 3.1

da albicans
      1.9%; Score 10; DB 14; Length 1461;
      100.0%; Pred. No. 51;
      0; Mismatches 0; Indels 0; Gaps 0;

DEEDD 343
|||||
DEEDD 1445

Application US/10073912
JS2003007703A1
CON:
i et al.
CON: Nucleic Acids, Proteins, and Antibodies
PTZ34C1
TION NUMBER: US/10/073,912
DATE: 2002-02-14
n removed - See file Wrapper or Palm
NOS: 18
In Ver. 2.0

sapiens
feature
CON: n equals a,t,g, or c

      1.9%; Score 10; DB 14; Length 1591;
      100.0%; Pred. No. 55;
      0; Mismatches 0; Indels 0; Gaps 0;

TAAAA 22
|||||

Db 795 AAAATTAAAA 804

RESULT 113
US-10-142-426-309
; Sequence 309, Application US/10142426
; Publication No. US2004004833A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; FILE REFERENCE: P3330R1C224
; CURRENT APPLICATION NUMBER: US/10/142,426
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 309
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1837
; OTHER INFORMATION: unknown base
US-10-142-426-309

Query Match 1.9%; Score 10; DB 12; Length 1843;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
|||||
Db 1826 AAAATTAAAA 1835

RESULT 114
US-10-123-155-309
; Sequence 309, Application US/10123155
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

```

11:33:40 2004

us-09-976-740-43.olg.rapb

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
P3330R1C30
TION NUMBER: US/10/123,155
DATE: 2002-04-15
n removed - See Palm or File Wrapper
D NOS: 550

Sapien

ure

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

TTAAAA 1835

Application US/10146731
US20030129692A1

ION:

er, Kevin P.
resini, Maureen
orge, Laura
noyers, Luc
lvaroff, Ellen
Wei-Qiang
ritsen, Mary E.
dard, Audrey
owski, Paul J.
ney, Austin L.
erwood, Steven
ith, Victoria
ewart, Timothy A.
as, Daniel
anabe, Colin K
d, William
ang, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ACIDS ENCODING THE SAME

P3330R1C323

ATION NUMBER: US/10/146,731

DATE: 2002-05-15

ion removed - See File Wrapper or Palm

ID NOS: 550

Sapien

ure

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

TTAAAA 1835

RESULT 116

US-10-140-472-309

; Sequence 309, Application US/10140472

; Publication No. US2003013888A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; FILE REFERENCE: P3330R1C168

; CURRENT APPLICATION NUMBER: US/10/140,472

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 309

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 1837

; OTHER INFORMATION: unknown base

US-10-140-472-309

Query Match

1.9%; Score 10; DB 14; Length 1843;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

|||||

Db 1826 AAAATTAAAA 1835

RESULT 117

US-10-141-761-309

; Sequence 309, Application US/10141761

; Publication No. US20030148432A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; FILE REFERENCE: P3330R1C168

; CURRENT APPLICATION NUMBER: US/10/140,472

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 309

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 1837

; OTHER INFORMATION: unknown base

US-10-140-472-309

P3330R1C198
ION NUMBER: US/10/141,761
DATE: 2002-05-08
on removed - See Palm or File Wrapper
D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1835

plication US/10142885
JS20030157604A1

ION:

r, Kevin P.

esini, Maureen

orge, Laura

oyers, Luc

varoff, Ellen

Wei-Qiang

ritsen, Mary E.

ard, Audrey

owski, Paul J.

ney, Austin L.

wood, Steven

th, Victoria

art, Timothy A.

as, Daniel

anabe, Colin K

d, William

ag, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ION: ACIDS ENCODING THE SAME

P3330R1C248

ION NUMBER: US/10/142,885

DATE: 2002-05-10

ion removed - See File Wrapper or Palm

D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1835

US-10-158-790-309
; Sequence 309, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; CURRENT APPLICATION NUMBER: US/10/158,790

; CURRENT FILING DATE: 2002-05-30

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 309

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 1837

; OTHER INFORMATION: unknown base

US-10-158-790-309

Query Match 1.9%; Score 10; DB 14; Length 1843;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22

|||||

Db 1826 AAAATTAAAA 1835

RESULT 120

US-10-137-871-309

; Sequence 309, Application US/10137871

; Publication No. US20030207350A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C153

; CURRENT APPLICATION NUMBER: US/10/137,871

DATE: 2002-05-03
on removed - See Palm or File Wrapper
D NOS: 550

Sapien

ire

ION: unknown base

1.9%; Score 10; DB 15; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1835

pplication US/10140923
US20030207355A1

ION:

er, Kevin P.

eresini, Maureen

orge, Laura

noyers, Luc

ilvaroff, Ellen

Wei-Qiang

ritsen, Mary E.

ddard, Audrey

owski, Paul J.

ney, Austin L.

erwood, Steven

th, Victoria

wart, Timothy A.

as, Daniel

anabe, Colin K

xd, William

ng, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ION: ACIDS ENCODING THE SAME

P3330R1C188

ATION NUMBER: US/10/140,923

DATE: 2002-05-07

on removed - See Palm or File Wrapper

D NOS: 550

Sapien

ire

7

ION: unknown base

1.9%; Score 10; DB 15; Length 1843;
arity 100.0%; Pred. No. 62;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATAAAA 22

|||||

ATAAAA 1835

pplication US/10141756

Publication No. US20030207359A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
FILE REFERENCE: P3330R1C200
CURRENT APPLICATION NUMBER: US/10/141,756
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 309
LENGTH: 1843
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 1837
OTHER INFORMATION: unknown base

US-10-141-756-309

Query Match 1.9%; Score 10; DB 15; Length 1843;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 13 AAAATTAAAA 22

Db 1826 AAAATTAAAA 1835

RESULT 123

US-10-141-759-309

Sequence 309, Application US/10141759

Publication No. US20030207361A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

FILE REFERENCE: P3330R1C197

CURRENT APPLICATION NUMBER: US/10/141,759

CURRENT FILING DATE: 2002-05-08

Prior Application removed - See File Wrapper or Palm

D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 15; Length 1843;
 arity 100.0%; Pred. No. 62; Mismatches 0; Indels 0; Gaps 0;

TAAAAA 22

TAAAAA 1835

plication US/10140805

US20030207417A1

ION:

r, Kevin P.

esini, Maureen

orge, Laura

noyers, Luc

varoff, Ellen

Wei-Qiang

ritsen, Mary E.

dard, Audrey

owski, Paul J.

ney, Austin L.

rwood, Steven

th, Victoria

wart, Timothy A.

as, Daniel

anabe, Colin K

d, William

ng, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME

P3330R1C176

ION NUMBER: US/10/140,805

DATE: 2002-05-07

ion removed - See File Wrapper or Palm

D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 15; Length 1843;
 arity 100.0%; Pred. No. 62; Mismatches 0; Indels 0; Gaps 0;

TAAAAA 22

TAAAAA 1835

plication US/10140864

US20030207419A1

ION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Deanoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

FILE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C184

CURRENT APPLICATION NUMBER: US/10/140,864

CURRENT FILING DATE: 2002-05-07

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 309

LENGTH: 1843

TYPE: DNA

ORGANISM: Homo Sapien

FEATURE:

NAME/KEY: unsure

LOCATION: 1837

OTHER INFORMATION: unknown base

US-10-140-864-309

Query Match

Best Local Similarity 1.9%; Score 10; DB 15; Length 1843;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22

Db 1826 AAAATTAAAA 1835

RESULT 126

US-10-369-493-22455

Sequence 22455, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR

FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 22455

LENGTH: 1887

TYPE: PRT

ORGANISM: Saccharomyces cerevisiae

US-10-369-493-22455

Query Match

Best Local Similarity 1.9%; Score 10; DB 15; Length 1887;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 137 PAPVAAAAA 146

Db 1826 AAAATTAAAA 1835

VAAAAA 134

plication US/10206915
US20040029221A1

TION:

er, Kevin P.

en, Jian

snoyers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TION: ACIDS ENCODING THE SAME

: P3430R1C513

ATION NUMBER: US/10/206,915

DATE: 2002-07-26

ION NUMBER: 10/052586

ATE: 2002-01-15

ION NUMBER: 60/059263

ATE: 1997-09-18

ION NUMBER: 60/059266

ATE: 1997-09-18

ION NUMBER: 60/062250

ATE: 1997-10-17

ION NUMBER: 60/063120

ATE: 1997-10-24

ION NUMBER: 60/063121

ATE: 1997-10-24

ION NUMBER: 60/063486

ATE: 1997-10-21

ION NUMBER: 60/063540

ATE: 1997-10-28

ION NUMBER: 60/063541

ATE: 1997-10-28

ION NUMBER: 60/063544

ATE: 1997-10-28

ION data removed - See File Wrapper or PALM.
ID NOS: 612

o Sapien

larity 1.9%; Score 10; DB 12; Length 1894;

Conservative 0; Pred. No. 64;

Mismatches 0; Indels 0; Gaps 0;

ATTAATA 22

|||||

ATTAATA 1060

plication US/10199670

US20040033560A1

TION:

er, Kevin P.

en, Jian

snoyers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C401

; CURRENT APPLICATION NUMBER: US/10/199,670

; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 97

; LENGTH: 1894

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-199-670-97

Query Match 1.9%; Score 10; DB 12; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

Db 1051 AAAATTAAAA 1060

RESULT 129

US-10-201-858-97

; Sequence 97, Application US/10201858

; Publication No. US20040038337A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C464

; CURRENT APPLICATION NUMBER: US/10/201,858

; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

ON NUMBER: 60/062250
TE: 1997-10-17
ON NUMBER: 60/063120
TE: 1997-10-24
ON NUMBER: 60/063121
TE: 1997-10-24
ON NUMBER: 60/063486
TE: 1997-10-21
ON NUMBER: 60/063540
TE: 1997-10-28
ON NUMBER: 60/063541
TE: 1997-10-28
ON NUMBER: 60/063544
TE: 1997-10-28
on data removed - See File Wrapper or PALM.
D NOS: 612

Sapien

1.9%; Score 10; DB 12; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
||||||
TTAAAA 1060

lication US/10205890
US20040048334A1
ION:
r, Kevin P.
a, Jian
noyers, Luc
lard, Audrey
owski, Paul J.
ey, Austin L.
, James
th, Victoria
anabe, Colin K.
d, William I.
ag, Zemin
ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ION: ACIDS ENCODING THE SAME
P3430R1C519
TION NUMBER: US/10/205,890
DATE: 2002-07-26
ON NUMBER: 10/052586
TE: 2002-01-15
ON NUMBER: 60/059263
TE: 1997-09-18
ON NUMBER: 60/059266
TE: 1997-09-18
ON NUMBER: 60/062250
TE: 1997-10-17
ON NUMBER: 60/063120
TE: 1997-10-24
ON NUMBER: 60/063121
TE: 1997-10-24
ON NUMBER: 60/063486
TE: 1997-10-21
ON NUMBER: 60/063540
TE: 1997-10-28
ON NUMBER: 60/063541
TE: 1997-10-28
ON NUMBER: 60/063544
TE: 1997-10-28
on data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-97

Query Match 1.9%; Score 10; DB 12; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C

Qy 13 AAAATTAAAA 22
||||||
Db 1051 AAAATTAAAA 1060

RESULT 131

US-10-208-024-97
; Sequence 97, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-208-024-97

Query Match 1.9%; Score 10; DB 12; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
||||||
Db 1051 AAAATTAAAA 1060

us-09-976-740-43.olg.rapb

Application US/10201853
US20040053358A1

TION:
r, Kevin P.
n, Jian
noyers, Luc
ddard, Audrey
owski, Paul J.
ney, Austin L.
t, James
ith, Victoria
anabe, Colin K.
g, William I.
ng, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
P343ORIC465
TION NUMBER: US/10/201,853
DATE: 2002-07-23
ON NUMBER: 60/052586
ATE: 2002-01-15
ON NUMBER: 60/059263
ATE: 1997-09-18
ON NUMBER: 60/059266
ATE: 1997-09-18
ON NUMBER: 60/062250
ATE: 1997-10-17
ON NUMBER: 60/063120
ATE: 1997-10-24
ON NUMBER: 60/063121
ATE: 1997-10-21
ON NUMBER: 60/063540
ATE: 1997-10-28
ON NUMBER: 60/063541
ATE: 1997-10-28
ON NUMBER: 60/063544
ATE: 1997-10-28
ON NUMBER: 60/063564
ATE: 1997-10-28
ON NUMBER: 60/063734
ATE: 1997-10-29
ON NUMBER: 60/063870
ATE: 1997-10-31
ON NUMBER: 60/064103
ATE: 1997-10-31
ON NUMBER: 60/065311
ATE: 1997-11-13
ON NUMBER: 60/066120
ATE: 1997-11-21
ON NUMBER: 60/066466
ATE: 1997-11-24
ON NUMBER: 60/066772
ATE: 1997-11-24
ON NUMBER: 60/069335
ATE: 1997-12-11
ON NUMBER: 60/069425
ATE: 1997-12-12
ON NUMBER: 60/069870
ATE: 1997-12-17
ON NUMBER: 60/068017
ATE: 1997-12-18
ON NUMBER: 60/077450
ATE: 1998-03-10
ON NUMBER: 60/077632
ATE: 1998-03-11
ON NUMBER: 60/077649
ATE: 1998-03-11
ON NUMBER: 60/078886
ATE: 1998-03-20
ON NUMBER: 60/078939
ATE: 1998-03-20
ON NUMBER: 60/079664
ATE: 1998-03-27
ON NUMBER: 60/079786
ATE: 1998-03-27
ON NUMBER: 60/080107
ATE: 1998-03-31
ON NUMBER: 60/080194
ATE: 1998-03-31
ON NUMBER: 60/080327
ATE: 1998-04-01
ON NUMBER: 60/080333
ATE: 1998-04-01
ON NUMBER: 60/081049
ATE: 1998-04-08

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score 10; DB 12; Length 1894;
Larity 100.0%; Pred.No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTTAAA 22
|||||
ATTTAAA 1060

lication US/10052586
US20020127584A1

TION:
er, Kevin P.
en, Jian
snoyers, Luc
ddard, Audrey
owski, Paul J.
rney, Austin L.
n, James
ith, Victoria
tanabe, Colin K.

1.9%; Score

IN NUMBER: 60/081070
TE: 1998-04-08
IN NUMBER: 60/081195
TE: 1998-04-09
IN NUMBER: 60/081838
TE: 1998-04-15
IN NUMBER: 60/082568
TE: 1998-04-21
IN NUMBER: 60/082569
TE: 1998-04-21
IN NUMBER: 60/082704
TE: 1998-04-22
IN NUMBER: 60/082797
TE: 1998-04-22
IN NUMBER: 60/083322
TE: 1998-04-28
IN NUMBER: 60/083495
TE: 1998-04-29
IN NUMBER: 60/083496
TE: 1998-04-29
IN NUMBER: 60/083499
TE: 1998-04-29
IN NUMBER: 60/083559
TE: 1998-04-29
IN NUMBER: 60/084366
TE: 1998-05-05
IN NUMBER: 60/084414
TE: 1998-05-06
IN NUMBER: 60/084639
TE: 1998-05-07
IN NUMBER: 60/084640
TE: 1998-05-07
IN NUMBER: 60/084643
TE: 1998-05-07
IN NUMBER: 60/085573
TE: 1998-05-15
IN NUMBER: 60/085579
TE: 1998-05-15
IN NUMBER: 60/085580
TE: 1998-05-15
IN NUMBER: 60/085582
TE: 1998-05-15
IN NUMBER: 60/085700
TE: 1998-05-15
IN NUMBER: 60/086023
TE: 1998-05-18
IN NUMBER: 60/086392
TE: 1998-05-22
IN NUMBER: 60/086486
TE: 1998-05-22
IN NUMBER: 60/087098
TE: 1998-05-28
IN NUMBER: 60/087208
TE: 1998-05-28
IN NUMBER: 60/087609
TE: 1998-06-02
IN NUMBER: 60/087759
TE: 1998-06-02
IN NUMBER: 60/087827
TE: 1998-06-03
IN NUMBER: 60/088025
TE: 1998-06-04
IN NUMBER: 60/088028
TE: 1998-06-04
IN NUMBER: 60/088029
TE: 1998-06-04
IN NUMBER: 60/088033
TE: 1998-06-04
IN NUMBER: 60/088167
TE: 1998-06-05
IN NUMBER: 60/088202
TE: 1998-06-05
IN NUMBER: 60/088212

IN PRIOR FILING DATE: 1998-06-05
IN PRIOR APPLICATION NUMBER: 60/088217
IN PRIOR FILING DATE: 1998-06-05
IN PRIOR APPLICATION NUMBER: 60/088326
IN PRIOR FILING DATE: 1998-06-04
IN PRIOR APPLICATION NUMBER: 60/088655
IN PRIOR FILING DATE: 1998-06-09
IN PRIOR APPLICATION NUMBER: 60/088722
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088738
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088740
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088811
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088824
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088825
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088826
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088861
IN PRIOR FILING DATE: 1998-06-11
IN PRIOR APPLICATION NUMBER: 60/088863
IN PRIOR FILING DATE: 1998-06-11
IN PRIOR APPLICATION NUMBER: 60/088876
IN PRIOR FILING DATE: 1998-06-11
IN PRIOR APPLICATION NUMBER: 60/089090
IN PRIOR FILING DATE: 1998-06-12
IN PRIOR APPLICATION NUMBER: 60/089105
IN PRIOR FILING DATE: 1998-06-12
IN PRIOR APPLICATION NUMBER: 60/089512
IN PRIOR FILING DATE: 1998-06-16
IN PRIOR APPLICATION NUMBER: 60/089514
IN PRIOR FILING DATE: 1998-06-16
IN PRIOR APPLICATION NUMBER: 60/089538
IN PRIOR FILING DATE: 1998-06-17
IN PRIOR APPLICATION NUMBER: 60/089598
IN PRIOR FILING DATE: 1998-06-17
IN PRIOR APPLICATION NUMBER: 60/089653
IN PRIOR FILING DATE: 1998-06-17
IN PRIOR APPLICATION NUMBER: 60/089908

Query Match 1.9%; Score 10; DB 13; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 13 AAAATTAAAA 22
|||||
Db 1051 AAAATTAAAA 1060

RESULT 134
US-10-174-590-97
; Sequence 97, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18

ion removed - See File Wrapper or Palm
ID NOS: 612

o Sapien

1.9%; Score 10; DB 14; Length 1894;
larity 100.0%; Pred. No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22

|||||
ATTAAAA 1060

plication US/10176758
US2003008353A1

TION:

er, Kevin P.

en, Jian

snoyers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ACIDS ENCODING THE SAME

: P3430R1C104

ATION NUMBER: US/10176,758

DATE: 2002-06-21

ion removed - See File Wrapper or Palm

ID NOS: 612

o Sapien

1.9%; Score 10; DB 14; Length 1894;
larity 100.0%; Pred. No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22

|||||
ATTAAAA 1060

plication US/10175737
US20030013153A1

TION:

er, Kevin P.

en, Jian

snoyers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

|||||

Db 1051 AAAATTAAAA 1060

RESULT 137

US-10-173-706-97

; Sequence 97, Application US/10173706

; Publication No. US20030022293A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C7

; CURRENT APPLICATION NUMBER: US/10/173,706

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 97

; LENGTH: 1894

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-706-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

|||||

Db 1051 AAAATTAAAA 1060

RESULT 138

US-10-175-738-97

; Sequence 97, Application US/10175738

; Publication No. US20030022294A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

g,Zemin
 ION: ACIDS ENCODING THE SAME
 P3430R1C45
 TION NUMBER: US/10/175,738
 DATE: 2002-06-19
 on removed - See File Wrapper or Palm
 D NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
 arity 100.0%; Pred. No. 64;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
 |||||
 ITAAAA 1060

lication US/10175752
 US20030022295A1

ION:
 r, Kevin P.
 a, Jian
 noyers, Luc
 dard, Audrey
 cwski, Paul J.
 ney, Austin L.
 , James
 th, Victoria
 anabe, Colin K.
 d, William I.
 g, Zemin
 ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ION: ACIDS ENCODING THE SAME
 P3430R1C60
 TION NUMBER: US/10/175,752
 DATE: 2002-06-19
 on removed - See File Wrapper or Palm
 D NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
 arity 100.0%; Pred. No. 64;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
 |||||
 ITAAAA 1060

lication US/10176482
 US20030022296A1

ION:
 r, Kevin P.
 a, Jian
 noyers, Luc
 dard, Audrey
 cwski, Paul J.
 ney, Austin L.
 , James

APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
 FILE REFERENCE: P3430R1C70
 CURRENT APPLICATION NUMBER: US/10/176,482
 CURRENT FILING DATE: 2002-06-20
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 97
 LENGTH: 1894
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-482-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
 |||||
 Db 1051 AAAATTAAAA 1060

RESULT 141

US-10-176-757-97
 Sequence 97, Application US/10176757
 Publication No. US20030022297A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
 FILE REFERENCE: P3430R1C86
 CURRENT APPLICATION NUMBER: US/10/176,757
 CURRENT FILING DATE: 2002-06-20
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 97
 LENGTH: 1894
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-757-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
 |||||
 Db 1051 AAAATTAAAA 1060

RESULT 142

US-10-176-913-97
 Sequence 97, Application US/10176913
 Publication No. US20030022298A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey

owski, Paul J.
ney, Austin L.
James
th, Victoria
anabe, Colin K.
d, William I.
ng, Zemin
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
P3430R1C66
TION NUMBER: US/10/176,913
DATE: 2002-06-20
on removed - See file Wrapper or Palm
ID NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||
ATTAAAA 1060

lication US/10180552
US20030022300A1
TION:

an, Jian
moyers, Luc
kard, Audrey
owski, Paul J.
ney, Austin L.
James
th, Victoria
anabe, Colin K.
d, William I.
ng, Zemin
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
P3430R1C153
TION NUMBER: US/10/180,552
on removed - See file Wrapper or Palm
ID NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||
ATTAAAA 1060

lication US/10180557
US20030022301A1
TION:
an, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 97
LENGTH: 1894
TYPE: PRT
ORGANISM: Homo Sapien
US-10-180-557-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22
|||||
DB 1051 AAAATTAAAA 1060

RESULT 145

US-10-173-700-97
Sequence 97, Application US/10173700
Publication No. US20030027262A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
CURRENT APPLICATION NUMBER: US/10/173,700
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 97
LENGTH: 1894
TYPE: PRT
ORGANISM: Homo Sapien
US-10-173-700-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22
|||||
DB 1051 AAAATTAAAA 1060

RESULT 146

US-10-174-572-97
Sequence 97, Application US/10174572

US20030027263A1
 ION: r, Kevin P.
 n, Jian
 noyers, Luc
 dard, Audrey
 owski, Paul J.
 ney, Austin L.
 , James
 th, Victoria
 anabe, Colin K.
 d, William I.
 ng, Zemin
 ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ION: ACIDS ENCODING THE SAME
 P3430R1C40
 TION NUMBER: US/10/174,572
 DATE: 2002-06-18
 ation removed - See File Wrapper or Palm
 NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
 arity 100.0%; Pred. No. 64;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
 |||||
 TTAATAA 1060

lication US/10174579
 US20030027264A1

ION: r, Kevin P.
 n, Jian
 noyers, Luc
 dard, Audrey
 owski, Paul J.
 ney, Austin L.
 , James
 th, Victoria
 anabe, Colin K.
 d, William I.
 ng, Zemin
 ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ION: ACIDS ENCODING THE SAME
 P3430R1C31
 TION NUMBER: US/10/174,579
 DATE: 2002-06-18
 on removed - See File Wrapper or Palm
 NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
 arity 100.0%; Pred. No. 64;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
 |||||
 TTAATAA 1060

RESULT 148

US-10-174-582-97
 ; Sequence 97, Application US/10174582
 ; Publication No. US20030027265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C36
 ; CURRENT APPLICATION NUMBER: US/10/174,582
 ; CURRENT FILING DATE: 2002-06-18
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 97
 ; LENGTH: 1894
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-174-582-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
 |||||
 Db 1051 AAAATTAAAA 1060

RESULT 149

US-10-174-588-97
 ; Sequence 97, Application US/10174588
 ; Publication No. US20030027266A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C28
 ; CURRENT APPLICATION NUMBER: US/10/174,588
 ; CURRENT FILING DATE: 2002-06-18
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 97
 ; LENGTH: 1894
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-174-588-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
 |||||

11:33:40 2004

us-09-976-740-43.olig.rapb

ATTAAAA 1060

Publication US/10175739

US20030027267A1

ION:

er, Kevin P.

en, Jian

snovers, Luc

ddard, Audrey

owski, Paul J.

ney, Austin L.

a, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ION: ACIDS ENCODING THE SAME

: P3430R1C46

ATION NUMBER: US/10/175,739

DATE: 2002-06-19

ion removed - See File Wrapper or Palm

ID NOS: 612

o Sapien

1.9%; Score 10; DB 14; Length 1894;

larity 100.0%; Pred. NO. 64;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22

|||||

ATTAAAA 1060

March 30, 2004, 15:05:55

3

GenCore version 5.1.6
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in search, using sw model

rch 30, 2004, 14:58:06 ; Search time 45 Seconds
(without alignments)
3772.195 Million cell updates/sec

-09-976-740-43

8

YAGPPALPPETAAATAA.....HIKVLQGHFDDDDPDGFLG 538

IGO

pop 60.0 , Gapext 60.0

17041 seqs, 315518202 residues

ts satisfying chosen parameters: 1017041

3th: 0

3th: 2000000000

isting first 150 summaries

PTREMBL 25:*

sp_arChaea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mhc:*

sp_organelle:*

sp_phase:*

: sp_plant:*

: sp_rodent:*

: sp_virus:*

: sp_vertebrate:*

: sp_unclassified:*

: sp_rvirus:*

: sp_bacteriap:*

: sp_arChaeap:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ad by analysis of the total score distribution.

SUMMARIES

ary	ch	Length	DB	ID	Description
1.1	239	4	Q96IM4		Q96IM4 homo sapien
2.2	361	5	Q9VBI3		Q9VBI3 drosophila
2.2	1928	5	Q8T9H1		Q8T9H1 drosophila
1.2	2280	5	Q9V8E6		Q9V8E6 drosophila
2.2	2302	5	Q9N693		Q9N693 drosophila
2.2	2310	5	Q9GRA9		Q9GRA9 drosophila
2.0	129	4	Q43180		Q43180 homo sapien
2.0	309	10	Q7XNY2		Q7XNY2 oryza sativ
2.0	317	12	Q64812		Q64812 autographa
2.0	422	10	Q8LP98		Q8LP98 oryza sativ
2.0	438	5	Q8WSL0		Q8WSL0 plasmodium
2.0	442	5	Q8WSL3		Q8WSL3 plasmodium
2.0	445	12	Q98174		Q98174 molluscum c
2.0	464	5	Q8WSL4		Q8WSL4 plasmodium
2.0	468	16	Q9LOP9		Q9LOP9 streptomyce
2.0	556	4	Q15411		Q15411 homo sapien

Q9R101 spe
Q8B916 rac
Q961K7 homc
Q96191 homc
Q9VTD0 dros
Q8RZ96 ory
Q8W2X4 ory
Q9AYL5 ory
Q7XBY6 ory
Q52494 rals
Q8XTH8 ral
Q7X9M6 zea
Q7WEQ2 bor
Q8BHG7 mus
Q7W3D2 bor
Q8PFD1 xar
Q8RZ96 ory
Q8Fdg3 esc
Q8PAJ7 xar
Q9HH51 meth
Q7WDB0 bor
Q65215 zea
Q8ML75 dros
Q86XT7 homc
Q7XRW4 ory
Q9FGF3 ara
Q9LWQ9 ory
Q89392 par
Q8S7N6 ory
Q9LWJ7 ory
Q8H616 zea
Q7UBI5 shi
Q8XAN5 esc
Q8341 shi
Q96151 plas
Q8DC21 vib
Q9VNR3 dros
Q9U0N1 plas
Q8LTK1 ory
Q8HXV1 oryc
Q9AB02 cau
Q9VCS3 dros
Q96210 dros
Q8LIF6 ory
Q8BK12 mus
Q9P4C6 pich
P97496 mus
Q9VY88 dros
Q02434 dros
Q28224 cerc
Q961R2 dros
Q9ESU6 mus
Q8VH18 mus
Q74297 neur
Q9BHL1 caen
Q8IAK3 plas
Q8NMS0 cor
Q9BMP6 culi
Q9SMS7 ara
Q7XNS7 ory
Q8LN81 ory
Q8L874 ara
Q9NAM5 ara
Q8LCW9 ara
Q8LEQ0 ara
Q9FIK9 ara
Q852J2 ory
Q9IA73 par
Q94190 atr
Q92KS8 rhi
Q9H4X1 homo
Q96AT3 homo

1.7 148 5 Q81P66
 1.7 149 11 Q9D7P2
 1.7 151 10 Q814D4
 1.7 153 16 Q88QD5
 1.7 154 10 Q8RZ52
 1.7 155 10 Q8H056
 1.7 168 12 Q9DHL7
 1.7 172 10 Q93815
 1.7 173 4 Q8N8T8
 1.7 173 10 Q92Q24
 1.7 185 10 Q92WF4
 1.7 187 5 Q9GRZ0
 1.7 194 4 Q96B02
 1.7 198 10 Q8H083
 1.7 214 10 Q9LWV3
 1.7 214 10 Q8H645
 1.7 217 10 P93426
 1.7 217 10 Q9M4Y5
 1.7 217 10 Q84545
 1.7 218 13 Q90764
 1.7 219 13 Q90575
 1.7 231 2 Q85939
 1.7 235 6 Q81008
 1.7 239 10 Q9AX02
 1.7 239 16 Q7WQEO
 1.7 241 16 Q7WCD5
 1.7 248 5 Q9VET8
 1.7 248 16 Q8XSS5
 1.7 252 10 Q8LHK1
 1.7 262 16 Q89LR9
 1.7 273 16 Q9A8M0
 1.7 274 5 Q9VDM8
 1.7 276 10 Q9SNS1
 1.7 278 10 Q8S1P7
 1.7 278 12 Q83418
 1.7 279 4 Q15415
 1.7 280 5 Q86NQ6
 1.7 281 10 Q9XE15
 1.7 282 10 Q8LFF27
 1.7 283 2 Q9RBF9
 1.7 283 5 Q81QD9
 1.7 287 5 Q814H9
 1.7 306 4 Q9B0P6
 1.7 308 2 Q93QT0
 1.7 309 2 Q93QT1
 1.7 316 5 Q9GRZ1
 1.7 316 5 Q9NHP0
 1.7 316 10 Q9LD92
 1.7 316 10 Q9AYL3
 1.7 316 10 Q7XBY4
 1.7 317 10 Q9M5M5
 1.7 320 10 Q7XM58
 1.7 320 5 Q95S20
 1.7 322 5 Q961E6
 1.7 325 4 Q86TG7
 1.7 325 10 Q7XPH4
 1.7 328 5 Q871D4
 1.7 328 5 Q86GY9
 1.7 333 4 Q86WB8
 1.7 333 10 Q84J51
 1.7 333 11 Q8C4L5

ALIGNMENTS

PRELIMINARY; PRT; 239 AA.

(TrEMBLrel. 19, Created)
 (TrEMBLrel. 19, Last sequence update)
 (TrEMBLrel. 23, Last annotation update)

Q81P66 drosophila
 Q9D7P2 mus musculus
 Q814D4 oryza sativ
 Q88QD5 pseudomonas
 Q8RZ52 oryza sativ
 Q8H056 oryza sativ
 Q9DHL7 yaba-like d
 Q93815 arabidopsis
 Q8N8T8 homo sapien
 Q92Q24 arabidopsis
 Q92WF4 oryza sativ
 Q9GRZ0 caenorhabdi
 Q96B02 homo sapien
 Q8H083 oryza sativ
 Q9LWV3 oryza sativ
 Q8H645 oryza sativ
 P93426 oryza sativ
 Q9M4Y5 oryza sativ
 Q84545 oryza sativ
 Q90764 gallus gall
 Q90575 gallus gall
 Q85939 sphingomona
 Q81008 felis silve
 Q9AX02 oryza sativ
 Q7WQEO bordetella
 Q7WCD5 bordetella
 Q9VET8 drosophila
 Q8XSS5 ralstonia s
 Q8LHK1 oryza sativ
 Q89LR9 bradyrhizob
 Q9A8M0 caulobacter
 Q9VDM8 drosophila
 Q9SNS1 oryza sativ
 Q8S1P7 oryza sativ
 Q83418 pseudorabie
 Q15415 homo sapien
 Q86NQ6 drosophila
 Q9XE15 oryza sativ
 Q8LFF27 arabidopsis
 Q9RBF9 alcaligenes
 Q81QD9 drosophila
 Q814H9 caenorhabdi
 Q9B0P6 homo sapien
 Q93QT0 mycobacteri
 Q93QT1 mycobacteri
 Q9GRZ1 caenorhabdi
 Q9NHP0 sarcophaga
 Q9LD92 oryza sativ
 Q9AYL3 oryza sativ
 Q7XBY4 oryza sativ
 Q9M5M5 euphorbia e
 Q7XM58 oryza sativ
 Q95S20 drosophila
 Q961E6 drosophila
 Q86TG7 homo sapien
 Q7XPH4 oryza sativ
 Q871D4 neurospora
 Q86GY9 rhizopcehal
 Q86WB8 homo sapien
 Q84J51 oryza sativ
 Q8C4L5 mus musculus

DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 R1 SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007384; AA07384.1; -.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00536; SAM; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00405; SAM_DOMAIN; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 239 AA; 25652 MW; 89A4CFD8760AFA0A CRC64;
 Query Match 44.1%; Score 237; DB 4; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.9e-201;
 Matches 237; Conservative 0; Mismatches 0; Indels 0;
 QY 302 RRCRAPPAAASAPSRKGGSERVLEKEEEDDDDEDEDEDDVSEGSVPESDRP
 DB 3 RRCRAPPAAASAPSRKGGSERVLEKEEEDDDDEDEDEDDVSEGSVPESDRP
 QY 362 HOLNBERGQSAKERVKEWTCGPHQGQDEGRGAPGSGTQVFSMAANKSGGT
 DB 63 HOLNBERGQSAKERVKEWTCGPHQGQDEGRGAPGSGTQVFSMAANKSGGT
 QY 422 GPDSPSPVLPKPKALPGADGTPGCPGRKEKPSDPVETVMDVVEYFTFAGF
 DB 123 GPDSPSPVLPKPKALPGADGTPGCPGRKEKPSDPVETVMDVVEYFTFAGF
 QY 482 AFQOEIDKSLLMORTDLVLTGLSIRLPALKIYEHHLKVLQOQHFDDEDDPGE
 DB 183 AFQOEIDKSLLMORTDLVLTGLSIRLPALKIYEHHLKVLQOQHFDDEDDPGE
 RESULT 2
 Q9VE13 PRELIMINARY; PRT; 361 AA.
 ID Q9VE13 Q95UT1;
 AC Q9VE13; Q95UT1;
 DT 01-MAY-2000 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG1057 protein (Microtubule-associated tau protein) (RE16764p).
 GN TAU OR CG5606 OR CG12881 OR CG31057.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 R1 SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.I.
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischma

rielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 G F., Gorrill J.H., Gu Z., Guan P., Harris M.,
 arvey D., Heiman T.J., Hernandez J.R., Houck J.,
 ston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 ush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 odira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
 B., McIntosh T.C., McLeod M.P., McPherson D.,
 alshina N.V., Mobarry C., Morris J., Moshrefi A.,
 y M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 elson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Pittman K.S., Pan S., Pollard J., Puri V., Reese M.G.,
 mington K., Saunders R.D.C., Scheeler F., Shen H.,
 en-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 dling A.C., Stapleton M., Strong R., Sun E.,
 ector C., Turner R., Venter E., Wang A.H., Wang X.,
 ssarman D.A., Weinstein G.M., Weissenbach J.,
 Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 ong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 ers E.W., Rubin G.M., Venter J.C.;
 quence of *Drosophila melanogaster*.";
 85-2195(2000).

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Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 cayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
 H., Baldwin D., Banzon J., Beeson K.Y., Busan D.A.,
 Center A., Champe M., Davenport L.B., Dietz S.M.,
 sett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 rise E., Galle R.F., Garg N.S., George R.A.,
 ouch J., Hoskins R.A., Hostin D., Howland T.J.,
 lali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 agas V., Park S., Patel S., Pfeiffer B.,
 S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 Strong R., Svirskas R., Tector C., Tyler D.,
 Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Drosophila melanogaster genome.";
 -2000) to the EMBL/GenBank/DBJ databases.

N.A.

by M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 uang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 gman C., Berman B., Carlson J.W., Celniker S.E.,
 dale R., Emmert D., Frise E., de Grey A., Harris N.,
 Marshall B., Millburn G., Richter J., Russo S.,
 Smith E., Shu S., Smutniak F., Whitfield E.,
 Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Drosophila melanogaster genome.";
 -2000) to the EMBL/GenBank/DBJ databases.

N.A.

lniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 -2000) to the EMBL/GenBank/DBJ databases.

N.A.

-2002) to the EMBL/GenBank/DBJ databases.

N.A.

84; PubMed11578871;
 rtini M.E.;
 n and characterization of the *Drosophila* tau homolog.";
 :171-178(2001).

N.A.

y;
 Brokstein P., Hong L., Agbayani A., Carlson J.,
 vez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 azale C., Guarin H., Kronmiller B., Li P., Liao G.,
 ngall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 ananavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR003761; AAF56732.2; -;
 DR EMBL; AY032977; AAK54556.1; -;
 DR EMBL; AY102697; ARM27526.1; -;
 DR FlyBase; FBgn0051057; tau.
 DR GO; GO:0007017; P: microtubule-based process; IEA.
 DR InterPro; IPR001084; Tubulin Tau.
 DR Pfam; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU MAP; 3.
 SQ SEQUENCE 361 AA; 38538 MW; B3DC50701DCF968A CRC64;

Query Match 2.2%; Score 12; DB 5; Length 361;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gc

QY 217 PPAPPOQQPPPP 228

Db 43 PPAPPOQQPPPP 54

RESULT 3

Q8T9H1

ID Q8T9H1 PRELIMINARY; PRT; 1928 AA.

AC Q8T9H1;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE SD01229p.

GN SBB OR CG5580.

OS *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]_TaxID=7227;

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY069769; AAL39914.1; -;

DR FlyBase; FBgn0010575; sbb.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:0007411; P:axon guidance; IMP.

DR GO; GO:0007412; P:axon target recognition; IMP.

DR GO; GO:0008346; P:larval walking behavior; IMP.

DR InterPro; IPR007087; Pfantne S.

DR Pfam; PF00096; zf-C2H2; 1.

DR SMART; SM00355; Znf C2H2; 1.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 1928 AA; 193764 MW; 7EE7D606C0D59C9B CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gc

QY 221 PQQQQPPPPPPQ 232

Db 1432 PQQQQPPPPPPQ 1443

RESULT 4

Q9V8E6

ID Q9V8E6 PRELIMINARY; PRT; 2280 AA.

AC Q9V8E6;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

(Tremblrel. 13, Last sequence update)
(Tremblrel. 25, Last annotation update)
in.

0.

elanogaster (Fruit fly).

etazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

pterygota; Diptera; Brachycera; Muscomorpha;

Drosophilidae; Drosophila.

227;

M N.A.

6006; PubMed=107311132;

Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

-G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

yle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Bencos P.V., Bernan B.P., Bhandari D., Bolshakov S.,

Botchan M.R., Bouck J., Brokstein P., Brattier P.,

Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cawley S., Dahlke C., Davenport L.B., Davies P.,

Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

oup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Evangelista C.C., Ferraz C., Ferrier A.S., Fleischmann W.,

abrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

uston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

i Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

ai B., McIntosh T.C., McLeod M.P., McPherson D.,

Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

oy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Remington K., Saunders R.D.C., Scheeler F., Shen H.,

iden-Klamos I., Simpson M., Skupski M.P., Smith T.,

radling A.C., Stapleton M., Strong R., Sun E.,

Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wassman D.A., Weinstock G.M., Weissbach J.,

Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

Myers E.W., Rubin G.M., Venter J.C.;

sequence of Drosophila melanogaster.";

2185-2195(2000).

00; AAF57721.1; -.

10010575; sbb.

34; C:nucleus; IDA.

11; P:axon guidance; IMP.

12; P:axon target recognition; IMP.

16; P:larval walking behavior; IMP.

R006162; Ppantne S.

R007087; Znf_C2H2.

5; zf-C2H2; 1.

55; Znf_C2H2; 1.

0012; PHOSPHOPANTHETINE; 1.

0028; ZINC_FINGER_C2H2_1; 1.

0157; ZINC_FINGER_C2H2_2; 1.

3; Zinc; Zinc-finger.

280 AA; 228107 MW; 1C2CDA27DC77B00B CRC64;

2.2%; Score 12; DB 5; Length 2280;

larity 100.0%; Pred. No. 0.28;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPPQPO 232

|||||

Db

1784 PQQQPPPPQPO 1795

RESULT 5

Q9N693

ID

Q9N693

AC

Q9N693

DT

01-OCT-2000

(Tremblrel. 15, Created)

DT

01-OCT-2000

(Tremblrel. 15, Last sequence update)

DT

01-OCT-2003

(Tremblrel. 25, Last annotation update)

DE

Brakeless-B (Scribbler long isoform).

GN

SBB OR BKS OR CG5580.

OS

Drosophila melanogaster (Fruit fly).

OC

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC

Ephidrotidae; Drosophilidae; Drosophila.

OX

NCBI_TaxID=7227;

RN

[1]

SEQUENCE FROM N.A.

RP

MEDLINE=20265906; PubMed=10804172;

RX

Senti K., Keleman K., Eisenhaber F., Dickson B.J.;

RA

"Brakeless" is required for lamina targeting of R1-R6 axons in th

RT

drosophila visual system.";

RL

Development 127:2291-2301(2000).

[2]

SEQUENCE FROM N.A.

RP

MEDLINE=20341319; PubMed=10880478;

RX

Yang P., Shaver S.A., Hilliker A.J., Sokolowski M.B.;

RA

"Abnormal turning behavior in Drosophila larvae: identification

RT

molecular analysis of scribbler (sbb).";

RL

Genetics 155:1161-1174(2000).

DR

EMBL; AF242194; AAF70256.1; -.

DR

EMBL; AF247562; AAF70256.1; -.

DR

FLYBase; FBgn0010575; sbb.

DR

GO; GO:0005634; C:nucleus; IDA.

DR

GO; GO:0007411; P:axon guidance; IMP.

DR

GO; GO:0007412; P:axon target recognition; IMP.

DR

GO; GO:0008346; P:larval walking behavior; IMP.

DR

InterPro; IPR0007087; Znf_C2H2.

DR

Pfam; PF00096; zf-C2H2; 1.

DR

SMART; SM00355; Znf_C2H2; 1.

DR

PROSITE; PS00012; PHOSPHOPANTHETINE; 1.

DR

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

DR

PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.

KW

Metal-binding; Zinc; Zinc-finger.

SQ

SEQUENCE 2302 AA; B35F759AE2C21729 CRC64;

Query Match 2.2%; Score 12; DB 5; Length 2302;

Best Local Similarity 100.0%; Pred. No. 0.28;

Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY

221 PQQQPPPPQPO 232

|||||

Db

1806 PQQQPPPPQPO 1817

|||||

RESULT 6

Q9GRA9

ID

Q9GRA9

AC

Q9GRA9

DT

01-MAR-2001

(Tremblrel. 16, Created)

DT

01-MAR-2001

(Tremblrel. 16, Last sequence update)

DT

01-OCT-2003

(Tremblrel. 25, Last annotation update)

DE

Master of thick veins.

GN

SBB OR MTV OR CG5580.

OS

Drosophila melanogaster (Fruit fly).

OC

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC

Ephidrotidae; Drosophilidae; Drosophila.

OX

NCBI_TaxID=7227;

RN

[1]

SEQUENCE FROM N.A.

discs;
 Minami M., Tabata T.;
 Gene that shapes the activity gradient of the Dpp
 ough regulation of thick veins.";
 N-2000) to the EMBL/GenBank/DBJ databases.
 3: BAB20792.1; -;
 0010575; sbd.
 4: C:nucleus; IDA.
 1: P:axon guidance; IMP.
 2: P:axon target recognition; IMP.
 6: P:larval walking behavior; IMP.
 006162; Ppantse.S.
 007087; Znf_C2H2.
 ; Zf-C2H2; 1.
 5: Znf_C2H2; 1.
 012; PHOSPHOPANTETHEINE; 1.
 028; ZINC_FINGER_C2H2_1; 1.
 157; ZINC_FINGER_C2H2_2; 1.
 ; Zinc; Zinc-finger.
 10 AA; 230954 MW; 3208AB65E51AEDF6 CRC64;

2.2%; Score 12; DB 5; Length 2310;
 arity 100.0%; Pred. No. 0.28;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPPQPQ 232
 |||||
 QPPPPQPQ 1825

RELIMINARY; PRT; 129 AA.

TREMBLrel. 06, Created)
 TREMBLrel. 06, Last sequence update)
 TREMBLrel. 22, Last annotation update)
 ar ataxia 7 (Fragment).

(Human).
 tazia; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Primates; Catarrhini; Hominidae; Homo.
 06;

N.A.
 nzw K.A., Bird T.D., Moseley M.L., Panum L.P.W.;
 9 of expanded trinucleotide repeat sequences.";
 0-0(1997).
 6; AAB87863.1; -;
 29 129
 9 AA; 14076 MW; B42FCB5972A34B3B CRC64;

2.0%; Score 11; DB 4; Length 129;
 arity 100.0%; Pred. No. 0.19;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

PPPPQPQ 232
 |||||
 PPPPQPQ 44

RELIMINARY; PRT; 309 AA.

TREMBLrel. 25, Created)
 TREMBLrel. 25, Last sequence update)
 TREMBLrel. 25, Last annotation update)
 .9 protein.
 (Rice).
 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
 RA Liu Y.B., Mu J., Yu Z., Chen L., Fan D.D., Weng Q.J., Zhang L.,
 RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li
 RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.
 RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
 RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin
 RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
 RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
 RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL662996; CAE03881.1; -;
 SQ SEQUENCE 309 AA; 32281 MW; C532040DE1D47768 CRC64;

Query Match 2.0%; Score 11; DB 10; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; C

Qy 133 PPPPPAPVAAA 143
 |||||
 Db 104 PPPPPAPVAAA 114

RESULT 9

Q64812
 ID Q64812 PRELIMINARY; PRT; 317 AA.
 AC Q64812;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Autographa californica nuclear polyhedrosis virus ORF2.
 OS Autographa californica nuclear polyhedrosis virus (ACMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolydnavirus.
 OX NCBI_TaxID=46015;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1.2;
 RX MEDLINE=95137388; PubMed=7835700;
 RA Oshresser M., Morin N., Cerutti M., Delsert C.;
 RT "Sequence analysis and transcriptional mapping of the orF-z gene
 RT Autographa californica nuclear polyhedrosis virus.";
 RL Gene 152:201-204(1995).
 DR EMBL; X78446; CAA55206.1; -;
 SQ SEQUENCE 317 AA; 36304 MW; 7C6DD5342355DE5A CRC64;

Query Match 2.0%; Score 11; DB 12; Length 317;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; C

Qy 212 PPPPPAPVAAA 222
 |||||
 Db 108 PPPPPAPVAAA 118

RESULT 10

Q8LP98
 ID Q8LP98 PRELIMINARY; PRT; 422 AA.
 AC Q8LP98;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Transcription factor PCF3 (Fragment).
 GN PCF3.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]

```

M N.A.
Ipponbare;
6562; PubMed=1200681;
hashi Y.;
and dimerization specificity and potential targets for
ein family.";
337-348(2002).
04; BAB92951.1; -.
P98; -.
R005333; TCP.
4; TCP; 1.
22 AA; 42877 MW; 2689E5553D5789E CRC64;
larity 100.0%; DB 10; Length 422;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAAPPPT 130
|||||
AAAAAPPPT 302

PRELIMINARY; PRT; 438 AA.
(TREMBLrel. 20, Created)
(TREMBLrel. 20, Last sequence update)
(TREMBLrel. 24, Last annotation update)
oite protein (Fragment).
inckei.
lveolata; Apicomplexa; Haemosporida; Plasmodium.
860;

M N.A.
Costa F., Letourner F., Walliker D., Landau I., Renia L.;
n the circumsporozoite protein genes of Plasmodium vinckei
;
UL-1999) to the EMBL/GenBank/DBJ databases.
04; AAL36457.1; -.
93; F:defense/immunity protein activity; IEA.
R003067; Crmsprzoite.
R000884; TSPI.
0; tsp 1; 1.
303; CRMSPRZOITE.
09; TSPI; 1.
0092; TSPI; 1.
438 438
38 AA; 45943 MW; 4BF9EAB97F59B9F3 CRC64;
larity 2.0%; Score 11; DB 5; Length 438;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DDEDEDEE 341
|||||
DDEDEDEE 83

PRELIMINARY; PRT; 442 AA.
(TREMBLrel. 20, Created)
(TREMBLrel. 20, Last sequence update)
(TREMBLrel. 24, Last annotation update)
oite protein.
inckei petteri.
lveolata; Apicomplexa; Haemosporida; Plasmodium.
38298;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Snounou G., Costa F., Letourner F., Walliker D., Landau I., Renia L.;
RT "Diversity in the circumsporozoite protein genes of Plasmodium
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162332; AAL36454.1; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Crmsprzoite.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00090; tsp_1; 1.
DR PRINTS; PRO1303; CRMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
SQ SEQUENCE 442 AA; 45626 MW; D7918F094AB25A0B CRC64;

Query Match 2.0%; Score 11; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 331 EEDDEDEDEE 341
|||||
DB 73 EEDDEDEDEE 83

RESULT 13
Q98174 PRELIMINARY; PRT; 445 AA.
AC Q98174; 1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE MC003L.
GN MC003L.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirir
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96325459; PubMed=8670425;
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RT "Genome sequence of a human tumorigenic poxvirus: Prediction of
RT specific host response-evasion genes.";
RL Science 273:813-816(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60315; AAC55131.1; -.
DR PIR; T30604; T30604.
SQ SEQUENCE 445 AA; 49447 MW; 2B3C59936F0058DE CRC64;

Query Match 2.0%; Score 11; DB 12; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 127 PPPTAPPPPP 137
|||||
DB 353 PPPTAPPPPP 363

RESULT 14
Q8WSL4 PRELIMINARY; PRT; 464 AA.
AC Q8WSL4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Circumsporozoite protein.
GN CS.

```

nckei lentum.
veolata; Apicomplexa; Haemosporida; Plasmodium.
8297;

N.A.
osta F., Letourneur F., Walliker D., Landau I., Renia I.,
the circumsporozoite protein genes of Plasmodium vinckei

N-1999) to the EMBL/GenBank/DBJ databases.

1; AAL36453.1; -.

3; F:defense/immunity protein activity; IEA.

003067; Crcmsprzoite.

000884; TSPL.

1; TSP.1; 1.

03; Crcmsprzoite.

9; TSPL; 1.

092; TSPL; 1.

4 AA; 48476 MW; 8AA595D8D6E97CF0 CRC64;

2.0%; Score 11; DB 5; Length 464;
arity 100.0%; Pred. No. 0.55;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDEDEE 341

|||||||

DEDEDEE 83

RELIMINARY; PRT; 468 AA.

TREMBLrel. 15, Created)

TREMBLrel. 15, Last sequence update)

TREMBLrel. 25, Last annotation update)

rane protein.

D8A.15C.

coelicol.

inobacteria; Actinobacteridae; Actinomycetales;

ae; Streptomycetaceae; Streptomycetes.

02;

N.A.

/ M145;

410; PubMed=12000953;

Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,

James K.D., Harris D.E., Quail M.A., Kieser H.,

teman A., Brown S., Chandra G., Chen C.W., Collins M.,

aser A., Goble A., Hidalgo J., Horneby T., Howarth S.,

Kieser T., Lark L., Murphy L., Oliver K., O'Neil S.,

E., Rajandream M.A., Rutherford K., Rutter S.,

nders D., Sharp S., Squares R., Squares S., Taylor K.,

tzorrek A., Woodward J., Barrell B.G., Parkhill J.,

ome sequence of the model actinomycete Streptomycetes

(2);

1-147(2002).

1; CAB7336.1; -.

08979; Gal_bind_like.

ome.

3 AA; 48544 MW; COF0487AA341CAC0 CRC64;

2.0%; Score 11; DB 16; Length 468;

arity 100.0%; Pred. No. 0.56;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPVAP 192

|||||||

APPVAP 195

ID O15411 PRELIMINARY; PRT; 556 AA.
AC O15411;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CAGH32 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369492; PubMed=9225980;
RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.,
RT "cDNAs with long CAG trinucleotide repeats from human brain."
RL Hum. Genet. 100:114-122(1997).
DR EMBL; U0743; AAB91441.1; -.
FT NON TER 1
SQ SEQUENCE 556 AA; 57588 MW; AAAF9DFEF77EE9E CRC64;

Query Match 2.0%; Score 11; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 225 QPPPPQPPPP 235

|||||||

Db 80 QPPPPQPPPP 90

RESULT 17

Q9R101

ID Q9R101 PRELIMINARY; PRT; 763 AA.

AC Q9R101;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hormone-sensitive lipase.

GN HSL.

OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;

OC Sperophilus.

OX NCBI_TaxID=43179;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=White adipose tissue;

RA Bauer V.W., Andrews M.T.;

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF177401; AAD51122.1; -.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002168; Lipolytic enzyme.

DR InterPro; IPR000379; Ser_estr.

DR PROSITE; PS01173; LIPASE GDHG HIS; 1.

DR PROSITE; PS01174; LIPASE GDHG SER; 1.

SQ SEQUENCE 763 AA; 83125 MW; E5516B02EFB8BE4D CRC64;

Query Match 2.0%; Score 11; DB 11; Length 763;

Best Local Similarity 100.0%; Pred. No. 0.84;

Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 119 PAAAAAAPP 129

|||||||

Db 752 PAAAAAAPP 762

RESULT 18

Q8B916

ID Q8B916 PRELIMINARY; PRT; 810 AA.

AC Q8B916;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
protein.
ou multiple nucleopolyhedrovirus.
na viruses, no RNA stage; Baculoviridae;
dovirus.
0366;

M N.A.

, Harrison R.L.;
usia ou multiple nucleopolyhedrovirus genome sequence."
UG-2002) to the EMBL/GenBank/DBJ databases.
71; AAN28017.1; -.

protein.
10 AA; 94066 MW; 717CDBD04EC226FE CRC64;

2.0%; Score 11; DB 12; Length 810;
larity 100.0%; Pred.No. 0.89; Indels 0; Gaps 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PQPAPQP 222

|||||

PQPAPQP 120

PRELIMINARY; PRT; 1157 AA.

(TrEMBLrel. 19, Created)

(TrEMBLrel. 19, Last sequence update)

(TrEMBLrel. 25, Last annotation update)

protein KIAA1818 (Fragment).

(Human).

etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
606;

M N.A.

5130; PubMed=11347906;

akayama M., Nakajima D., Kikuno R., Ohara O.;

of the coding sequences of unidentified human genes. XX.

sequences of 100 new cDNA clones from brain which code

teins in vitro."

5-95(2001).

21; BAB47447.1; -.

34; C:nucleus; IEA.

77; F:DNA binding; IEA.

2001005; Myb_DNA_binding.

17; SANT; 1.

0090; MYB_3; 1.

protein.

1

L57 AA; 125525 MW; B08A6AE50B1A9E01 CRC64;

2.0%; Score 11; DB 4; Length 1157;

larity 100.0%; Pred.No. 1.2;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PQPAPQP 235

|||||

PQPAPQP 549

PRELIMINARY; PRT; 3124 AA.

(TrEMBLrel. 19, Created)

(TrEMBLrel. 19, Last sequence update)

(TrEMBLrel. 25, Last annotation update)

P400 SW12/SNF2-related protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21400441; PubMed=11509179;

RA Fuchs M., Gerber J., Drapkin R., Sif S., Ikura T., Ogryzko V.,

Lane W.S., Nakatani Y., Livingston D.M.;

RT "The p400 complex is an essential E1A transformation target."

RL Cell 106:297-307(2001).

DR EMBL; AY044869; AAK97789.1; -.

DR Genbank; HGNC:11958; EP400.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001650; Helicase_C.

DR InterPro; IPR006562; HSA.

DR InterPro; IPR001005; Myb_DNA_binding.

DR InterPro; IPR000330; SNF2_N.

DR Pfam; PF00271; helicase_C; 1.

DR Pfam; PF00176; SNF2_N; 2.

DR SMART; SM00487; DEXDc; 1.

DR SMART; SM00573; HSA; 1.

DR SMART; SM00717; SANT; 1.

DR PROSITE; PS50090; MYB_3; 1.

DR ATP-binding; Helicase; Hydrolase.

SK SEQUENCE 3124 AA; 340146 MW; B8F57FD6C7BD01E9 CRC64;

Query Match 2.0%; Score 11; DB 4; Length 3124;

Best Local Similarity 100.0%; Pred.No. 2.8;

Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 225 QPPPPQPQPPP 235

|||||

Db 2506 QPPPPQPQPPP 2516

RESULT 21

Q9VTD0

ID Q9VTD0 PRELIMINARY; PRT; 96 AA.

AC Q9VTD0;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE CG14148 protein.

DE CG14148.

GN CG14148.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.I

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B

RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.I

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Fabrics B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W., Brielan A.E., Garg N.S., Gelbart W.M., Glasser K., ng F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Helman T.J., Hernandez J.R., Houck J., ueston K.A., Howland T.J., Wei M.-H., Ibegwan C., lueh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., i B., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., i B., McIntosh T.C., McLeod M.P., McPherson D., yllshina N.V., Mobarry C., Morris J., Moshrefi A., y M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., emington K., Saunders R.D.C., Scheeler F., Shen H., den-Kiamos I., Simpson M., Skupski M.P., Smith T., adling A.C., Stapleton M., Strong R., Sun E., tector C., Turner R., Venter E., Wang A.H., Wang X., asarman D.A., Weinstein G.M., Weissbach J., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., hong F.N., Zhong W., Zhou X., Zhao Q., Zheng L., yers E.W., Rubin G.M., Venter J.C.; equence of *Drosophila melanogaster*; 185-2195(2000). 5; AAF50122.1; 3040821; CG14148. AA; 10884 MW; A17E2752CE1DCA7D CRC64; 1.9%; Score 10; DB 5; Length 96; arity 100.0%; Pred. No. 1.1; nservative 0; Mismatches 0; Indels 0; Gaps 0; AAPP 129 ||||| AAPP 32 RELIMINARY; PRT; 166 AA. TrEMBLrel. 21, Created) TrEMBLrel. 21, Last sequence update) TrEMBLrel. 25, Last annotation update) .2 protein. .2. (japonica cultivar-group). cidiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryzae; Oryza. 347; N.A. onbare; sumoto T., Yamamoto K.; nipponbare(GA3) Genomic DNA, chromosome 1, BAC 63G05." V-2001) to the EMBL/GenBank/DBJ databases.); BAB90493.1; -. 36; -. ; F:DNA binding; IEA. ; P:regulation of transcription, DNA-dependent; IEA. 300910; HMG_12_box. ; HMG_box; 1. 3; HMG; 1. 118; HMG_BOX.2; 1. 5 AA; 18791 MW; 3D4E911025FEAFCA CRC64; 1.9%; Score 10; DB 10; Length 166; arity 100.0%; Pred. No. 1.8; nservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 PPPPQQPPPP 235
| | | | |
Db 74 PPPPQQPPPP 83
|| | | | |
RESULT 23
Q8W2X4 PRELIMINARY; PRT; 172 AA.
AC Q8W2X4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNB0060105.14 OR OSJNB0040D23.6.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=O.sativa; STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Teitlin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbus Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0060105 genomic sequence." Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitirini T., Krol M.I., Jarrabi B.B., Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Sun B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C. "Oryza sativa chromosome 10 BAC OSJNB0040D23 genomic sequence." Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL [3]
RN SEQUENCE FROM N.A.
RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice chromosome 10." Science 300:1566-1569(2003).
RL [4]
RN SEQUENCE FROM N.A.
RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092697; AAL58119.1; -
DR EMBL; AC074196; AAM76345.1; -
DR EMBL; AE017115; AAF54812.1; -
DR Gramene; Q8W2X4; -
DR GO; GO:0004185; F:serine carboxypeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001563; Peptidase_S10
DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
KW Hypothetical protein.
SQ SEQUENCE 172 AA; 17950 MW; 049DF2321C0E4D12 CRC64;
Query Match 1.9%; Score 10; DB 10; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G.

Qy 13 AAAATTAATAA 22
| | | | |
Db 12 AAAATTAATAA 21
|| | | | |
RESULT 24


```

PRELIMINARY;          PRT;    212 AA.
(TREMBLrel. 17, Created)
(TREMBLrel. 17, Last sequence update)
(TREMBLrel. 25, Last annotation update)
Protein.
3.2.
Iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
3; Oryzae; Oryza.
530;

4 N.A.
ipponbare;
Juan O., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
Pai G., Bowman C.L., Fujii C.V., VanAken S.E.,
Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
J., White O., Salzberg S.L., Fraser C.M.;
a chromosome 10 BAC OSUNBA0003019 genomic sequence.;
3B-2001) to the EMBL/GenBank/DBJ databases.
55; AAK00445.1; -.
YL5; -.
Protein.
12 AA; 23084 MW; BBAID03553465083 CRC64;

    1.9%; Score 10; DB 10; Length 212;
    Identity 100.0%; Pred. No. 2.2;
    Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAPPP 129
|||||
AAAAPPP 205

PRELIMINARY;          PRT;    212 AA.
(TREMBLrel. 25, Created)
(TREMBLrel. 25, Last sequence update)
(TREMBLrel. 25, Last annotation update)
Protein.
3.2.
(Japonica cultivar-group).
Iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
3; Oryzae; Oryza.
9947;

4 N.A.
ipponbare;
Genome 10 Sequencing Consortium;
sw of structure, activity, and evolution of rice
0.;
1566-1569(2003).

4 N.A.
ipponbare;
Wing R.A., McCombie W.R., Messing J., Yuan Q.;
AY-2003) to the EMBL/GenBank/DBJ databases.
21; AAP55122.1; -.
Protein.
12 AA; 23084 MW; BBAID03553465083 CRC64;

    1.9%; Score 10; DB 10; Length 212;
    Identity 100.0%; Pred. No. 2.2;
    Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAPPP 129
|||||
AAAAPPP 205

PRELIMINARY;          PRT;    301 AA.
(TREMBLrel. 01, Created)
(TREMBLrel. 01, Last sequence update)
(TREMBLrel. 24, Last annotation update)
HrpF protein.
GN HRPF.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
NCBI_TaxID=305;
[1]
RN RP SEQUENCE FROM N.A.
STRAIN=GM11000;
RC MEDLINE=20253307; PubMed=10792715;
RX Gueneron M., Timmers A.C.J., Boucher C., Arlat M.;
"Two novel proteins, PopB, which has functional nuclear localiza
RT signals, and PopC, which has a large leucine-rich repeat domain,
RT secreted through the Hrp-secretion apparatus of Ralstonia
RT solanacearum."
RL Mol. Microbiol. 36:261-277(2000).
RN [2]
RN RP SEQUENCE FROM N.A.
STRAIN=GM11000;
RC MEDLINE=95349395; PubMed=7623665;
RX Van Gijsegem F., Gough C.L., Zischek C., Genin S., Niqueux E.,
Arlat M., Barberis P., German S., Castello P., Boucher C.A.;
"The hrp gene locus of Pseudomonas solanacearum which controls a
RT III secretion system, encodes eight proteins related to component
RT the flagellar biogenesis complex."
RL Mol. Microbiol. 15:1095-1114(1995).
RN [3]
RN RP SEQUENCE FROM N.A.
STRAIN=GM11000;
RC MEDLINE=93125128; PubMed=1479894;
RX Genin S., Gough C.L., Zischek C., Boucher C.A.;
"Evidence that the hrpB gene encodes a positive regulator of
RT pathogenicity genes from Pseudomonas solanacearum."
RL Mol. Microbiol. 6:3065-3076(1992).
RN [4]
RN RP SEQUENCE FROM N.A.
STRAIN=GM11000;
RC MEDLINE=93113006; PubMed=1472716;
RX Gough C.L., Genin S., Zischek C., Boucher C.A.;
"hrp genes of Pseudomonas solanacearum are homologous to pathoge
RT determinants of animal pathogenic bacteria and are conserved amon
RT plant pathogenic bacteria."
RL Mol. Plant Microbe Interact. 5:384-389(1992).
RN [5]
RN RP SEQUENCE FROM N.A.
STRAIN=GM11000;
RC MEDLINE=93302711; PubMed=8316211;
RX Gough C.L., Genin S., Lopes V., Boucher C.A.;
"Homology between the HrpO protein of Pseudomonas solanacearum a
RT bacterial proteins implicated in a signal peptide-independent sec
RT mechanism."
RL Mol. Gen. Genet. 239:378-392(1993).
RN [6]
RN RP SEQUENCE FROM N.A.
STRAIN=GM11000;
RC MEDLINE=96347139; PubMed=8736546;
RX Bogdanove A.J., Beer S.V., Bonas U., Boucher C.A., Collmer A.,
Coplin D.L., Cornelis G.R., Huang H.C., Hutcheson S.W.,
Panopoulos N.J., Van Gijsegem F.;
"Unified nomenclature for broadly conserved hrp genes of
RT phytopathogenic bacteria."
RL Mol. Microbiol. 20:681-683(1996).
RN [7]
RN RP SEQUENCE FROM N.A.

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> ;
> 01; PubMed=8313899;
> Gijsegem F., Huet J., Pernollet J., Boucher C.A.;
> ein which induces a hypersensitivity-like response on
> ia genotypes, is secreted via the Hrp pathway of
> anacearum.";
> 3-553(1994)).
> N.A.
> ;
> 349; PubMed=8190064;
> cher C.A.;
> / of proteins involved in different secretion pathways in
> bacteria: modular structure and specificity of N-terminal
> st. 243:112-118(1994)).
> 1; CAB58256.1; -.
> 362087.
> 1 AA; 32331 MW; F3DA387F2CF95464 CRC64;
> 1.9%; Score 10; DB 2; Length 301;
> arity 100.0%; Pred.No. 2.9;
> onservative 0; Mismatches 0; Indels 0; Gaps 0;
> EDEDD 343
> |||||
> EDEDD 300
>
> RELIMINARY; PRT; 301 AA.
> TrEMBLrel. 20, Created)
> TrEMBLrel. 20, Last sequence update)
> TrEMBLrel. 24, Last annotation update)
>
> 69 OR RS01640.
> anacearum (Pseudomonas solanacearum).
> laamid.
> teobacteria; Betaproteobacteria; Burkholderiales;
> eae; Ralstonia.
> 5;
> N.A.
> 379; PubMed=11823852;
> , Genin S., Artiguenave F., Gouzy J., Mangenot S.,
> lault A., Brottier P., Camus J.C., Cattolico L.,
> Choisine N., Claudel-Renard C., Cunnac S., Demange N.,
> vie M., Moisan A., Robert C., Saurin W., Schiex T.,
> ebault P., Whalen M., Wincker P., Levy M.,
> ., Boucher C.A.;
> ace of the plant pathogen Ralstonia solanacearum.";
> 7-502(2002)).
> 1; CAD18020.1; -.
> 1; C:extrachromosomal DNA; IEA.
> lete proteome.
> 1 AA; 32732 MW; 5ED1E267293C2967 CRC64;
> 1.9%; Score 10; DB 16; Length 301;
> arity 100.0%; Pred.No. 2.9;
> onservative 0; Mismatches 0; Indels 0; Gaps 0;
> EDEDD 343
> |||||
> EDEDD 300
>
> RELIMINARY; PRT; 308 AA.

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DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Substrate of serine protease (Cpsid).
GN U126.5.
OS Bovine herpesvirus type 1 (strain Jura).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jura;
RA Schwytzer M., Vlcek C., Lowery D.E., Bello L.J., Meyer G., Misra V
RT "Gene contents in a 37-kb segment centered in the UL part of the
RL bovine herpesvirus 1 genome: the last gap.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Jura;
RA Schwytzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,
RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vlcek C.;
RT "Complete DNA sequence of bovine herpesvirus 1.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ004801; CA006108.1; -.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001847; Peptidase S21.
DR Pfam; PF00716; Peptidase S21; I.
SQ SEQUENCE 308 AA; 31187 MW; 676CD234E3D8C8D3 CRC64;

Query Match 1.9%; Score 10; DB 12; Length 308;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 120 AAAAAAAAAPPP 129
Db |||||
55 AAAAAAAAAPPP 64

RESULT 29
Q7X9M6 PRELIMINARY; PRT; 320 AA.
ID Q7X9M6
AC Q7X9M6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Yabby10 protein
OS Zea mays (Maize)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73; TISSUE=Vegetative apex;
RA Juarez M.T., Twigg R.W., Timmermans M.C.P.;
RT "Reversal of dorsoventral polarity in the maize leaf.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY313904; AAP79887.1; -.
SQ SEQUENCE 320 AA; 33396 MW; FB65FCB8CDD4C6E6 CRC64;

Query Match 1.9%; Score 10; DB 10; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 120 AAAAAAAAAPPP 129
Db |||||
103 AAAAAAAAAPPP 112

RESULT 30
Q7WEQ2 PRELIMINARY; PRT; 326 AA.
ID Q7WEQ2

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(TREMBLrel. 25, Created)
(TREMBLrel. 25, Last sequence update)
(TREMBLrel. 25, Last annotation update)
ochrome c.

conchiseptica (Alcaligenes bronchisepticus).
teobacteria; Betaproteobacteria; Burkholderiales;
ae; Bordetella.

4 N.A.
/ ATCC BAA-588;
7954; PubMed=12910271;
Sebahia M., Preston A., Murphy L.D., Thomson N.,
Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
aga A.M., Temple L., James K., Harris B., Quail M.A.,
Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Collins M., Cronin A., Davis P., Doggett J.,
Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
le S., Norberczak H., O'Neill S., Ormond D., Price C.,
monds M., Skelton J., Squares R., Squares S., Stevens K.,
thead S., Barrell B.G., Maskell D.J.;
analysis of the genome sequences of Bordetella pertussis,
arapertussis and Bordetella bronchiseptica.";
35:32-40(2003).
51; CAB39444.1; -.
eome.
26 AA; 32865 MW; 1B1AD7E9FEC191B8 CRC64;

1.9%; Score 10; DB 16; Length 326;
larity 100.0%; Pred. No. 3.2;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAAP 127
|||||
AAAAAAP 236

PRELIMINARY; PRT; 327 AA.

(TREMBLrel. 23, Created)
(TREMBLrel. 23, Last sequence update)
(TREMBLrel. 24, Last annotation update)
protein (Fragment).
K.
(Mouse).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0090;

M N.A.
/6J; TISSUE=Brain, and Hypothalamus;
4683; PubMed=12466851;
onsortium,
nome Exploration Research Group Phase I & II Team;
the mouse transcriptome based on functional annotation of
length cDNAs.";
53-573(2002).
96; BAC32675.1; -.
48; BAC37680.1; -.
PT0675.
4804; A230054D04Rik.
protein.
327 327
27 AA; 34826 MW; 20320E4E36DE7E8B CRC64;

1.9%; Score 10; DB 11; Length 327;
larity 100.0%; Pred. No. 3.2;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 226 PPPPQQPPPP 235
Db 16 PPPPQQPPPP 25

RESULT 32
Q7W3D2 PRELIMINARY; PRT; 334 AA.
AC Q7W3D2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative cytochrome c.
GN BPP4111.
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
[1]
SEQUENCE FROM N.A.
RP STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Churcher C.M., Bentley S.D., Mungall K.L., Harris B., Quail M.A., Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Fellwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price R., Rabinowitsch E., Rutter S., Saunders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Steve Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis and Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640435; CAE39391.1; -.
KW Complete proteome.
SQ SEQUENCE 334 AA; 33750 MW; 1C2BA3F19282EA80 CRC64;

Query Match 1.9%; Score 10; DB 16; Length 334;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 118 APAAAAAAP 127
Db 235 APAAAAAAP 244

RESULT 33
Q8PFD1 PRELIMINARY; PRT; 336 AA.
AC Q8PFD1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE TonB-like protein.
GN XAC4052.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
[1]
SEQUENCE FROM N.A.
RP STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Caramoté G., Cannavan F., Cardozo J., Chamargo F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.S., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

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49; F: dihydrolipoamide S-succinyltransferase acti. . . ; IEA.
 15; F: protein binding; IEA.
 40; F: transferase activity; IEA.
 52; P: metabolism; IEA.
 99; P: tricarboxylic acid cycle; IEA.
 R001078; 2-oxoacid dh.
 R000089; biotin_lipoyl.
 R004167; E3_binding.
 R003016; Lipoyl_BS.
 R006255; SucB.
 9; 2-oxoacid dh; 1.
 4; biotin_lipoyl; 1.
 7; e3_binding; 1.
 1115; 2-oxoacid dh; 1.
 GR01347; sucB; 1.
 0189; LIPOYL; 1.
 Complete proteome.
 04 AA; 42414 MW; B4FED8E9556D1977 CRC64;
 1.9%; Score 10; DB 16; Length 404;
 larity 100.0%; Pred. No. 3.8;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAAAP 127
 |||||
 AAAAAAP 115
 PRELIMINARY; PRT; 406 AA.
 (TrEMBLrel. 16, Created)
 (TrEMBLrel. 16, Last sequence update)
 (TrEMBLrel. 19, Last annotation update)
 actural protein.
 rium wolfei.
 yarchaeota; Methanobacteria; Methanobacteriales;
 riaceae; Methanothermobacter.
 45261;
 M N.A.
 9258; PubMed11544247;
 cer P., Leisinger T., Wasserfallen A.;
 of Archaeal Prophage PsiM100 Encodes the Lytic Enzyme
 for Autolysis of Methanothermobacter wolfei.";
 . 183:5788-5792(2001).
 M N.A.
 UG-2000) to the EMBL/GenBank/DBJ databases.
 75; AAG39960.1; -.
 06 AA; 46062 MW; 30B27CB36A6428A6 CRC64;
 1.9%; Score 10; DB 1; Length 406;
 larity 100.0%; Pred. No. 3.8;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DDEDED 339
 |||||
 DDEDED 356
 PRELIMINARY; PRT; 406 AA.
 (TrEMBLrel. 25, Created)
 (TrEMBLrel. 25, Last sequence update)
 (TrEMBLrel. 25, Last annotation update)
 mide succinyltransferase component of 2-oxoglutarate
 e complex (2-oxoglutarate dehydrogenase complex, E2
 EC 2.3.1.61).

GN ODH OR SUB OR B33668.
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=518;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=RB50 / ATCC BAA-588;
 RC MEDLINE=22827954; PubMed=12910271;
 RX Parkhill J., Sebaihia M., Preston A., Churcher C.M., Bentley S.D., Mungall
 RA Harris D.E., Holden M.T.G., Churcher C.M., James K., Harris B., Quail M.A.
 RA Cardeno-Tarraga A.M., Temple L., Basham D., Bason N., Cherevach I
 RA Achman M., Atkin R., Baker S., Bason N., Cronin A., Davis P., Doggett J.,
 RA Chillingworth T., Collins M., Hamlin N., Hauser H., Holroyd S., Jagels
 RA Fellwell T., Goble S., Norberczak H., O'Neill S., Ormond D., Price
 RA Leather S., Moule S., Norberczak H., O'Neill S., Saunders D., Seeger K.,
 RA Rabinowitsch E., Rutter S., Sanders M., Squares R., Squares S., Steve
 RA Sharp S., Simmonds M., Skelton J., Skelton J., Skelton J., Skelton J.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pert
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL: BX640448; CAE35641.1; -.
 KW Acyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 406 AA; 41997 MW; 723C1E8E82FFD81A CRC64;
 Query Match 1.9%; Score 10; DB 16; Length 406;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 118 AAAAAAAAP 127
 Db 93 AAAAAAAAP 102
 RESULT 39
 O65215 PRELIMINARY; PRT; 436 AA.
 ID O65215; PRELIMINARY; PRT; 436 AA.
 AC O65215; PRELIMINARY; PRT; 436 AA.
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Zinc finger protein ID1.
 GN ID1.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Immature leaf;
 RC MEDLINE=98265970; PubMed=9604934;
 RX Colasanti J., Yuan Z., Sundaresan V.;
 RA "The indeterminate gene encodes a zinc finger protein and regula
 RT leaf-generated signal required for the transition to flowering i
 RT maize.";
 RL Cell 93:593-603(1998).
 DR EMBL: AF058757; AAC18941.1; -.
 DR PIR: T01652; T01652.
 DR TRANSFAC; T03994; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf_C2H2; 3.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 436 AA; 46746 MW; 6A9AD06320413BD5 CRC64;
 Query Match 1.9%; Score 10; DB 10; Length 436;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;

SPQPPA 219
|||||
SPQPPA 54

RELIMINARY; PRT; 466 AA.

TrEMBLrel. 22, Created)
TrEMBLrel. 22, Last sequence update)
TrEMBLrel. 23, Last annotation update)

lanogaster (Fruit fly).

tazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
pterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.

27;

N.A.

ey; PubMed=10731132;

006; elniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Wormman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
le C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
ghayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,
Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
otchan M.R., Bouck J., Brokstein P., Brottier P.,
Susam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cawley S., Dahle C., Davenport L.B., Davies P.,
Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Briellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
ng F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harvey D., Helman T.J., Hernandez J.R., Houck J.,
uston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
lush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
i B., McIntosh A.A., Li J., Li Z., Liang Y., Lin X.,
Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
oy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
emington K., Saunders R.D.C., Scheeler F., Shen H.,
den-Kiamos I., Simpson M., Skupski M.P., Smith T.,
adling A.C., Stapleton M., Strong R., Sun E.,
Tector C., Turner R., Venter E., Wang A.H., Wang X.,
assarman D.A., Weinstein G.M., Weissbach J.,
Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
, F., Zaveri J.S., Zhan M., Zhang Q., Zhou X., Zheng L.,
hong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
yers E.W., Rubin G.M., Venter J.C.;
quence of *Drosophila melanogaster*;
185-2195(2000).

N.A.

, Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
ocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Center A., Champe M., Davenport L.B., Dietz S.M.,
rsett V., Doup I.E., Doyle C., Dresnek D., Farfan D.,
Frise E., Galle R.F., Garg N.S., George R.A.,
Houck J., Hoskins R.A., Hostin D., Howland T.J.,
alali M., Kruse D., Li P., Mattei B., Moshrefi A.,
, Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
ragas V., Park S., Patel S., Pfeiffer B.,

Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of *Drosophila melanogaster* genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN

RP SEQUENCE FROM N.A.

RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Ciamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of *Drosophila melanogaster* genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RT

RN

RP SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;

RL

RN

RP SEQUENCE FROM N.A.

RA FlyBase;

RL Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

DR

DR

DR

DR

SQ

SEQUENCE 466 AA; 53179 MW; 22EA4D68BDD64BEA CRC64;

Query Match 1.9%; Score 10; DB 5; Length 466;

Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 10; Conservative 0; Mismatches 0; Indels 0; C

Oy

Db

14 AAATTAAAS 23

276 AAATTAAAS 285

RESULT 41

Q86XT7

ID Q86XT7 PRELIMINARY; PRT; 489 AA.

AC Q86XT7;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Similar to forkhead box O1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Strausberg R.;

RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC050072; AAS0072.1;

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA

DR InterPro; IPR001766; TF_Fork_head.

DR Pfam; PF00250; Fork head; 1.

DR PRINTS; PR00053; FORKHEAD.

DR ProDom; PD000425; TF_Fork_head; 1.

DR SMART; SM00339; FH; 1.

DR PROSITE; PS00657; FORK HEAD_1; 1.

DR PROSITE; PS00658; FORK HEAD_2; 1.

DR PROSITE; PS00339; FORK HEAD_3; 1.

SQ SEQUENCE 489 AA; 52369 MW; 3EB55F4B503E058C CRC64;

Query Match 1.9%; Score 10; DB 4; Length 489;

Best Local Similarity 100.0%; Pred. No. 4.5;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Oy

220 PPQQQPPPP 229

|||||
 QQQPPPP 77

PRELIMINARY; PRT; 489 AA.

(TREMBLrel. 25, Created)
 (TREMBLrel. 25, Last sequence update)
 (TREMBLrel. 25, Last annotation update)

12.5 protein.

12.5.

(Rice).

Aridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 a; Magnoliophyta; Liliopsida; Poales; Poaceae;
 e; Oryzae; Oryza.

530;

M N.A.

(Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
 J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
 S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
 H., Jia P.X., Qian Y.M., Yang K., Zhou B., Chen Z.H.,
 G L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
 G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
 i Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
 ng X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
 n S.T., Ni L., Zhu F.H., Hong G.F.;
 EC-2001) to the EMBL/GenBank/DBJ databases.

105; CAE02257.1; -- 126F4480EBB0B1D CRC64;
 89 AA; 54725 MW; 126F4480EBB0B1D CRC64;

1.9%; Score 10; DB 10; Length 489;

1arity 100.0%; Pred. No. 4.5;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAPPP 129

|||||

AAAAPPP 14

PRELIMINARY; PRT; 513 AA.

(TREMBLrel. 16, Created)
 (TREMBLrel. 16, Last sequence update)
 (TREMBLrel. 25, Last annotation update)
 o unknown protein (Hypothetical protein)

12B11.2 OR ATSG64430.

thaliana (Mouse-ear cress).

iridiplantae; Streptophyta; Embryophyta; Tracheophyta;

a; Magnoliophyta; eudicotyledons; core eudicots; rosids;

Brassicales; Brassicaceae; Arabidopsis.

702;

M N.A.

bia;

atoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,

analysis of Arabidopsis thaliana chromosome 5. XI."

.PR-1999) to the EMBL/GenBank/DBJ databases.

M N.A.

, Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,

owser L., Jones T., Bann J., Carninci P., Chen H.,

ung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

eoologis A., Davis R.W.;

(OV-2001) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.
 RP Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kaw
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

[4]

RN SEQUENCE FROM N.A.

RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
 RA Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusa
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat
 RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis ORF Clones";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB025640; BAB11604.1; -

DR EMBL; AY062534; AAL32612.1; -

DR EMBL; AY092962; AAM12961.1; -

DR EMBL; AY093313; AAM13312.1; -

DR EMBL; BT008878; AAF68317.1; -

DR InterPro; IPR000270; OPR_PBI.

DR Pfam; PF00564; PBI; 1.

DR SMART; SM00666; PBI; 1.

KW Hypothetical protein.

SQ SEQUENCE 513 AA; 56441 MW; 255A63F2079726AA CRC64;

Query Match

Best Local Similarity 100.0%; Score 10; DB 10; Length 513;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 222 QQQQPPPPQ 231

Db 414 QQQQPPPPQ 423

RESULT 44

Q9LWQ9

ID Q9LWQ9 PRELIMINARY; PRT; 525 AA.

AC Q9LWQ9;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Similar to Arabidopsis thaliana chromosome II BAC T9122 genomic

DE sequence.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

RT clone:P0431F01";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP001550; BAA92994.1; -

DR Gramene; Q9LWQ9; -

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 7.

DR PRINTS; PR00320; GPROTEINRPT.

DR SMART; SM00320; WD40; 5.

DR PROSITE; PS00082; WD_REPEATS_2; 3.

DR PROSITE; PS00294; WD_REPEATS_REGION; 1.

KW Repeat; WD repeat.

SQ SEQUENCE 525 AA; 55187 MW; 8C302D45D6E5BC1 CRC64;

Query Match

Best Local Similarity 100.0%; Score 10; DB 10; Length 525;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

conservative 0; Mismatches 0; Indels 0; Gaps 0;
EDDED 337
|||||
EDDED 453

RELIMINARY; PRT; 544 AA.

TrEMBLrel. 01, Created)
TrEMBLrel. 01, Last sequence update)
TrEMBLrel. 25, Last annotation update)

rsaria chlorella virus 1 (PBCV-1).
A viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
506;

N.A.
167; PubMed=7831789;
Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;
45 kb of DNA located at the left end of the chlorella
genome.";
339-352(1995).

N.A.
326; PubMed=10544099;
Ilmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Ickerson K.W., Van Etten J.L.;
PBCV-1 encodes a functional homosperridine
254-262(1999).

N.A.
354; PubMed=11021991;
J.R., Adams B.J., Graves M.V., Van Etten J.L.;
ion of a beta-1,3-glucanase encoded by chlorella virus
27-36(2000).

N.A.
; 1995) to the EMBL/GenBank/DBJ databases.
N.A.
(-1997) to the EMBL/GenBank/DBJ databases.
N.A.
; 1997) to the EMBL/GenBank/DBJ databases.
N.A.
an Etten J.L.;
(-1998) to the EMBL/GenBank/DBJ databases.
N.A.
an Etten J.L.;
(-1999) to the EMBL/GenBank/DBJ databases.
N.A.
Graves M.V., Van Etten J.L.;
(-2000) to the EMBL/GenBank/DBJ databases.
AAC96425.1; -.
117547.
4 AA; 59361 MW; 6680655754F034E5 CRC64;
arity 1.9%; Score 10; DB 12; Length 544;
arity 100.0%; Pred.No.4.9;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 PPPTAPAPPPP 136
|||||
Db 379 PPPTAPAPPPP 388

RESULT 46
Q8S7N6 PRELIMINARY; PRT; 570 AA.

AC Q8S7N6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative pyruvate kinase (EC 2.7.1.40) (PK).
GN OSUNBA0095C07.5.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Ganeberg K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbus
Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSUNBA0095C07 genomic sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
chromosome 10.";
RL Science 300:1566-1569(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + PYRUVATE = ADP + PHOSPHOENOLPYRUVAT
-1- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS; FINAL STEP.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
DR EMBL; AC077693; AAL86487.1; -.
DR EMBL; AE017121; AAP55104.1; -.
DR Gramene; Q8S7N6; -.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004743; F:pyruvate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF00224; PK; 1.
DR Pfam; PF02887; PK_C; 1.
DR PRINTS; PR01050; PYRUVTKINASE.
DR ProDom; PD001009; Pyruvate kinase; 1.
DR TIGRFAMs; TIGR01064; pyruv_kin; 1.
DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
KM Glycolysis; Kinase; Magnesium; Pyruvate; Transferase.
SQ SEQUENCE 570 AA; 61645 MW; 00CA46020AFF6D8A CRC64;

Query Match 1.9%; Score 10; DB 10; Length 570;
Best Local Similarity 100.0%; Pred.No.5.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 119 PAAAAAAPP 128
|||||
Db 26 PAAAAAAPP 35

RESULT 47


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PRELIMINARY; PRT; 580 AA.
(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
(E60543) corresponds to a region of the predicted
(Rice).
iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
530;
M N.A.
ipponbare;
atsumoto T., Yamamoto K.;
a nipponbare (GA3) genomic DNA, chromosome 6, PAC
04.;
AY-2000) to the EMBL/GenBank/DBJ databases.
69; BAA95818.1; -.
WJ7; -.
R001026; ENTH.
R008943; PI_bind_N.
7; ENTH; 1.
73; ENTH; 1.
80 AA; 64048 MW; 7E26B931100A7144 CRC64;
1.9%; Score 10; DB 10; Length 580;
Larity 100.0%; Pred.No.5.1;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAPPP 129
|||||
AAAAPPP 531

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PRELIMINARY; PRT; 607 AA.
(TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
protein.
iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Panicoideae; Andropogoneae; Zea.
577;
M N.A.
SS853;
3764; PubMed=12368247;
ca V., Messing J.;
nization of Orthologous Sequences in Grass Genomes.";
121:1549-1555(2002).
65; AAN40027.1; -.
R005516; Remorin_C.
3; Remorin_C; 1.
protein.
07 AA; 64780 MW; 8C699253452700EF CRC64;
1.9%; Score 10; DB 10; Length 607;
Larity 100.0%; Pred.No.5.3;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
EEDDED 337
|||||
EEDDED 296

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RESULT 49
Q7UBI5 PRELIMINARY; PRT; 608 AA.
ID Q7UBI5
AC Q7UBI5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sigmad(70) factor of RNA polymerase.
DE RPOD OR S313.
GN Shigella flexneri.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016988; AAP18396.1; -.
SQ SEQUENCE 608 AA; 69601 MW; E07A9E0169699DA1 CRC64;
Query Match 1.9%; Score 10; DB 16; Length 608;
Best Local Similarity 100.0%; Pred.No.5.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY 333 DDEDEDEED 342
DB 191 DDEDEDEED 200
|||||
|||||
RESULT 50
Q8XAN5 PRELIMINARY; PRT; 613 AA.
ID Q8XAN5
AC Q8XAN5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA polymerase, sigma(70) factor, regulation of proteins induced
DE high temperatures (RNA polymerase sigma 70 factor RpoD).
GN RPOD OR 24420 OR ECS3950.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Rosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya
RA Han C.-G., Ohtaubo E., Nakayama K., Murata T., Tanaka M., Tobe T
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RNA Res. 8:11-22(2001).

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DR	InterPro; IPR009042; Sigma70_r1_2.	
DR	InterPro; IPR007627; Sigma70_r2.	
DR	InterPro; IPR007624; Sigma70_r3.	
DR	InterPro; IPR007630; Sigma70_r4.	
DR	InterPro; IPR000943; Sigma70_r5.	
DR	Pfam; PF04546; sigma70_rer; 1.	
DR	Pfam; PF03979; sigma70_r1_1; 1.	
DR	Pfam; PF00140; sigma70_r1_2; 1.	
DR	Pfam; PF04542; sigma70_r2; 1.	
DR	Pfam; PF04539; sigma70_r3; 1.	
DR	Pfam; PF04545; sigma70_r4; 1.	
DR	PRINTS; PR00046; SIGMA70FOCT.	
DR	PROSITE; PS00715; SIGMA70_1; 1.	
DR	PROSITE; PS00716; SIGMA70_2; 1.	
KW	Complete proteome.	
QY	SEQUENCE 613 AA; 70207 MW; 5B4CC1D0C382AA9E CRC64;	
DB	Query Match 1.9%; Score 10; DB 16; Length 613;	
	Best Local Similarity 100.0%; Pred. No. 5.4;	
	Matches 10; Conservative 0; Mismatches 0; Indels 0;	
QY	333 DDDEDEDEED 342	
DB	191 DDDEDEDEED 200	
RESULT 52		
Q96151		
ID	O96151 PRELIMINARY; PRT; 635 AA.	
AC	O96151;	
DT	01-MAY-1999 (TrEMBLrel. 10, Created)	
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)	
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Hypothetical protein.	
GN	PF0250W.	
OS	Plasmodium falciparum.	
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	
OX	NCBI_TaxID=5833;	
ON	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=99021743; PubMed=9804551;	
RA	Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind I.	
RA	Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Pederson J.,	
RA	Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,	
RA	Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.	
RA	Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;	
RT	"Chromosome 2 sequence of the human malaria parasite Plasmodium	
RT	falciparum."	
RL	Science 282:1126-1132(1998).	
DR	EMBL; AE001382; AAC71839.1; -.	
DR	PIR; A71620; A71620.	
KW	Hypothetical protein.	
QY	SEQUENCE 635 AA; 70649 MW; DDB063DC15C15459 CRC64;	
	Query Match 1.9%; Score 10; DB 5; Length 635;	
	Best Local Similarity 100.0%; Pred. No. 5.6;	
	Matches 10; Conservative 0; Mismatches 0; Indels 0;	
QY	334 DDDEDEDEED 343	
DB	577 DDDEDEDEED 586	
RESULT 53		
Q8DC21		
ID	Q8DC21 PRELIMINARY; PRT; 636 AA.	
AC	Q8DC21;	
DT	01-MAR-2003 (TrEMBLrel. 23, Created)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide	
GN	acyltransferase component.	
GN	VW11631.	

ficus.
 oteobacteria; Gammaproteobacteria; Vibrionales;
 ; Vibrio.
 72;
 M N.A.
 im S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 nome sequence of *Vibrio vulnificus* CMCP6.";
 EC-2002) to the EMBL/GenBank/DBJ databases.
 02; AAOL0050.1; -.
 54; C-pyruvate dehydrogenase complex; IEA.
 15; F:acyltransferase activity; IEA.
 42; F:diacylglycerolipase S-acyltransferase activity; IEA.
 15; F:protein binding; IEA.
 96; P:glycolysis; IEA.
 52; P:metabolism; IEA.
 R001078; 20xoxacid dh.
 R006256; AceF.
 R004167; Biotin lipoyl.
 R003016; Lipoyl BS.
 3; 2-oxoacid dh; 1.
 4; biotin lipoyl; 3.
 7; e3 binding; 1.
 1115; 20xoxacid dh; 1.
 GR01348; PDHac trf_long; 1.
 0189; LIPOYL; 3.
 teome.
 36 AA; 65712 MW; 845B61BDB8CA23327 CRC64;
 laxity 1.9%; Score 10; DB 16; Length 636;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 VAAAAPA 146
 |||||
 VAAAAPA 196
 PRELIMINARY; PRT; 660 AA.
 (TREMBlrel. 13, Created)
 (TREMBlrel. 13, Last sequence update)
 (TREMBlrel. 25, Last annotation update)
 4.
 elanogaster (Fruit fly).
 stazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 dopterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 227;
 M N.A.
 ley;
 6006; PubMed=10731132;
 Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Lewis S.E., Smith R.L., Holt R.A., White R.F.,
 Wortman J.R., Richards S., Ashburner M., Henderson S.N.,
 Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 yle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Achayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cawley S., Dahlke C., Davenport L.B., Davies P.,
 Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 oup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischma
 RA Posler C., Gabriellian A.E., Gaig N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003609; AAF52249.1; -.
 DR HSSP; P24781; 1XBR.
 DR FlyBase; FBgn0016660; H15.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IE
 DR InterPro; IPR008967; P53-like.
 DR InterPro; IPR001699; TF T-box.
 DR Pfam; PF00907; T-box; 1.
 DR PRINTS; PR00937; TBOX.
 DR SMART; SM00425; TBOX; 1.
 DR PROSITE; PS01283; TBOX_1; 1.
 DR PROSITE; PS0252; TBOX_3; 1.
 SQ SEQUENCE 660 AA; 72370 MW; 904BEF9AE684B58F CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 660;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 13 AAAATTAATAA 22
 Db 141 AAAATTAATAA 150
 RESULT 55
 Q9U0N1 PRELIMINARY; PRT; 673 AA.
 ID Q9U0N1
 AC Q9U0N1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical gap protein.
 GN GARP.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RC STRAIN=3D7;
 RP SEQUENCE FROM N.A.
 RA Bowman S., Churcher C., Harris B., Harris D., Lawson D., Quail M
 RA Barrell B.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031746; CAB63561.1; -.
 SQ SEQUENCE 673 AA; 79795 MW; 7A7FFE921D83DA26 CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 673;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;

```

QV DEDEDE 340
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DE DEDEDE 645

RELIMINARY; PRT; 714 AA.

TREMBLrel. 22, Created)
TREMBLrel. 22, Last sequence update)
TREMBLrel. 24, Last annotation update)
rotein.

(japonica cultivar-group).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Oryzaeae; Oryza.
947;

N.A.
pponbare;
tsunoto T., Yamamoto K.;
nipponbare(GA3) genomic DNA, chromosome 1, PAC
7.";
V-2000) to the EMBL/GenBank/DBJ databases.
0; BAB92117.1; -.
KI; -.
1; C:integral to membrane; IEA.
004695; C4dc/mal.transpt.
; C4dic.mal.tran.1.
4 AA; 78219 MW; A52C833843B619FE CRC64;

arity 1.9%; Score 10; DB 10; Length 714;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAT 157
|||||
AAAAAT 167

RELIMINARY; PRT; 759 AA.

TREMBLrel. 23, Created)
TREMBLrel. 23, Last sequence update)
TREMBLrel. 25, Last annotation update)
assium channel Kv3.3.

uniculus (Rabbit).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
neria; Lagomorpha; Leporidae; Oryctolagus.
86;

N.A.
1 endothelium;
529; PubMed=10712820;
pard A.R.;
ium channels in lens epithelium and corneal
; 70:339-348(2000).

N.A.
1 endothelium;
pard A.R.;
G-2002) to the EMBL/GenBank/DBJ databases.
9; AAN15930.1; -.
1; C:integral to membrane; IEA.
5; C:voltage-gated potassium channel complex; IEA.
5; F:protein binding; IEA.
9; F:voltage-gated potassium channel activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB POZ.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel pore.
DR InterPro; IPR005404; KV3.3 channel.
DR InterPro; IPR003968; KV_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K tetra.
DR InterPro; IPR005820; M-channel nlg.
DR InterPro; IPR003974; Shaw channel.
DR Pfam; PF00520; ion.trans.1.
DR Pfam; PF02214; K_tetra.1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01582; KV33CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01498; SHAWCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ionic channel.
SQ SEQUENCE 759 AA; 80499 MW; 746486F967D6E7AF CRC64;

Query Match 1.9%; Score 10; DB 6; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C

QV 226 PPPPQQPPPP 235
DB 36 PPPPQQPPPP 45

RESULT 58
Q9AB02
ID Q9AB02 PRELIMINARY; PRT; 762 AA.
AC Q9AB02;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Chemotaxis protein CheA.
GN CC0433.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RA MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Ely
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Sait J., Craven M.B., Khouri H., Shetty J., Berry K
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whit
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
DR EMBL; AE005716; AAK22420.1; -.
DR PTR; H87302; H87302.
DR HSP; O56310; I3Q.
DR TIGR; CC0433; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0000455; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.

```

R002545; Chew.
 R004105; H-kinase dim.
 R005467; His Kinase.
 R002114; HPr_Serp_S.
 R008207; Hpt_N.
 R008208; Hpt_N.
 4; Chew; 1.
 5; H-kinase_dim; 1.
 8; HATase_c; 1.
 7; Hpt; 1.
 344; BCTRLSENSOR.
 3142; Hpt_N; 1.
 60; Chew; 1.
 87; HATase_c; 1.
 73; HPT; 1.
 0851; CHEW; 1.
 0109; HIS_KIN; 1.
 0894; HPT; 1.
 0589; PTS_HPR_SER; 1.
 phosphorylation; Sensory transduction; Transferase;
 teome.
 62 AA; 80149 MW; 95E9D16BE4F5AC2A CRC64;
 1.9%; Score 10; DB 16; Length 762;
 larity 100.0%; Pred. No. 6.5; Indels 0; Gaps 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAAAP 127
 |||||
 AAAAAAP 347
 PRELIMINARY; PRT; 806 AA.
 (TREMBLrel. 13, Created)
 (TREMBLrel. 13, Last sequence update)
 (TREMBLrel. 24, Last annotation update)
 in (Zinc finger transcription factor).
 7.
 elanogaster (Fruit fly).
 elazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 dopterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 227;
 M N.A.
 ley;
 606; PubMed=10731132;
 Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Yle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cawley S., Dahlke C., Davenport L.B., Davies P.,
 Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 Evangelista C.C., Ferraz C., Ferrera S., Fleischmann M.,
 Abrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 i Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 ei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.I.
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese N.
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smiti
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RP Ruiz-Gomez M., Coutts N., Suster M.L., Landgraf M., Bate M.;
 RA "myoblasts incompetent encodes a zinc finger transcription factor
 RT required to specify fusion competent myoblasts in Drosophila";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003741; AAF56082.1; -;
 DR EMBL; AJ311850; CAC51080.1; -;
 DR HSP; P08151; 2GLI
 DR FlyBase; FBgn0039039; lmd.
 DR GO; GO:0007525; P:somatic muscle development; IMP.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zfc2h2; 5.
 DR ProDom; PD000003; Znf_C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 806 AA; 89406 MW; CD2F5254D934EBD7 CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 806;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 20 AAASSSAASP 29
 |||||
 DB 214 AAASSSAASP 223
 RESULT 60
 Q96210
 ID Q96210 PRELIMINARY; PRT; 866 AA.
 AC Q96210;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 GN LMD OR CG4677.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RN SEQUENCE FROM N.A.
 RP Duan H., Nguyen H.T.;
 RT "A novel Zn finger protein that is essential for myogenesis";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkeley.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.
 RA Celniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

RN	[7]
RP	SEQUENCE FROM N.A.
RA	FlyBase;
RRL	Submitted (SBP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL:	AY032609; AA39641.1; -
EMBL:	AY121651; AAM51978.1; -
EMBL:	AE003741; AAN13923.1; -
DR	FlyBase; FBgn0039039; lmd.
DR	GO:0007525; P:somatic muscle development; IMP.
DR	InterPro; IPR007087; Znf_C2H2.
DR	Pfam; PF00096; zf-C2H2; 5.
DR	ProDom; PD00060; Znf_C2H2; 1.
DR	PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR	PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
KW	Metal-binding; zinc; Zinc-finger.
SK	SEQUENCE 866 AA; 96040 MW; 596394F14FBAB0EC CRC64;
QY	Query Match 1.9%; Score 10; DB 5; Length 866;
Db	Best Local Similarity 100.0%; Pred. No. 7.2;
	Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY	20 AAASSSAASP 29
Db	235 AAASSSAASP 244
RESULT 61	
Q8LIF6	PRELIMINARY;
ID Q8LIF6	PRT; 888 AA.
AC Q8LIF6;	
CD 01-OCT-2002	(TrEMBLrel. 22, Created)
DT 01-OCT-2002	(TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE QJ1316 A04.5 protein [P0503D09.22 protein].	
GN QJ1316_A04.5 OR P0503D09.22;	
OS Oryza sativa (japonica cultivar-group).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta	
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC Ehrhartoidae; Oryzaceae; Oryza.	
OX NCBI_TaxID=39947;	
XP 11	
RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Nipponbare;	
CC Sasaki T., Matsumoto T., Yamamoto K.;	
RT "Oryza sativa nipponbare (CA3) genomic DNA, chromosome 7, BAC	
RT clone:OJ1316 A04.";	
RT Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	
RP SEQUENCE FROM N.A.	
RC STRAIN=cv. Nipponbare;	
CC Sasaki T., Matsumoto T., Katayose Y.;	
RT "Oryza sativa nipponbare (CA3) genomic DNA, chromosome 7, PAC	
RT clone:P0503D09.";	
RT Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.	
EMBL: AP003822; BAC06989.1; -	
EMBL: AP005455; BAC16733.1; -	
DR Gramene; Q8LIF6; -	
DR InterPro; IPR007527; Znf_SWIM.	
DR Pfam; PF04434; SWIM; 1.	
SK SEQUENCE 888 AA; 100868 MW; AA78854BF338E542 CRC64;	
QY	Query Match 1.9%; Score 10; DB 10; Length 888;
Db	Best Local Similarity 100.0%; Pred. No. 7.4;
	Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY	151 AAAAATAPP 160
Db	119 AAAAATAPP 128
RESULT 62	
Q8BK12	PRELIMINARY;
ID O8BK12	PRT; 943 AA.

(TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
K. proline-rich region containing protein.
(Mouse).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0090;

M N.A.
/6J; TISSUE=Eye;
4683; PubMed=12466851;
Ensortium,

name Exploration Research Group Phase I & II Team;
the mouse transcriptome based on functional annotation of
length cDNAs";
53-573(2002).
22, BAC34813.1; -.
PT0698.
3730; D230019K20Rik.
protein.
43 AA; 99939 MW; 8B2D3326D09B5426 CRC64;

1.9%; Score 10; DB 11; Length 943;
larity 100.0%; Pred.No.7.8;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPPQP 231
|||||||
QPPPPQP 832

PRELIMINARY; PRT; 1038 AA.

(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)

ris (Yeast).
ungi; Ascomycota; Saccharomycotina; Saccharomycetes;
tales; Saccharomycetaceae; Pichia.
922;

M N.A.

2858; PubMed=10923020;
Kaiser C.A., Bevis B.J., Soderholm J., Fu D., Sears I.B.,
f Pichia pastoris genes involved in ER-to-Golgi

-993(2000).
60; AAF27636.1; -.
R000886; ER_target_S.
R001680; WD40.
20; WD40; 1.
0014; ER_TARGET; 1.
epest.

038 AA; 114600 MW; FE23F286859EBB36 CRC64;

1.9%; Score 10; DB 3; Length 1038;
larity 100.0%; Pred.No.8.4;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

EDDDEDE 338
|||||||
EDDDEDE 1019

RESULT 64
P97496

ID P97496 PRELIMINARY; PRT; 1100 AA.
AC P97496;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SRG3.
GN SMARCC1 OR SRG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Jeon S.H., Kang M.G., Kim Y.H., Lee C., Park S.D., Seong R.H.;
RT "A new mouse gene, SRG3, related to the SWI3 of Saccharomyces
RT cerevisiae";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
DR EMBL; U85614; AAB42085.1; -.
DR PIR; T30967; T30967.
DR MGD; MGI:1203524; Smarcc1.
DR GO; GO:0009887; P.organoogenesis; IMP.
DR InterPro; IPR001357; BRCT.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR001005; Myb DNA_binding.
DR InterPro; IPR007526; SWIRM.
DR Pfam; PF00533; BRCT; 1.
DR Pfam; PF00249; myb DNA-binding; 1.
DR Pfam; PF04433; SWIRM; 1.
DR SMART; SM00298; CHROMO; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS50030; MYB_3; 1.
DR DNA-binding; Nuclear Protein.
KW DNA-binding; Nuclear Protein.
SQ SEQUENCE 1100 AA; 123276 MW; 0321A9E95FDBAB4A CRC64;

Query Match 1.9%; Score 10; DB 11; Length 1100;
Best Local Similarity 100.0%; Pred.No.8.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 220 PQQQQQPPPP 229
DB 1073 PQQQQQPPPP 1082

RESULT 65
Q9VY88

ID Q9VY88 PRELIMINARY; PRT; 1250 AA.
AC Q9VY88;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RDGB protein.
GN RDGB OR CG1111.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.
RA Wan X.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin

BA Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 BE Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 BR Otchan M.R., Bouck J., Brokstein P., Brottier P.,
 CA Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 CC Cawley S., Dahlke C., Davenport L.B., Davies P.,
 CD Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 CE up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 CF Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 CG briellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 CH ng F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 CI Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 CJ uston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 CK lush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 CL Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 CM Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 CN i B., McIntosh T.C., McLeod M.P., McPherson D.,
 CO Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 CP oy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 CQ Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 CR Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 CS emington K., Saunders R.D.C., Scheeler F., Shen H.,
 CT den-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 CU adling A.C., Stapleton M., Strong R., Sun E.,
 CV Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 CW assarman D.A., Weinstock G.M., Weissbach J.,
 CX Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 CY -F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 CZ hong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 DT Yers E.W., Rubin G.M., Venter J.C.;
 EY sequence of *Drosophila melanogaster*;
 FQ 185-2195(2000).
 GA 3; AAF48315.1; -.
 GB 0003218; rdgB.
 GC 9; C:subrhabdomeral cisterna; NAS.
 GD 5; P:phosphatidylcholine transporter activity; IDA.
 GE 6; P:phosphatidylcholine transporter activity; IDA.
 GF 9; P:deactivation of rhodopsin mediated signaling; IMP.
 GG 8; P:olfaction; IMP.
 GH 6; P:rhodopsin mediated signaling; IMP.
 GI 004177; DDHD dom.
 GJ 001666; PI transfer.
 GK ; DDHD; 1.
 GL ; IP transfer; 1.
 GM 91; PITRANSFER.
 GN 50 AA; 137840 MW; E4E78525D1BDAE2A CRC64;
 HO 1.9%; Score 10; DB 5; Length 1250;
 HP arity 100.0%; Pred. No. 9.9;
 HQ nservative 0; Mismatches 0; Indels 0; Gaps 0;
 HU DDEDE 338
 HV |||||
 HW DDEDE 333
 HX
 HY
 HZ
 IY
 IZ
 JY
 JZ
 KY
 KZ
 LY
 LZ
 MY
 MZ
 NY
 NZ
 OY
 OZ
 PY
 PZ
 QY
 QZ
 RY
 RZ
 SY
 SZ
 TY
 TZ
 UY
 UZ
 VY
 VZ
 WY
 WZ
 XY
 XZ
 YY
 YZ
 ZY
 ZZ

RA Rubboli F., Bulfone A., Bogni S., Marchitello A., Zollo M.,
 RB Borsani G., Ballabio A., Banfi S.,
 RC "A mammalian homologue of the *Drosophila* retinal degeneration B,
 RD implications for the evolution of phototransduction mechanisms.",
 RE Genes Funct. 1:205-214(1997).
 RF [2]
 RG SEQUENCE FROM N.A.
 RH RP STRAIN=ORCON-R; TISSUE=Head;
 RI RC MEDLINE=91231170; PubMed=1903119;
 RJ RX Vitelic T.S., Hyde D.R., O'Tousa J.E.;
 RK "Isolation and characterization of the *Drosophila* retinal degene;
 RL B (rdgB) gene.",
 RM Genet. 127:761-768(1991).
 RN DR EMBL; Y08035; CAA69291.1; -.
 RO DR FlyBase; FBgn0003218; rdgB.
 RP DR GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
 RQ DR GO; GO:0008525; P:phosphatidylcholine transporter activity; IDA.
 RS DR GO; GO:0008536; P:phosphatidylcholine transporter activity; IDA.
 RT DR GO; GO:0016059; P:deactivation of rhodopsin mediated signaling; I
 RU DR GO; GO:0007608; P:olfaction; IMP.
 RV DR GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
 RW DR InterPro; IPR004177; DDHD dom.
 RX DR InterPro; IPR001666; PI_transfer.
 RY DR Pfam; PF02862; DDHD; 1.
 RZ DR Pfam; PF02121; IP transfer; 1.
 SA DR PRINTS; PR00391; PITRANSFER.
 SB SQ SEQUENCE 1250 AA; 137777 MW; 3CC926ABBA40AGF28 CRC64;
 SC
 SD
 SE
 SF
 SG
 SH
 SI
 SJ
 SK
 SL
 SM
 SN
 SO
 SP
 SQ
 SR
 SS
 ST
 SU
 SV
 SW
 SX
 SY
 SZ
 TA
 TB
 TC
 TD
 TE
 TF
 TG
 TH
 TI
 TJ
 TK
 TL
 TM
 TN
 TO
 TP
 TQ
 TR
 TS
 TT
 TU
 TV
 TW
 TX
 TY
 TZ
 UY
 UZ
 VY
 VZ
 WY
 WZ
 XY
 XZ
 YY
 YZ
 ZY
 ZZ

Query Match 1.9%; Score 10; DB 6; Length 1251;
 389; PubMed=9680295;

larity 100.0%; Pred. No. 9.9;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
JASSMAAS 28
|||||||
JASSMAAS 1050

PRELIMINARY; PRT; 1259 AA.
(TREMBLrel. 19, Created)
(TREMBLrel. 19, Last sequence update)
(TREMBLrel. 25, Last annotation update)
11111-PA).
111.
melanogaster (Fruit fly).
etazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
dopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
227;
M N.A.
ley;
Brokstein P., Hong L., Aghayani A., Carlson J.,
havez C., Dorsett V., Farfan D., Frise E., George R.,
Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
cleb J., Faragas V., Park S., Phouanavong S., Wan K.,
S.E., Rubin G.M., Celnikier S.;
UG-2001) to the EMBL/GenBank/DBJ databases.
M N.A.
6006; PubMed=10731132;
Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
yle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Aghayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cawley S., Dahlke C., Davenport L.B., Davies P.,
Belcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
cup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Evangeliata C.C., Ferraz C., Ferreira S., Fleischmann W.,
abrielian A.E., Garg N.S., Gelbart W.M., Glasse K.,
ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
uston K.A., Howland T.J., Wei M.H., Ibegwan C.,
alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
i Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
ai B., McIntosh T.C., McLeod M.P., McPherson D.,
Milehina N.V., Mobarri C., Morris J., Moshrefi A.,
Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Remington K., Saunders R.D., Scheeler F., Shen H.,
iden-Klamas I., Simpson M., Skupski M.P., Smith T.,
radling A.C., Stapleton M., Strong R., Sun E.,
Tector C., Turner R., Venter E., Wang A.H., Wang X.,
assarman D.A., Weinstein G.M., Weissbach J.,
., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Jeri J.S., Zhong M., Zhong G., Zhao Q., Zheng L.,
Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Myers E.W., Rubin G.M., Venter J.C.;
sequence of *Drosophila melanogaster*.
2185-2195 (2000).

SEQUENCE FROM N.A.
RA Celnikier S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers
RA Banon J., An H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan I
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler I
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler I
RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell
RA Hradscky P., Huang Y., Kaminker J.S., Prochman S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnikier S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.
RA "Annotation of *Drosophila melanogaster* genome."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnikier S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051422; AAK92846.1;
DR EMBL; AE003493; AAF48316.2;
DR FlyBase; FBgn0003218; rdbg.
DR GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
DR GO; GO:0008525; F:phosphatidylcholine transporter activity; IDA.
DR GO; GO:0008526; F:phosphatidylcholine transporter activity; IDA.
DR GO; GO:0016059; P:deactivation of rhodopsin mediated signaling;
DR GO; GO:0007608; P:olfaction; IMP.
DR GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
DR InterPro; IPR004177; DDHD dom.
DR InterPro; IPR001666; PI_transfer.
DR Pfam; PF02862; DDHD; 1.
DR Pfam; PF02121; IP_trans; 1.
DR PRINTS; PR00391; PITRANSFER.
SQ SEQUENCE 1259 AA; 138895 MW; 9DD40B76EB1079F7 CRC64;
Query Match 1.9%; Score 10; DB 5; Length 1259;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY 329 EEEEDDEDE 338
Db 324 EEEEDDEDE 333
|||||||
|||||||
RESULT 69
Q9ESU6 PRELIMINARY; PRT; 1400 AA.
AC Q9ESU6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cell proliferation related protein CAP.
GN BRD4 OR CAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mur
OX NCBI_TaxID=10090;

N.A.
 30; PubMed=10938129;
 erg J., Farina A., Coleman A.E., Maruyama T.,
 Lippincott-Schwartz J., Ozato K.;
 protein, MCPAP, associates with mitotic chromosomes and
 o-M transition.";
 1. 20:6537-6549(2000).
 ; AAG02191.1; -;
 1B91.
 20; Brd4.
 01487; Bromodomain.
 bromodomain; 2.
 13; BROMODOMAIN.
 ; BROMO; 2.
 133; BROMODOMAIN 1; 1.
 114; BROMODOMAIN 2; 2.
 10 AA; 155923 MW; 9902BFF7B00ADB59 CRC64;
 1.9%; Score 10; DB 11; Length 1400;
 100.0%; Pred. No. 11;
 0; Mismatches 0; Indels 0; Gaps 0;
 0; Gaps 0;
 PPOPPP 235
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 PPOPPP 989
 ELIMINARY; PRT; 1400 AA.
 REMBLrel. 20, Created)
 REMBLrel. 20, Last sequence update)
 REMBLrel. 25, Last annotation update)
 ntaining protein BRD4 long variant.
 (Mouse).
 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Rodentia; Sciurognathi; Muridae; Mus.
 190;
 N.A.
 , Bullock S.L., Lynch D.B., Grigorieva E.F.,
 eddington R.S.P.;
 uly post implantation defects in mice mutant for the
 ntaining protein Brd4.";
 2001) to the EMBL/GenBank/DBJ databases.
 ; AAL67833.1; -;
 120; Brd4.
 01487; Bromodomain.
 bromodomain; 2.
 13; BROMODOMAIN.
 ; BROMO; 2.
 133; BROMODOMAIN 1; 1.
 114; BROMODOMAIN 2; 2.
 10 AA; 155925 MW; 89952B9E75501BC4 CRC64;
 1.9%; Score 10; DB 11; Length 1400;
 100.0%; Pred. No. 11;
 0; Mismatches 0; Indels 0; Gaps 0;
 0; Gaps 0;
 PPOPPP 235
 |||||
 PPOPPP 989
 ELIMINARY; PRT; 1646 AA.
 REMBLrel. 08, Created)
 REMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CPC3 protein.
 GN CPC-3 OR B10H4.070.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WT 74-OR23-1A;
 RX MEDLINE=98352081; PubMed=9685394;
 RA Sattlegger E., Hinnebusch A.G., Barthelmess I.B.;
 RT "cpc-3, the Neurospora crassa homologue of yeast GCN2, encodes a
 RT polypeptide with juxtaposed eIF2 (alpha) kinase and histidyl-tRNA
 RT synthetase-related domains required for general amino acid contro
 RL J. Biol. Chem. 273:20404-20416(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; X91867; CAA62973.1; -;
 DR EMBL; AL670010; CAD21394.1; -;
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006520; P:amino acid metabolism; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR006575; RWD_kinase.
 DR InterPro; IPR000634; S/T dehydrtse_BS.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; kinase; 2.
 DR Pfam; PF05773; RWD; 1.
 DR ProDom; PD000001; Prot_kinase; 3.
 DR SMART; SM00591; RWD; 1.
 DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 2.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00908; RWD; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase
 SQ SEQUENCE 1646 AA; 184903 MW; 2415219DD99A56A4 CRC64;
 Query Match 1.9%; Score 10; DB 3; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G
 QY 330 EEEDEDEDED 339
 DB 727 EEEDEDEDED 736
 |||||
 RESULT 72
 Q9BHL1 PRELIMINARY; PRT; 1722 AA.
 ID Q9BHL1
 AC Q9BHL1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein Y111B2A.23.
 GN Y111B2A.23.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoid;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

```

31 N2;
9613; PubMed-9851916;
ence of the nematode C.elegans: A platform for
biology";
2012-2018(1998).
4 N.A.
31 N2;
AY-2003) to the EMBL/GenBank/DBJ databases.
04; CAC35852.2; -.
1B2A.23; CE34109.
24; F:ATP binding; IEA.
26; F:ATP dependent helicase activity; IEA.
77; F:DNA binding; IEA.
R001410; DEAD.
R001650; Helicase_C.
R006562; HSA.
R000330; SNF2_N.
1; helicase_C; 1.
6; SNF2_N; 1.
87; DEXDC; 1.
90; HELIC; 1.
73; HSA; 1.
protein.
722 AA; 196920 MW; B6B864925F31B643 CRC64;
1.9%; Score 10; DB 5; Length 1722;
latity 100.0%; Pred. No. 13;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TPAPPPP 136
|||||
TPAPPPP 163

PRELIMINARY; PRT; 2980 AA.
(TREMBLrel. 23, Created)
(TREMBLrel. 23, Last sequence update)
(TREMBLrel. 25, Last annotation update)
membrane protein 1 (PFEMP1).
alcaparum (isolate 3D7).
lveolata; Apicomplexa; Haemosporida; Plasmodium.
5329;

4 N.A.
Arphy L., Harris D., Berriman M., Pain A., Hall N.,
crell B.;
3P-2002) to the EMBL/GenBank/DBJ databases.
07; CAD51361.1; -.
39; F:glycosaminoglycan binding; IEA.
05; P:patogenesis; IEA.
3004258; PFEMP.
1; PFEMP; 2.
380 AA; 340609 MW; 52B1B2CD078DB34C CRC64;
1.9%; Score 10; DB 5; Length 2980;
latity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DEDEED 343
|||||
DEDEED 1670

PRELIMINARY; PRT; 2993 AA.

AC Q8NMS0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE 3-oxoacyl-(acyl-carrier-protein) synthase (EC 2.3.1.85).
GN CGL2495.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AP005281; BAB99888.1; -.
DR GO; GO:0005835; C:fatty-acid synthase complex; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact.
DR GO; GO:0004312; F:fatty-acid synthase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001227; Ac trans.
DR InterPro; IPR003965; Fatty acid synth.
DR InterPro; IPR000794; Ketoacyl synth.
DR InterPro; IPR002539; Maoc dehydratas.
DR InterPro; IPR001638; SBP_bac_3.
DR Pfam; PF00698; Acyl_transf; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt C; 1.
DR Pfam; PF01575; Maoc dehydratas; 1.
DR PRINTS; PR01483; FASYNTHASE.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS01039; SBP_BACTERIAL_3; 1.
DR Transferase; Acyltransferase; Complete proteome.
KW SEQUENCE 2993 AA; 316347 MW; 14CCEA44FAC3561B CRC64;
Query Match 1.9%; Score 10; DB 16; Length 2993;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 137 PAPVAAAPA 146
|||||
Db 1696 PAPVAAAPA 1705

RESULT 75
Q9BMP6 PRELIMINARY; PRT; 78 AA.
AC Q9BMP6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Ribosomal P0 protein (Fragment).
OS Culicoides nubeculosus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Ceratopogonidae; Ceratopogoninae; Culicoides.
OX NCBI_TaxID=144565;
RN [1]
RP SEQUENCE FROM N.A.
RA Althaus H., Marti E., Mueller N.;
RT "Cloning and sequencing of a partial cDNA expressing a recombin
RT Culicoides nubeculosus ribosomal P0 protein.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AF314650; AAK00899.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

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1; P:translational elongation; IEA.
001813; Ribosomal_60S.
1
AA; 8372 MW; A2C63F35E38F124A CRC64;
arity 1.7%; Score 9; DB 5; Length 78;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATAP 159
|||||
AAATAP 48

RELIMINARY; PRT; 100 AA.

TrEMBLrel. 13, Created)
TrEMBLrel. 13, Last sequence update)
TrEMBLrel. 25, Last annotation update)
protein.
AT4G09270 OR AT4G09220.
Maliana (Mouse-ear cress).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; eudicotyledons; core eudicots; rosids;
brassicales; Brassicaceae; Arabidopsis.
02;

N.A.
Der Schueren J., Chuang Y.J., Voet M., Robben J.,
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
p-1999) to the EMBL/GenBank/DBJ databases.

N.A.
s sequencing project;
p-1999) to the EMBL/GenBank/DBJ databases.

N.A.
ymonprez B., Volckaert G., Spiegel L.A., Huang E.N.,
J., de la Bastide M., Vil D.M., Preston R.R., Matero A.,
ughnessy A., Rodriguez M., Shekher M., Schutz K.,
oy I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
r-2000) to the EMBL/GenBank/DBJ databases.

N.A.
s sequencing project;
r-2000) to the EMBL/GenBank/DBJ databases.

N.A.
Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
chutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
smcke K., Mayer K.F.X.;
r-2000) to the EMBL/GenBank/DBJ databases.
5; CAB55690.1; -.
4; CAB78050.1; -.
4; CAB78046.1; -.
I17126.
protein.
0 AA; 10935 MW; C6FD13466A73F754 CRC64;
arity 1.7%; Score 9; DB 10; Length 100;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPP 229
|||||
QPPPP 73

1; P:translational elongation; IEA.
001813; Ribosomal_60S.
1
AA; 8372 MW; A2C63F35E38F124A CRC64;
arity 1.7%; Score 9; DB 5; Length 78;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATAP 159
|||||
AAATAP 48

RELIMINARY; PRT; 100 AA.

TrEMBLrel. 13, Created)
TrEMBLrel. 13, Last sequence update)
TrEMBLrel. 25, Last annotation update)
protein.
AT4G09270 OR AT4G09220.
Maliana (Mouse-ear cress).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; eudicotyledons; core eudicots; rosids;
brassicales; Brassicaceae; Arabidopsis.
02;

N.A.
Der Schueren J., Chuang Y.J., Voet M., Robben J.,
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
p-1999) to the EMBL/GenBank/DBJ databases.

N.A.
s sequencing project;
p-1999) to the EMBL/GenBank/DBJ databases.

N.A.
ymonprez B., Volckaert G., Spiegel L.A., Huang E.N.,
J., de la Bastide M., Vil D.M., Preston R.R., Matero A.,
ughnessy A., Rodriguez M., Shekher M., Schutz K.,
oy I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
r-2000) to the EMBL/GenBank/DBJ databases.

N.A.
s sequencing project;
r-2000) to the EMBL/GenBank/DBJ databases.

N.A.
Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
chutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
smcke K., Mayer K.F.X.;
r-2000) to the EMBL/GenBank/DBJ databases.
5; CAB55690.1; -.
4; CAB78050.1; -.
4; CAB78046.1; -.
I17126.
protein.
0 AA; 10935 MW; C6FD13466A73F754 CRC64;
arity 1.7%; Score 9; DB 10; Length 100;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPP 229
|||||
QPPPP 73

RESULT 77
Q7XNS7 PRELIMINARY; PRT; 102 AA.
AC O7XNS7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB OSJNB0085H11.10 protein.
GN OSJNB0085H11.10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu W.F., Tu Y.F., Jia J., Yin
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606995; CAB03961.1; -.
SQ SEQUENCE 102 AA; 11560 MW; 1C9C896BD238CAFC CRC64;

Query Match 1.7%; Score 9; DB 10; Length 102;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
Qy 13 AAAATTAAA 21
Db 84 AAAATTAAA 92

RESULT 78
Q8LN81 PRELIMINARY; PRT; 103 AA.
AC Q8LN81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNB0091N21.34.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.
RA "Oryza sativa chromosome 10 BAC OSJNB0091N21 genomic sequence."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RA chromosome 10."
RL Science 300:1566-1569(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;

```

Y-2003) to the EMBL/GenBank/DBJ databases.
 2; AAM94936.1; -;
 1; AAP54558.1; -;
 181; -;
 protein.
 3 AA; 11065 MW; 3296B0DB35681B7F CRC64;
 1.7%; Score 9; DB 10; Length 103;
 arity 100.0%; Pred. No. 9.1;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAATA 158
 |||||
 AAATA 56

RELIMINARY; PRT; 105 AA.
 (TrEMBLrel. 22, Created)
 (TrEMBLrel. 22, Last sequence update)
 (TrEMBLrel. 23, Last annotation update)
 protein.
 124.17.
 thaliana (Mouse-ear cross).
 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Magnoliophyta; eudicotyledons; core eudicots; rosids;
 Brassicales; Brassicaceae; Arabidopsis.
 02;
 I.N.A.
 k M.K., Ishmael N., Kumar N., Redman J., Riedmuller S.,
 Whitelaw C.A., Fraser C.M., Town C.D.;
 Sequencing of Full-length cDNAs for Hypothetical Genes
 me 2 of Arabidopsis thaliana."
 Y-2002) to the EMBL/GenBank/DBJ databases.
 8; AAM96823.1; -;
 protein.
 15 AA; 11920 MW; 068D2845C47BC58F CRC64;
 1.7%; Score 9; DB 10; Length 105;
 arity 100.0%; Pred. No. 9.3;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 EEDDD 335
 |||||
 EEDDD 85

RELIMINARY; PRT; 112 AA.
 (TrEMBLrel. 15, Created)
 (TrEMBLrel. 15, Last sequence update)
 (TrEMBLrel. 25, Last annotation update)
 active acidic ribosomal protein P1).
 WIG01100.
 thaliana (Mouse-ear cross).
 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Magnoliophyta; eudicotyledons; core eudicots; rosids;
 Brassicales; Brassicaceae; Arabidopsis.
 102;
 I.N.A.
 n P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Lam B.,
 way A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 C., Li J., Liu A., Liu K., Liu S., Mukharbeky N.,
 alm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
 Ecker J.R.;

RT "Genomic sequence for Arabidopsis thaliana BAC T25K16 from chrom:
 I.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 Carninci P., Chen H., Cheuk R., Hayaishizaki Y., Ishida J., Jones
 Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam I.
 Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.,
 Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.
 Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 "Full length cDNA of gene T25K16.9 (GI:6715644).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 Carninci P., Chen H., Cheuk R., Hayaishizaki Y., Ishida J., Jones
 Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki
 Davis R.W., Ecker J.R., Theologis A.;
 "Arabidopsis Open Reading Frame (ORF) Clones."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007323; AAF26471.1; -;
 DR EMBL; AY050975; AAK93652.1; -;
 DR EMBL; AY091176; AAM14115.1; -;
 DR PIR; E86141; E86141
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
 DR GO; GO:006414; P:translational elongation; IEA.
 DR InterPro; IPR001813; Ribosomal 60S.
 DR Pfam; PF00428; 60s_ribosomal; I.
 KW Ribosomal protein.
 QY SEQUENCE 112 AA; 11162 MW; 6D086DD332205E7A CRC64;
 DB

Query Match 1.7%; Score 9; DB 10; Length 112;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 138 APVAAAAPA 146
 |||||
 DB 71 APVAAAAPA 79

RESULT 81
 QBLCW9 PRELIMINARY; PRT; 112 AA.
 AC QBLCW9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Acidic ribosomal protein, putative.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; ros.
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volfovsky N., Town C.D., Troughan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 "Full-length messenger RNA sequences greatly improve genome
 annotation."
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;

```

DNA from Arabidopsis thaliana.;
?-2002) to the EMBL/GenBank/DBJ databases.
; AM64427.1; -.
; C:intracellular; IEA.
; C:ribosome; IEA.
; P:structural constituent of ribosome; IEA.
; P:translational elongation; IEA.
; 60s_ribosomal; I.
ein.
2 AA; 11192 MW; 6D087D8277245E7A CRC64;
1.7%; Score 9; DB 10; Length 112;
arity 100.0%; Pred.No.9.8;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAPA 146
|||||
AAAPA 79
ELIMINARY; PRT; 113 AA.
REMBLrel. 22, Created)
REMBLrel. 25, Last sequence update)
osomal protein P1-like protein.
aliana (Mouse-ear cress).
idiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; eudicotyledons; core eudicots; rosids;
; Brassicales; Brassicaceae; Arabidopsis.
2;
N.A.
fovsky N., Town C.D., Troukhan M., Alexandrov N.,
Flavell R.B., White O., Salzberg S.L.;
essenger RNA sequences greatly improve genome
):0-0(2002).
N.A.
ukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
DNA from Arabidopsis thaliana.;
?-2002) to the EMBL/GenBank/DBJ databases.
; AM62534.1; -.
; C:intracellular; IEA.
; C:ribosome; IEA.
; P:structural constituent of ribosome; IEA.
; P:translational elongation; IEA.
; 60s_ribosomal; I.
ein.
; AA; 11270 MW; 1A2D792A052DA8B9 CRC64;
1.7%; Score 9; DB 10; Length 113;
arity 100.0%; Pred.No.9.9;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAPA 146
|||||
AAAPA 79
ELIMINARY; PRT; 113 AA.
REMBLrel. 16, Created)
REMBLrel. 16, Last sequence update)
REMBLrel. 25, Last annotation update)

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DE Putative 60S acidic ribosomal protein P1.
GN AT5G47700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosi
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia.
EX MEDLINE=99156233; PubMed=10048488;
RA Aamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seven
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:379-391(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.
RA Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At5g47700 (GI:15238170).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Sakurai T., Shinn P.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016886; BAB1317.1; -.
DR EMBL; AY070049; AAL49806.1; -.
DR EMBL; AY096430; AAM20070.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR001813; Ribosomal_60S.
DR Pfam; PF00428; 60s_ribosomal; I.
KW Ribosomal protein.
SQ SEQUENCE 113 AA; 11247 MW; FAB300CD9B5D3FB6 CRC64;
Query Match 1.7%; Score 9; DB 10; Length 113;
Best Local Similarity 100.0%; Pred.No.9.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 138 APVAAAAPA 146
DB 71 APVAAAAPA 79
|||||
RESULT 84
Q852J2 PRELIMINARY; PRT; 118 AA.
AC Q852J2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OSJNB0060J21.32.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

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(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)

Qy 325 VLEKEEED 333
|||
Db 49 VLEKEEED 57

[illegible]


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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0053C23.9 OR OSJNBB0038A07.21.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.B., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.
RA "Oryza sativa chromosome 10 BAC OSJNBB0038A07 genomic sequence."
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.B., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.
RA "Oryza sativa chromosome 10 BAC OSJNBB0038A07 genomic sequence."
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL [3]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RL Science 300:1566-1569(2003).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC092389; AAM8616.1; -.
DR EMBL; AC113948; AAM94527.1; -.
DR EMBL; AB017114; AAP54771.1; -.
DR Gramene; Q8L4D4; -.
KW Hypothetical protein.
SQ SEQUENCE 151 AA; 15015 MW; 8E2A692E8A922E19 CRC64;
Query Match 1.7%; Score 9; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; (
QY 14 AAATTAAAA 22
DB 32 AAATTAAAA 40
RESULT 93
Q88QD5 PRELIMINARY; PRT; 153 AA.
AC Q88QD5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acetyl-CoA carboxylase, biotin carboxyl carrier protein.
GN ACCB OR PP0559.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]_
RP SEQUENCE FROM N.A.

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060: PubMed=12534463;
 Weinert C., Paulsen I.T., Dodson R.J., Hilbert H.,
 Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 Eanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 Lison W., White O., Peterson J., Kouri H., Hance I.,
 Holtzapple E., Scanlan D., Tran K., Moazzes A.,
 Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
 Jendancic D., Hoheisel J., Straetz M., Heim S.,
 Isen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 ome sequence and comparative analysis of the
 versatile Pseudomonas putida KT2440.";
 obiol. 4:799-808(2002).
 6; AAN66186.1; --.
 7; C:acetyl-CoA carboxylase complex; IEA.
 9; F:acetyl-CoA carboxylase activity; IEA.
 4; P:biotin binding; IEA.
 3; P:fatty acid biosynthesis; IEA.
 001249; ACoA_biotinCC.
 001882; Biotin_BS.
 000089; Biotin_lipoyl.
 71; biotin_lipoyl; 1.
 71; ACOABiotinCC.
 188; BIOTIN; 1.
 some.
 3 AA; 16186 MW; 9CFEFP311AA3DB54 CRC64;
 1.7%; Score 9; DB 16; Length 153;
 arity 100.0%; Pred.No.13;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAPA 146
 |||||
 AAAPA 65
 RELIMINARY; PRT; 154 AA.
 TrEMBLrel. 21, Created
 TrEMBLrel. 21, Last sequence update)
 TrEMBLrel. 22, Last annotation update)
 protein.
 (japonica cultivar-group).
 cidipiantae; Streptophyta; Embryophyta; Tracheophyta;
 ; Magnoliophyta; Liliopsida; Poales; Poaceae;
 ; Oryzaeae; Oryza.
 347;
 N.A.
 sponbare;
 sumoto T., Yamamoto K.;
 (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 209.";
 4-2001) to the EMBL/GenBank/DBJ databases.
 2; BAB89199.1; --.
 52; --.
 1 AA; 15967 MW; 173BD51BFC478013 CRC64;
 1.7%; Score 9; DB 10; Length 154;
 arity 100.0%; Pred.No.13;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TTAAA 21
 |||||
 TTAAA 41

Q8H056 PRELIMINARY; PRT; 155 AA.
 Q8H056;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN OSUNBA001406.16.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
 RA Currie J., Collura K.;
 RT "Rice Genomic Sequence."
 RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC105928; AAN77309.1; --.
 KW Hypothetical protein.
 SQ SEQUENCE 155 AA; 15618 MW; A4D4E0C8ACA320CC CRC64;
 Query Match 1.7%; Score 9; DB 10; Length 155;
 Best Local Similarity 100.0%; Pred.No.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 Qy 120 AAAAAAAPP 128
 |||||
 Db 127 AAAAAAAPP 135
 RESULT 96
 Q9DHL7 PRELIMINARY; PRT; 168 AA.
 ID Q9DHL7
 AC Q9DHL7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 96R protein.
 GN 96R.
 OS Yaba-like disease virus (YLDV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirina
 OC Yatapoxvirus.
 OX NCBI_TaxID=132475;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee H.J.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21176366; PubMed=11277691;
 RA Lee H.J., Essani K., Smith G.L.;
 RT "The genome sequence of Yaba-like disease virus, a yatapoxvirus."
 RL Virology 281:170-192(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lee H.J.;
 RL Thesis (2000), Sir William Dunn School of Pathology, University o
 DR EMBL; AJ293568; CAC21334.1; --.
 DR InterPro; IPR007984; Pox_RNA_Pol_19.
 DR Fram; PF05320; Pox_RNA_Pol_19; 1.
 SQ SEQUENCE 168 AA; 19253 MW; 19FA374984C8AE2D CRC64;
 Query Match 1.7%; Score 9; DB 12; Length 168;
 Best Local Similarity 100.0%; Pred.No.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 Qy 331 EDDDEDED 339
 |||||
 Db 13 EDDDEDED 21
 RESULT 97

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PRELIMINARY; PRT; 172 AA.
(TREMBLrel. 03, Created)
(TREMBLrel. 03, Last sequence update)
(TREMBLrel. 24, Last annotation update)

thaliana (Mouse-ear cress).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Brassicales; Brassicaceae; Arabidopsis.
102;

4 N.A.
columbia;
; Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G.,
Conway A.B., Conway A.R., Dewar K., Feng J., Kim C.,
Y., Shinn P., Sun H., Davis R.W., Ecker J.R.,
A., Theologis A.;
3 of BAC F1919 from Arabidopsis thaliana chromosome 1.;
AN-1997) to the EMBL/GenBank/DBJ databases.

4 N.A.
columbia;
; AR-1999) to the EMBL/GenBank/DBJ databases.
04; AAB70430.1; -.
F86176.
3007087; Znf C2H2.
5; zf-C2H2.1.
35; Znf C2H2.1.
1028; ZINC_FINGER_C2H2_1; 1.
1057; ZINC_FINGER_C2H2_2; 1.
3; Zinc; Zinc-finger.
72 AA; 19204 MW; 03473071616E37FF CRC64;

1.7%; Score 9; DB 10; Length 172;
Larity 100.0%; Pred. No. 14;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAP 127
|||||
AAAAAP 50

PRELIMINARY; PRT; 173 AA.
(TREMBLrel. 22, Created)
(TREMBLrel. 22, Last sequence update)
(TREMBLrel. 23, Last annotation update)
protein FLJ38877.
(Human).
atazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
506;

4 N.A.
Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
to T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
uki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
wai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
agai K., Isogai T.;
cDNA sequencing project.";
JL-2002) to the EMBL/GenBank/DBJ databases.
96; BAC04724.1; -.
protein.
73 AA; 18626 MW; A0D11696F08F211B CRC64;

Query Match 1.7%; Score 9; DB 4; Length 173;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 120 AAAAAAAP 128
|||||
Db 61 AAAAAAAP 69

RESULT 99
Q9ZQ24 PRELIMINARY; PRT; 183 AA.
ID Q9ZQ24;
AC Q9ZQ24;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE AT2924440 protein (Hypothetical protein).
GN AT2924440 OR AT2924440/T28124.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyt.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; ros
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 0:0-0 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Xiao Y., Ishmael N., Kumar N., Redman J., Riedmuller S., Utterba
RA Whitelaw C.A., Fraser C.M., Town C.D.;
RT "Cloning and sequencing of full-length cDNAs for hypothetical ge
RT from chromosome 2 of Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006403; AAD18115.1; -.
DR EMBL; AY085501; AAM62725.1; -.
DR EMBL; AY102544; AAM76749.1; -.
DR PIR; F84636; F84636.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20712 MW; 3CA61F0BD0B33F82 CRC64;

Query Match 1.7%; Score 9; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

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BEDDD 335
|||||
BEDDD 85

RELIMINARY; PRT; 185 AA.
TREMBLrel. 10, Created)
TREMBLrel. 10, Last sequence update)
TREMBLrel. 25, Last annotation update)
somal protein L12.
67ID01.16.
(Rice), and
(japonica cultivar-group),
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Oryzae; Oryza.
30, 39947;

N.A.
iva; STRAIN=cv. Nipponbare; TISSUE=Green leaf;
Arimura S.;
N-1999) to the EMBL/GenBank/DBJ databases.

N.A.
iva; STRAIN=cv. Nipponbare; TISSUE=Green leaf;
rashige M., Hirai A., Tautumi N.;
tion of two rice genes for nuclear-encoded chloroplast
tein L12 and phylogenetic analysis of the acquisition of
des and gene duplication.";
Genet. 97:110-115(1998).

N.A.
iva (japonica cultivar-group); STRAIN=cv. Nipponbare;
sumoto T., Yamamoto K.;
(japonica cultivar-group) genomic DNA, chromosome 1, PAC
1.";
3-2001) to the EMBL/GenBank/DBJ databases.
4; BAA37171.1; -.
4; BAB91739.1; -.
PC4267.
ICTF.
34; -.
2; C:intracellular; IEA.
3; C:ribosome; IEA.
5; P:structural constituent of ribosome; IEA.
2; P:protein biosynthesis; IEA.
00206; Ribosomal L12.
08932; Ribos L12/7_olig.
; Ribosomal L12; 1.
326; Ribosomal L12; 1.
R00855; L12; 1.
tein.
5 AA; 18590 MW; EBBFA7FFC98609AB CRC64;
arity 1.7%; Score 9; DB 10; Length 185;
nservative 100.0%; Pred. No. 15;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 127
|||||
AAAAA 29

RELIMINARY; PRT; 187 AA.
TREMBLrel. 16, Created)
TREMBLrel. 16, Last sequence update)

01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Y59A8B.9 protein.
Y59A8B.9.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoic
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RA Sulston J.E.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
Science 282:2012-2018(1998).
RL EMBL; AL32898; CAC14409.1; -.
DR WormPep; Y59A8B.9; CE26218.
DR GO; GO:0008017; F:microtubule binding; IEA.
DR InterPro; IPR004953; B1.
DR Pfam; PF03271; B1; 1.
DR SEQUENCE 187 AA; 19601 MW; B869998562FA1340 CRC64;

Query Match 1.7%; Score 9; DB 5; Length 187;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 120 AAAAAAAAAAPP 128
|||||
Db 89 AAAAAAAAAAPP 97

RESULT 102
Q96BU2 PRELIMINARY; PRT; 194 AA.
AC Q96BU2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015174; AAH15174.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05CBD3C CRC64;

Query Match 1.7%; Score 9; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 227 PPPQPQPPP 235
|||||
Db 127 PPPQPQPPP 135

RESULT 103
Q8H083 PRELIMINARY; PRT; 198 AA.
AC Q8H083;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.

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2.8.
(japonica cultivar-group).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
3947; Oryzae; Oryza.
M.N.A.
Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
Allura K.;
Sequence."
SC-2002) to the EMBL/GenBank/DBJ databases.
34; AAN87736.1; -.
3007087; Znf.C2H2.
5; Zf.C2H2.1.
0028; ZINC_FINGER_C2H2_1; 1.
0157; ZINC_FINGER_C2H2_2; 1.
protein.
98 AA; 21161 MW; 753E11BECF71D7E5 CRC64;
1.7%; Score 9; DB 10; Length 198;
Larity 100.0%; Pred.No.16;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TPAPPP 135
|||||
CPAPPP 99
PRELIMINARY; PRT; 214 AA.
(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 24, Last annotation update)
UNA for DREB1A.
(Rice).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
330; Oryzae; Oryza.
1 N.A.
pnonbare;
tsumoto T., Yamamoto K.;
nipponbare (GA3) genomic DNA, chromosome 6, PAC
12."
18; BAA90812.1; -.
2GCC.
W3; -.
14; C:nucleus; IEA.
10; F:transcription factor activity; IEA.
1001471; TF_ERF.
167; ETHRSPELEMT.
423; TF_ERF; 1.
10; AP2; 1.
4 AA; 23110 MW; 8838D48CBB151F69 CRC64;
1.7%; Score 9; DB 10; Length 214;
arity 100.0%; Pred.No.17;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ASSAA 27
|||||
ASSAA 135
1 N.A.
pnonbare;
tsumoto T., Yamamoto K.;
nipponbare (GA3) genomic DNA, chromosome 6, PAC
12."
18; BAA90812.1; -.
2GCC.
W3; -.
14; C:nucleus; IEA.
10; F:transcription factor activity; IEA.
1001471; TF_ERF.
167; ETHRSPELEMT.
423; TF_ERF; 1.
10; AP2; 1.
4 AA; 23110 MW; 8838D48CBB151F69 CRC64;
1.7%; Score 9; DB 10; Length 214;
arity 100.0%; Pred.No.17;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ASSAA 27
|||||
ASSAA 135
1 N.A.
pnonbare;
tsumoto T., Yamamoto K.;
nipponbare (GA3) genomic DNA, chromosome 6, PAC
12."
18; BAA90812.1; -.
2GCC.
W3; -.
14; C:nucleus; IEA.
10; F:transcription factor activity; IEA.
1001471; TF_ERF.
167; ETHRSPELEMT.
423; TF_ERF; 1.
10; AP2; 1.
4 AA; 23110 MW; 8838D48CBB151F69 CRC64;
1.7%; Score 9; DB 10; Length 214;
arity 100.0%; Pred.No.17;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ASSAA 27
|||||
ASSAA 135
1 N.A.
pnonbare;
tsumoto T., Yamamoto K.;
nipponbare (GA3) genomic DNA, chromosome 6, BAC
157; Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone-OSJNBa0038F22."
Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
(2)
SEQUENCE FROM N.A.
QuanHong Y., Rihe P., Aisheng X.;
"Isolation of rice DREBs, transcription factors involved in
RT dehydration- and cold-inducible gene expression."
Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF002838; BAC24831.1; -.
DR EMBL; AY327040; AAP92125.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001471; TF_ERF.
DR Pfam; PF00847; AP2-domain; 1.
DR PRINTS; PR00367; ETHRSPELEMT.
DR ProDom; PD001423; TF_ERF; 1.
DR SMART; SM00380; AP2; 1.
SQ SEQUENCE 214 AA; 23110 MW; 8838D48CBB151F69 CRC64;
Query Match 1.7%; Score 9; DB 10; Length 214;
Best Local Similarity 100.0%; Pred.No.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 19 AAAASSAA 27
|||||
DB 127 AAAASSAA 135
RESULT 106
P93426
PRELIMINARY; PRT; 217 AA.
ID P93426
AC P93426;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Leucine zipper protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Tainung 67; TISSUE=Seed;
RA Hsing Y.C., Tsao C.V., Chow T., Hsieh J., Chen Z.;
"Rice early embryogenesis gene."
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
DR EMBL; U25283; AAB39320.1; -.
DR PIR; T04353; T04353.
DR Gramene; P93426; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
InterPro; IPR008917; Euk_transcr_DNA.

```

04827; TF_BZIP.

bZIP; 1.7%;

17; BZIP; 1.7%;

136; BZIP_BASIC; 1.7%;

nuclear protein.

AA; 23178 MW; C71B4189FAFFAF8 CRC64;

1.7%; Score 9; DB 10; Length 217;

urity 100.0%; Pred. No. 17;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 127

|||||

AAAA 60

ELIMINARY; PRT; 217 AA.

EMBLrel. 15, Created)

EMBLrel. 15, Last sequence update)

EMBLrel. 25, Last annotation update)

Rice).

idiplantae; Streptophyta; Embryophyta; Tracheophyta;

Magnoliophyta; Liliopsida; Poales; Poaceae;

Oryzae; Oryza.

0;

N.A.

4; Chow T.-Y., Chang Z.-T., Chen Z.-Y., Chung M.-C.,

ieh J.-S.;

ion of a rice early embryogenesis specific gene OSE2.;

-2000) to the EMBL/GenBank/DBJ databases.

; BELONGS TO THE BZIP FAMILY.

; AAF65459.1; -.

5; -.

; C:nucleus; IEA.

; F:DNA binding; IEA.

; P:regulation of transcription, DNA-dependent; IEA.

08917; Euk transcr_DNA.

04827; TF_BZIP.

bZIP; 1.7%;

17; BZIP; 1.7%;

36; BZIP_BASIC; 1.7%;

nuclear protein.

AA; 23192 MW; CE6F8BACE7C3C203 CRC64;

1.7%; Score 9; DB 10; Length 217;

urity 100.0%; Pred. No. 17;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 127

|||||

AAAA 60

ELIMINARY; PRT; 217 AA.

EMBLrel. 24, Created)

EMBLrel. 24, Last sequence update)

EMBLrel. 25, Last annotation update)

protein.

japonica cultivar-group).

idiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzae; Oryza.

OC NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Sasaki T., Matsumoto T., Katayose Y.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC

clone:OJ9990 A01.1";

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AP005847; BAC65071.1; -.

DR InterPro; IPR004893; DUF260.

DR PROSITE; PS00891; LOB; 1.

SQ SEQUENCE 217 AA; 23641 MW; 1D6EC23E52DFBC3C CRC64;

Query Match 1.7%; Score 9; DB 10; Length 217;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDDEDEEE 341

Db 163 DDDEDEEE 171

RESULT 109

Q90764

ID Q90764 PRELIMINARY; PRT; 218 AA.

AC Q90764;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Transcriptional regulator.

GN ASH.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasian

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Wang S., Kirby M.L.;

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

CC -! SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMIL

CC TRANSCRIPTION FACTORS.

DR EMBL; L11871; AAA03722.1; -.

DR InterPro; IPR001092; HLH_basic.

DR Pfam; PF00010; HLH; 1.

DR SMART; SM00353; HLH; 1.

DR PROSITE; PS00038; HLH 1; 1.

DR PROSITE; PS00888; HLH 2; 1.

SQ SEQUENCE 218 AA; 22884 MW; A80B11AEC09B8211 CRC64;

Query Match 1.7%; Score 9; DB 13; Length 218;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Ga

QY 120 AAAAAAPP 128

Db 28 AAAAAAPP 36

RESULT 110

Q90575

ID Q90575 PRELIMINARY; PRT; 219 AA.

AC Q90575;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Achaete-scute homologue.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasian

OC 31; [N.A.
 RX 365; PubMed=7600956;
 RA Walker M.B., Morris M.D., Reh T.A.;
 RI haete-scute homolog (CASH-1) is expressed in a temporally
 RI discrete manner in the developing nervous system.";
 RL 20:769-783(1994).
 RL Y: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 RL PROTEIN FACTORS.
 DE AAC59658.1; -.
 DE I51382.
 DE J001092; HLH_basic.
 DE); HLH; 1.
 DE J3; HLH; 1.
 DE J038; HLH_1; 1.
 DE J888; HLH_2; 1.
 DE 9 AA; 22980 MW; 31AE76764BC58B43 CRC64;
 DE 1.7%; Score 9; DB 13; Length 219;
 DE Identity 100.0%; Pred. No. 17;
 DE Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE AAAAPP 128
 DE |||||
 DE AAAAPP 36
 DE
 DE PRELIMINARY; PRT; 231 AA.
 DE (TREMBLrel. 08, Created)
 DE (TREMBLrel. 08, Last sequence update)
 DE (TREMBLrel. 24, Last annotation update)
 DE sembly and synthesis protein precursor.
 DE aromaticivorans.
 DE
 DE teobacteria; Alphaproteobacteria; Sphingomonadales;
 DE iceae; Novosphingobium.
 DE J935;
 DE 4 N.A.
 DE Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C.,
 DE Gaasterland T., Saffer J.D., Fredrickson J.K.;
 DE nence of a 184 kb catabolic plasmid from Sphingomonas
 DE ms strain F199.";
 DE JL-1998) to the EMBL/GenBank/DBJ databases.
 DE J7; AAD03955.1; -.
 DE T31231.
 DE J1; C:extrachromosomal DNA; IEA.
 DE 1. 27 POTENTIAL.
 DE J1 AA; 24710 MW; 27F3C1F6664F258B CRC64;
 DE 1.7%; Score 9; DB 2; Length 231;
 DE Identity 100.0%; Pred. No. 18;
 DE Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE APARAP 149
 DE |||||
 DE APARAP 222
 DE
 DE PRELIMINARY; PRT; 235 AA.
 DE (TREMBLrel. 23, Created)
 DE (TREMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Bcl-2 protein.
 GN BCL-2.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Carnivora; Felidae; Felis.
 OC NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamazaki J., Sano J., Kano R., Hasegawa A.;
 RL "Felis catus mRNA for bcl-2, complete cds.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DE EMBL; AB096611; BAC24136.1; IEA.
 DE GO; GO:0016020; C:membrane; IEA.
 DE GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DE GO; GO:0006915; P:apoptosis; IEA.
 DE InterPro; IPR00712; Bcl2_BH.
 DE InterPro; IPR003093; Bcl2_BH4.
 DE InterPro; IPR002475; BCL2_family.
 DE InterPro; IPR004725; Bcl2_reg.
 DE Pfam; PF00452; Bcl-2; 1.
 DE Pfam; PF02180; BH4; 1.
 DE SMART; SM00337; BCL; 1.
 DE SMART; SM00265; BH4; 1.
 DE TIGRFAMs; TIGR00865; bcl-2; 1.
 DE PROSITE; PS50062; BCL2_FAMILY; 1.
 DE PROSITE; PS01080; BH1; 1.
 DE PROSITE; PS01258; BH2; 1.
 DE PROSITE; PS01259; BH3; 1.
 DE PROSITE; PS50063; BH4_2; 1.
 DE SEQUENCE 235 AA; 25621 MW; 2320B57C96B64548 CRC64;
 SQ
 Query Match 1.7%; Score 9; DB 6; Length 235;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 118 APAAAAAA 126
 DB |||||
 DB 70 APAAAAAA 78
 RESULT 113
 Q9AX02
 ID Q9AX02 PRELIMINARY; PRT; 239 AA.
 AC Q9AX02;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE P0492F05.10 protein (P0443E07.2 protein).
 GN P0492F05.10 OR P0443E07.2.
 OS Oryza sativa (Rice), and
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530, 39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O. sativa; STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0492F05.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases;
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O. sativa (japonica cultivar-group); STRAIN=cv. Nipponbare
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0443E07.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DE EMBL; AP002902; BAB32708.1; -.
 DE EMBL; AP002900; BAB92099.1; -.
 DE Gramene; Q9AX02; -.

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AA; 25914 MW; ACECLIFE777F78339 CRC64;
1.7%; Score 9; DB 10; Length 239;
rity 100.0%; Pred. No. 19;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAT 157
|||||
AAAT 194

RELIMINARY; PRT; 239 AA.

TREMBlrel. 25, Created)
TREMBlrel. 25, Last sequence update)
TREMBlrel. 25, Last annotation update)
protein.

nchiseptica (Alcaligenes bronchisepticus).
eobacteria; Betaproteobacteria; Burkholderiales;
; Bordetella.
;

N.A.
ATCC BAA-588;
954; PubMed=12910271;
Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Ja A.M., Temple L., James K., Harris B., Quail M.A.,
Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
T., Collins M., Cronin A., Davis P., Doggett J.,
Goble S., Norberczak H., O'Neill S., Ormond D., Price C.,
Rutter S., Saunders M., Saunders D., Seeger K.,
Woods M., Skelton J., Squares R., Squares S., Stevens K.,
Whithead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis,
capertussis and Bordetella bronchiseptica."
5:32-40(2003).
3; CAE30891.1; -.
protein; Complete proteome.
9 AA; 24495 MW; 5F6AB75BA5856581 CRC64;

arity 1.7%; Score 9; DB 16; Length 239;
rity 100.0%; Pred. No. 19;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||
AAAPA 161

RELIMINARY; PRT; 241 AA.

TREMBlrel. 25, Created)
TREMBlrel. 25, Last sequence update)
TREMBlrel. 25, Last annotation update)
protein.

teobacteria; Betaproteobacteria; Burkholderiales;
; Bordetella.
9;

N.A.
/ ATCC BAA-587;
954; PubMed=12910271;
Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

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RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Saunders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Steven;
RA Unwin L., Whithead S., Barrell B.G., Maskell D.J.;
RA "Comparative analysis of the genome sequences of Bordetella pertu
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640424; CAE35975.1; -.
KW Hydrothermal protein; Complete proteome.
SQ SEQUENCE 241 AA; 24663 MW; 5E49B6BL6P8A326F CRC64;

Query Match 1.7%; Score 9; DB 16; Length 241;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 138 APVAAAAAPA 146
Db 153 APVAAAAAPA 161
|||||

RESULT 116
Q9VET8 PRELIMINARY; PRT; 248 AA.
AC Q9VET8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG11769 protein.
GN CG11769.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananaitides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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RA assarman D.A., Weinstock G.M., Weissenbach J.,
RA Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA -F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA hong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA yers E.W., Rubin G.M., Venter J.C.,
RA sequence of Drosophila melanogaster."
RA 185-2195(2000).
RA 3; AAF55330.1; -.
RA 0038441; CG11769.
RA 8 AA; 26831 MW; 1E55A2CFF296C0F1 CRC64;
RA
RA 1.7%; Score 9; DB 5; Length 248;
RA arity 100.0%; Pred. No. 19;
RA conservative 0; Mismatches 0; Indels 0; Gaps 0;
RA
RA 'AAAA 23
RA '|||||
RA 'AAAA 41
RA
RA PRELIMINARY; PRT; 248 AA.
RA
RA (TREMBLrel. 20, Created)
RA (TREMBLrel. 20, Last sequence update)
RA (TREMBLrel. 24, Last annotation update)
RA yellow assembly protein FLIH.
RA 192 OR RS00820.
RA anacearum (Pseudomonas solanacearum).
RA blasmid.
RA teobacteria; Betaproteobacteria; Burkholderiales;
RA ceae; Ralstonia.
RA 05;
RA
RA 4 N.A.
RA 00;
RA 1879; PubMed=11823852;
RA Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA ilault A., Bottier P., Camus J.C., Cattolico L.,
RA Choise N., Claudel-Renard C., Cunac S., Demange N.,
RA vie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA thebault P., Whalen M., Wincker P., Levy M.,
RA J., Boucher C.A.;
RA ence of the plant pathogen Ralstonia solanacearum."
RA 97-502(2002).
RA
RA 78; CAD17543.1; -.
RA 21; C:extrachromosomal DNA; IEA.
RA 88; C:flagellum (sensu Bacteria); IEA.
RA 74; F:motor activity; IEA.
RA 39; P:ciliary/flagellar motility; IEA.
RA R000563; Flag_FliH.
RA 8; FliH; I.
RA 003; FLGFLIH.
RA plete proteome.
RA 48 AA; 26993 MW; 9CA196E0BC549D47 CRC64;
RA
RA 1.7%; Score 9; DB 16; Length 248;
RA larity 100.0%; Pred. No. 19;
RA conservative 0; Mismatches 0; Indels 0; Gaps 0;
RA
RA AAAPPP 129
RA '|||||
RA AAAPPP 38
RA
RA PRELIMINARY; PRT; 252 AA.
RA
RA (TREMBLrel. 22, Created)
RA (TREMBLrel. 22, Last sequence update)
RA (TREMBLrel. 25, Last annotation update)

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DE P0524E08.25 protein.
GN P0524E08.25.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_taxid=39947;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nipponbare;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0524E08."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004341; BAC10856.1; -.
DR Gramene; Q8LHK1; -.
DR InterPro; IPR008889; VQ.
DR Pfam; PF05678; VQ; 1.
DR SQ SEQUENCE 252 AA; 25166 MW; 9453D1A134A6634C CRC64;
DR
DR Query Match 1.7%; Score 9; DB 10; Length 252;
DR Best Local Similarity 100.0%; Pred. No. 19;
DR Matches 9; Conservative 0; Mismatches 0; Indels 0;
DR
DR QY 120 AAAAAAAPP 128
DR Db '|||||
DR 191 AAAAAAAPP 199
DR
DR RESULT 119
DR Q89LR9 PRELIMINARY; PRT; 262 AA.
DR AC Q89LR9;
DR DT 01-JUN-2003 (TREMBLrel. 24, Created)
DR DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DR DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DR DE BLR4474 protein.
DR BLR4474.
DR GN Bradyrhizobium japonicum.
DR OS Bradyrhizobium japonicum.
DR OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
DR OC Bradyrhizobiaceae; Bradyrhizobium.
DR OX NCBI_TaxID=375;
DR [1]
DR RN SEQUENCE FROM N.A.
DR RP STRAIN=USDA 110;
DR RC MEDLINE=22484998; PubMed=12597275;
DR RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
DR RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
DR RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada
DR RA Tabata S.;
DR RT "Complete genomic sequence of nitrogen-fixing symbiotic bacteriu
DR RT Bradyrhizobium japonicum USDA110."
DR RL DNA Res. 9:189-197(2002).
DR EMBL; AP005951; BAC49739.1; -.
DR KW Complete proteome.
DR SQ SEQUENCE 262 AA; 27675 MW; 1F590E2B275473E9 CRC64;
DR
DR Query Match 1.7%; Score 9; DB 16; Length 262;
DR Best Local Similarity 100.0%; Pred. No. 20;
DR Matches 9; Conservative 0; Mismatches 0; Indels 0;
DR
DR QY 131 PAPPPPAP 139
DR Db '|||||
DR 81 PAPPPPAP 89
DR
DR RESULT 120
DR Q9A8M0 PRELIMINARY; PRT; 273 AA.
DR ID Q9A8M0
DR AC Q9A8M0;
DR DT 01-JUN-2001 (TREMBLrel. 17, Created)
DR DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DR DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

```

a polymerase-related protein.
 centus.
 eobacteria; Alphaproteobacteria; Caulobacterales;
 eae; Caulobacter.
 5892;
 N.A.
 3089 / CBJ5;
 598; PubMed=11259647;
 Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 Jørgensen J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 Oson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 Venter J.C., Shapiro L., Fraser C.M.;
 "The genome sequence of Caulobacter crescentus";
 cad. Sci. U.S.A. 98:4136-4141(2001).
 8; AAK23314.1; --
 F87414.
 --
 005273; SP01polNrel.
 005122; UDNA_glycylisef.
 ; UDG; 1.
 R00758; SP01polNrel; 1.
 some.
 3 AA; 29214 MW; CR54307D81568194 CRC64;
 1.7%; Score 9; DB 16; Length 273;
 arity 100.0%; Pred.No.21;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PAPVA 141
 |||||
 PAPVA 55
 RELIMINARY; PRT; 274 AA.
 TREMBLrel. 13, Created
 TREMBLrel. 13, Last sequence update)
 TREMBLrel. 22, Last annotation update)
 in.
 lanogaster (Fruit fly).
 tacea; Arthropoda; Hexapoda; Insecta; Pterygota;
 opterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 27;
 N.A.
 ey;
 006; PubMed=10731132;
 elinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 He C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Ghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Busam D.A., Butler H., Center A., Center A., Chandra I.,
 Cawley S., Dahlke C., Davenport L.B., Davies P.,
 DeLcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Eup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR FlyBase; FBgn0038794; CG17205.
 SQ SEQUENCE 274 AA; 30624 MW; 1AA91C5120C2DDF7 CRC64;
 Query Match 1.7%; Score 9; DB 5; Length 274;
 Best Local Similarity 100.0%; Pred.No.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; C

Qy 335 DEDEDEDD 343
 |||||
 Db 129 DEDEDEDD 137
 RESULT 122
 Q9SNS1 PRELIMINARY; PRT; 276 AA.
 AC Q9SNS1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
 clone:FO535G04";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP000399; BAA8355.1; --
 DR Gramene; Q9SNS1; --
 KW Hypothetical protein.
 SQ SEQUENCE 276 AA; 29463 MW; 62B4AA1069536447 CRC64;
 Query Match 1.7%; Score 9; DB 10; Length 276;
 Best Local Similarity 100.0%; Pred.No.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; C

Qy 121 AAAAAPP 129
 |||||
 Db 79 AAAAAPP 87
 RESULT 123
 Q9S1P7 PRELIMINARY; PRT; 278 AA.
 ID Q9S1P7;
 AC Q9S1P7;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)

TREMBLrel. 21, Last sequence update)
TREMBLrel. 25, Last annotation update)
binding protein.

(japonica cultivar-group).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Oryzaeae; Oryza.
947;

[N.A.
pponbare;
tsumoto T., Yamamoto K.;
nipponbare (GA3) genomic DNA, chromosome 1, PAC
B-2001) to the EMBL/GenBank/DBJ databases.
Y: BELONGS TO THE BZIP FAMILY.
6; BAB9789.1; -.
P7; -.
4; C:nucleus; IEA.
7; P:DNA binding; IEA.
5; P:regulation of transcription, DNA-dependent; IEA.
004827; TF_BZIP.
; BZIP; 1.
8; BRLZ; 1.
0217; BZIP; 1.
0036; BZIP BASIC; 1.
Nuclear protein.
18 AA; 29688 MW; 9425F64C16D2A0FA CRC64;

1.7%; Score 9; DB 10; Length 278;
larity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAP 127

AAAAAP 108

PRELIMINARY; PRT; 278 AA.

(TREMBLrel. 01, Created)
(TREMBLrel. 01, Last sequence update)
(TREMBLrel. 25, Last annotation update)
ise.

virus (strain Kaplan) (PRV).
NA viruses, no RNA stage; Herpesviridae;
irinae; Varicellovirus.
3703;

4 N.A.

1;
9740; PubMed=8806172;

Bras F., Vende P., Simonet B., Nguyen X., Flamand A.,

ragment 9 of pseudorabies virus contains genes homologous
UL25, UL26, and UL26.5 genes of herpes simplex virus

2:27-39(1996).

; CAA65010.1; -.
001; -.
33; F:peptidase activity; IEA.

78 AA; 28198 MW; E0AD4E74C395273F CRC64;

1.7%; Score 9; DB 12; Length 278;
larity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAA 126

Db 212 APAAAAAA 220
|||||

RESULT 125

Q15415 PRELIMINARY; PRT; 279 AA.

ID O15415;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE CAGH3.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97369492; PubMed=9225980;

RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.

RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;

RT "CDNAS with long CAG trinucleotide repeats from human brain.;"

RL Hum. Genet. 100:114-122(1997).

DR EMBL; U80747; AAB91445.1; -.
DR Genbank; HGNC:11966; TNRC3.

DR GO; GO:0005634; C:nucleus; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.

DR GO; GO:0007393; P:neurogenesis; TAS.

SQ SEQUENCE 279 AA; 31630 MW; 3C571297D422DA04 CRC64;

Query Match 1.7%; Score 9; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 21;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 222 QQQQPPPPQ 230

Db 175 QQQQPPPPQ 183

RESULT 126

Q86NQ6

ID Q86NQ6 PRELIMINARY; PRT; 280 AA.

AC Q86NQ6;

DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE RE01075P.

GN ECT.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Y;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Dreenek D., Farfan D., Friese E

RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.

RA Miranda A., Mungali C.J., Nunoo J., Pacleb J., Paragas V., Park

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M

RA Celniker S.;

RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BT003781; AAC41462.1; -.
DR EMBL; BT003781; AAC41462.1; -.
SQ SEQUENCE 280 AA; 29519 MW; 73BECA0FC7A7C10 CRC64;

Query Match 1.7%; Score 9; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 21;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 330 EEDDEDE 338

|||||
DEDE 87

ELIMINARY; PRT; 281 AA.

EMBLrel. 12, Created)
EMBLrel. 12, Last sequence update)
EMBLrel. 24, Last annotation update)
ative SWI/SNF complex subunit BAF170.
(Rice).

idiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryzae; Oryza.

10;

N.A.

ponbare;
sumoto T., Yamamoto K.;
Nipponbare (GA3) genomic DNA, chromosome 2, PAC

(Contig b).";
1999) to the EMBL/GenBank/DBJ databases.

7; BAA82389.1; -.

L5; -.

007526; SWIRM.

SWIRM; 1.

1 AA; 28773 MW; AACCE096AC53156 CRC64;

arity 100.0%; Pred. No. 21; Length 281;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126

|||||

AAAAA 79

ELIMINARY; PRT; 282 AA.

EMBLrel. 22, Created)

EMBLrel. 22, Last sequence update)

EMBLrel. 24, Last annotation update)

tein L4.

haliana (Mouse-ear cress).

ridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Magnoliophyta; eudicotyledons; core eudicots; rosids;

Brassicales; Brassicaceae; Arabidopsis.

02;

N.A.

lfovsky N., Town C.D., Troukhan M., Alexandrov N.,

Flavell R.B., White O., Salzberg S.L.;

messenger RNA sequences greatly improve genome

0:0-0(2002).

1 N.A.

oukhan M., Alexandrov N., Lu Y.-P., Flavell R.,

CDNA from Arabidopsis thaliana";

R-2002) to the EMBL/GenBank/DBJ databases.

1; AAM61637.1; -.

2; C:intracellular; IEA.

0; C:ribosome; IEA.

5; F:structural constituent of ribosome; IEA.

2; P:protein biosynthesis; IEA.

002136; Ribosomal_L4/LuE.

; Ribosomal L4; 1.

12 AA; 30584 MW; 0809CC09EA60E79C CRC64;

Query Match 1.7%; Score 9; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G.

QY 330 EEEDDEDE 338

DB 267 EEEDDEDE 275

RESULT 129

Q9RBF9 PRELIMINARY; PRT; 283 AA.

ID Q9RBF9

AC Q9RBF9

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Alcaligenes eutrophus (Ralstonia eutropha).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Ralstonia.

OX NCBI_TaxID=510;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=335; Schloemann M.;

RA "Characterization of a Gene Cluster Encoding the Maleylacetate

RT Reductase from Ralstonia eutropha 335, an Enzyme Recruited for Gr

RT with 4-Fluorobenzoate.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF130250; AAD55888.1; -.

DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact.;

DR GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.

DR InterPro; IPR001853; DSBA.

DR Pfam; PF01323; DSBA; 1.

KW Hypothetical protein.

SQ SEQUENCE 283 AA; 31479 MW; 4FCD36A6C0C70518 CRC64;

Query Match 1.7%; Score 9; DB 2; Length 283;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 117 GAPAAAAA 125

DB 20 GAPAAAAA 28

RESULT 130

Q8IQD9

ID Q8IQD9

AC Q8IQD9

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CG6611-PC.

GN ECT OR CG6611 OR CG11965.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Spheroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.

RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkuch C., Baldwin I

RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.N

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Botchan M.R., Bouck J., Brokstein P., Brottier P., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I., Cawley S., Dahle C., Davenport L.B., Davies P., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Iribeliana A.E., Garg N.S., Gelbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Huston K.A., Howland T.J., Wei M.H., Ibegwam C., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X., Li Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Shi B., McIntosh T.C., McLeod M.P., McPherson D., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Remington K., Saunders R.D., Scheeler F., Shen H., Iden-Kiamos I., Simpson M., Skupski M.P., Smith T., Tardif A.C., Stapleton M., Strong R., Sun E., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wasserman D.A., Weinstein G.M., Weissbach J., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Veri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Myers E.W., Rubin G.M., Venter J.C.; sequence of *Drosophila melanogaster*.; 2185-2195(2000).

OM N.A.
Adams M.D., Krontz B., Wan K.H., Holt R.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D., Bonzon J., Beeson K.Y., Busam D.A., Center A., Champs D., Davenport L.B., Dietz S.M., Dorsett V., Dou P.L., Doyle C., Dresnek D., Farfan D., Frise E., Galle R.F., Garg N.S., George R.A., Houck J., Hoskins R.A., Hostin D., Howland T.J., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Paragas V., Park S., Patel S., Pfeiffer B., Pittman G.S., Puri V., Richards S., Scheeler F., Strong R., Svirskaas R., Tector C., Tyler D., Vaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; of *Drosophila melanogaster* genome.;

VAR-2000) to the EMBL/GenBank/DBJ databases.

OM N.A.
Rooby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D., Bergman C., Berman B., Carlson J.W., Celniker S.E., Rysdale R., Emmert D., Frise E., de Grey A., Harris N., Marshall B., Millburn G., Richter J., Russo S., Smith E., Shu S., Smutnicki F., Whitfield E., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; of *Drosophila melanogaster* genome.;

VAR-2000) to the EMBL/GenBank/DBJ databases.

OM N.A.
Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; MAR-2000) to the EMBL/GenBank/DBJ databases.

OM N.A.

(SEP-2002) to the EMBL/GenBank/DBJ databases.

1549; AAN11922.1; -

3900000451; ect.

283 AA; 30272 MW; 3E7B16C02CEB1C2C CRC64;

1.7%; Score 9; DB 5; Length 283;

ilarity 100.0%; Pred. No. 22; 0; Indels

Conservative 0; Mismatches

0; Gaps 0;

0;

QY 330 EEDDEDE 338
Db 79 EEDDEDE 87
RESULT 131
Q814H9 PRELIMINARY; PRT; 287 AA.
ID Q814H9
AC Q814H9
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE C. elegans sdn-1 protein (corresponding sequence F57C7.3b).
GN F57C7.3 OR SDN-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditos
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RX [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z69646; CAD44142.1; -.
DR WormPep; F57C7.3b; CE32681.
DR GO; GO:0016020; C:membrane; IEA.
DR DR GO; GO:0008032; F:cytoskeletal protein binding; IEA.
DR DR InterPro; IPR001050; Syndecan.
DR DR Pfam; PF01034; Syndecan; 1.
DR DR PROSITE; PS00964; SYNDSCAN; 1.
SQ SEQUENCE 287 AA; 30851 MW; C947CF0A7FC95B5C CRC64;

Query Match 1.7%; Score 9; DB 5; Length 287;

Best Local Similarity 100.0%; Pred. No. 22; 0; Indels

Matches 9; Conservative

0; Mismatches

0;

QY 332 EDDDEDE 340

Db 144 EDDDEDE 152

RESULT 132

Q9BUP6 PRELIMINARY; PRT; 306 AA.

ID Q9BUP6

AC Q9BUP6

DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom

OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg K.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler C.

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.I.

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheet;

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne I

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huly

DE Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 ON E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 OS Adan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 OC Touchman J.W., Green E.D., Dickson M.C.,
 OC Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 OX I., Skalska U., Smalish D.E., Schermer A., Schein J.E.,
 RN Arria M.A.,
 RP and initial analysis of more than 15,000 full-length human
 RX A sequences.";
 RA cad. Sci. U.S.A. 99:16899-16903 (2002).
 RT N.A.
 RL B-2001) to the EMBL/GenBank/DBJ databases.
 DR 1; AA02431.2; -.
 DR protein.
 KW 6 AA; 34992 MW; A48380BC0452841B CRC64;
 FT 1.7%; Score 9; DB 4; Length 306;
 FT arity 100.0%; Pred.No.23;
 FT conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ AATAP 159
 AATAP 17
 RELIMINARY; PRT; 308 AA.
 TREMBLrel. 19, Created)
 TREMBLrel. 19, Last sequence update)
 TREMBLrel. 25, Last annotation update)
 ULcerans.
 inobacteria; Actinobacteridae; Actinomycetales;
 neae; Mycobacteriaceae; Mycobacterium.
 09;
 [N.A.
 '541; PubMed=11496008;
 L., Picardeau M., Raynaud C., Rauzier J.,
 Salmoniere Y.-O., Barker L., Bigi F., Cataldi A.,
 'eyrat J.-M.,
 'acellular protein family specific to mycobacteria.";
 147:2315-2320(2001).
 4; AAK82955.1; -.
 008164; XGLTT_repeat.
 ; GLTT; 1.
 1 22 POTENTIAL.
 23 308 ERP.
 08 AA; 29436 MW; 86D5D06C184EFEC2 CRC64;
 1.7%; Score 9; DB 2; Length 308;
 arity 100.0%; Pred.No.23;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAAA 126
 AAAAAA 303
 PRELIMINARY; PRT; 309 AA.
 (TREMBLrel. 19, Created)
 (TREMBLrel. 19, Last sequence update)
 (TREMBLrel. 25, Last annotation update)

DE Exp precursor.
 GN ERP.
 OS Mycobacterium marinum.
 OC Bacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21387541; PubMed=11496008;
 RA Mendonca-Lima L., Picardeau M., Raynaud C., Rauzier J.,
 RA Goguet de al Salmoniere Y.-O., Barker L., Bigi F., Cataldi A.,
 RA Gicquel B., Reytrat J.-M.;
 RT "Exp, an extracellular protein family specific to mycobacteria.";
 RL Microbiology 147:2315-2320(2001).
 DR EMBL; AF213153; AAK82954.1; -.
 DR InterPro; IPR008164; XGLTT_repeat.
 DR Pfam; PF01744; GLTT; 1.
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 309 ERP.
 SQ SEQUENCE 309 AA; 29492 MW; 1BBEE6DF1C39C53 CRC64;
 Query Match 1.7%; Score 9; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred.No.23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 QY 118 AAAAAAAAAA 126
 DB 296 AAAAAAAAAA 304
 RESULT 135
 Q9GRZ1
 ID Q9GRZ1 PRELIMINARY; PRT; 316 AA.
 AC Q9GRZ1;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Y59A8B.7 protein.
 GN Y59A8B.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoi;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sulston J.E.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; AL132898; CAC14408.1; -.
 DR WormP; Y59A8B.7; CE26217.
 DR GO; GO:008017; F:microtubule binding; IEA.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR004953; EBI.
 DR Pfam; PF03037; CH; 1.
 DR Pfam; PF03271; EBI; 1.
 DR SQ SEQUENCE 316 AA; 34854 MW; CA505FD16E3387E4 CRC64;
 Query Match 1.7%; Score 9; DB 5; Length 316;
 Best Local Similarity 100.0%; Pred.No.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 120 AAAAAAAPP 128
 DB 218 AAAAAAAPP 226

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PRELIMINARY; PRT; 316 AA.
(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 25, Last annotation update)
ribosomal protein P0.
casipalpis.
stazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Pterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
3; Sarcophaga.
3312;

M N.A.
0706; PubMed=11024299;
Denlinger D.L.;
3 transcription patterns of 60S ribosomal protein P0, a
ulated AP endonuclease in the flesh fly, Sarcophaga
";
-388 (2000).
39; AAF31449.1; -.
22; C:intracellular; IEA.
40; C:ribosome; IEA.
35; F:structural constituent of ribosome; IEA.
14; P:translational elongation; IEA.
R001813; Ribosomal_L10.
R001790; Ribosomal_L10.
8; 60S ribosomal; I.
5; Ribosomal_L10; 1.
otein.
16 AA; 34095 MW; 0EF6152DA9A77572 CRC64;

1.7%; Score 9; DB 5; Length 316;
larity 100.0%; Pred. No. 24;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATAP 159
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AAATAP 284

PRELIMINARY; PRT; 316 AA.
(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 24, Last annotation update)
rabidopsis thaliana chromosome 5 BAC clone F21E10.
(Rice).
iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
e; Oryzae; Oryza.
530;

M N.A.
ipponbare;
atsumoto T., Yamamoto K.;
a nipponbare(GA3) genomic DNA, chromosome 1, PAC
'05.";
UN-2000) to the EMBL/GenBank/DBJ databases.

M N.A.
ipponbare;
atsumoto T., Yamamoto K.;
a nipponbare(GA3) genomic DNA, chromosome 1, PAC
'01.";
IAR-2000) to the EMBL/GenBank/DBJ databases.
ILAR LOCATION: NUCLEAR (BY SIMILARITY).
TY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
; 80; BAA96556.1; -.

EMBL; AP002070; BAA95850.1; -.
DR Gramene; Q9LD92; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regul
SQ SEQUENCE 316 AA; 34240 MW; DB4E00CD509EF819 CRC64;

Query Match 1.7%; Score 9; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 131 PAPPPPPPAP 139
Db 179 PAPPPPPPAP 187

RESULT 138
Q9AYL3 PRELIMINARY; PRT; 316 AA.
AC Q9AYL3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative carnitine/acylcarnitine translocase.
GN OSUNBA003019.8.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RA "Oryza sativa chromosome 10 BAC OSUNBA003019 genomic sequence."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC060755; AAK00443.1; -.
DR Gramene; Q9AYL3; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 316 AA; 31554 MW; 61B69BB6012BCB86 CRC64;

Query Match 1.7%; Score 9; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 118 APAAAAAA 126
Db 142 APAAAAAA 150

RESULT 139
Q7XBY4 PRELIMINARY; PRT; 316 AA.
ID Q7XBY4
AC Q7XBY4;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative carnitine/acylcarnitine translocase.

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26 1.8.
27 (japonica cultivar-group).
28 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
29 ; Magnoliophyta; Liliopsida; Poales; Poaceae;
30 ; Oryzae; Oryza.
31 947;
32 N.A.
33 pponbare;
34 mosome 10 Sequencing Consortium;
35 w of structure, activity, and evolution of rice
36 ;
37 566-1569(2003).
38 N.A.
39 pponbare;
40 ing R.A., McCombie W.R., Messing J., Yuan Q.;
41 Y-2003) to the EMBL/GenBank/DBJ databases.
42 1; AAP5124.1; -.
43 6 AA; 31554 MW; 61869BB6012BCB86 CRC64;
44 1.7%; Score 9; DB 10; Length 316;
45 arity 100.0%; Pred. No. 24;
46 conservative 0; Mismatches 0; Indels 0; Gaps 0;
47
48 AAAAA 126
49 |||||
50 AAAAA 150
51
52 RELIMINARY; PRT; 317 AA.
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54 TREMBLrel. 15, Created)
55 TREMBLrel. 15, Last sequence update)
56 TREMBLrel. 25, Last annotation update)
57 bosomal protein PO (Fragment).
58 lla (leafy spurge).
59 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
60 ; Magnoliophyta; eudicotyledons; core eudicots; rosids;
61 Malpighiales; Euphorbiaceae; Euphorbiaceae; Euphorbiaceae;
62 193;
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64 N.A.
65 , Horvath D.P.;
66 on of mRNAs expressed in underground adventitious buds of
67 lla (leafy spurge).";
68 N-2000) to the EMBL/GenBank/DBJ databases.
69 12; AAF34767.1; -.
70 12; C:intracellular; IEA.
71 0; C:ribosome; IEA.
72 5; F:structural constituent of ribosome; IEA.
73 4; P:translational elongation; IEA.
74 001813; Ribosomal_L10.
75 001790; Ribosomal_L10.
76 60s ribosomal; 1.
77 ; Ribosomal_L10; 1.
78 stein.
79 1
80 .7 AA; 33738 MW; 3761F2EE62AF4F4A CRC64;
81 1.7%; Score 9; DB 10; Length 317;
82 larity 100.0%; Pred. No. 24;
83 conservative 0; Mismatches 0; Indels 0; Gaps 0;
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85 AAAAA 146
86 |||||
87 AAAAA 288
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ilarity 100.0%; Pred. No. 24;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 39

PRELIMINARY; PRT; 322 AA.

(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)

elanogaster (Fruit fly).
stazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
227;

M N.A.

ley;
Brokstein P., Hong L., Agbavani A., Carlson J.,
havez C., Dorsett V., Farfan D., Frise E., George R.,
Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
cleb J., Fargas V., Park S., Phouanavong S., Wan K.,
S.E., Rubin G.M., Celnikier S.;
UG-2001) to the EMBL/GenBank/DBJ databases.
36; AAK93060.1; -
n0031965; CG7093.
22 AA; 35090 MW; BD70B7CCE322EA4F CRC64;

1.7%; Score 9; DB 5; Length 322;

ilarity 100.0%; Pred. No. 24;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDEED 342
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DEDEED 151

PRELIMINARY; PRT; 325 AA.

(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
xpressed 10.
(Human).

etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
606;

M N.A.

heral Nervous System;

..;
PR-2003) to the EMBL/GenBank/DBJ databases.
59; AAH50659.1; -
76; P-nucleic acid binding; IEA.
R005162; Retrotrans_gag.
R001878; Znf_CCHC.
2; Retrotrans_gag; 1.
18; ZF-CCHC; 1.
1939; C2HCZNFINGER.
10158; ZF_CCHC; 1.
125 AA; 36965 MW; 118E4CFAF97F2A76 CRC64;

1.7%; Score 9; DB 4; Length 325;
ilarity 100.0%; Pred. No. 24;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 121 AAAAAAPP 129
|||||
DB 64 AAAAAAPP 72

RESULT 145

Q7XPH4 PRELIMINARY; PRT; 325 AA.

AC Q7XPH4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE OSJNB0003B01.9 protein.
GN OSJNB0003B01.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Wu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., L
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606649; CAE03618.1; -
SQ SEQUENCE 325 AA; 35096 MW; 3F1C483A61C0FCAD CRC64;

Query Match 1.7%; Score 9; DB 10; Length 325;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 19 AAAAASSAA 27
|||||
DB 33 AAAAASSAA 41

RESULT 146

Q871D4 PRELIMINARY; PRT; 328 AA.

AC Q871D4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT Hypothetical protein B8G12.135.
GN B8G12.135.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Hollar
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX294027; CAD71073.1; -
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 34350 MW; 760420D2C40A6EB5 CRC64;

Query Match 1.7%; Score 9; DB 3; Length 328;

Best Local Similarity 100.0%; Pred. No. 24;

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nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAPP 128
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AAAPP 280

RELIMINARY; PRT; 328 AA.

TrEMBLrel. 24, Created)
TrEMBLrel. 24, Last sequence update)
TrEMBLrel. 25, Last annotation update)
tin-like protein.
appendiculatus (Brown ear tick).
araoa; Arthropoda; Chelicerata; Arachnida; Acari;
s; Ixodida; Ixodidae; Rhipicephalus.
531;

N.A.
igimoto C., Onuma M.;
s appendiculatus midgut galleitin-like protein.";
3-2002) to the EMBL/GenBank/DBJ databases.
7; AAC60051.1; -.
008985; ConA like lec_gl.
001079; Galleitin.
; Gal-bind_lectin; 1.
5; GLECT; 2.
3 AA; 36185 MW; 90BFD7322818CAB CRC64;

1.7%; Score 9; DB 5; Length 328;
arity 100.0%; Pred.No. 24;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 298

RELIMINARY; PRT; 333 AA.

TrEMBLrel. 24, Created)
TrEMBLrel. 24, Last sequence update)
TrEMBLrel. 25, Last annotation update)
form of TSLC-1.
(Human).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
06;

N.A.

y., Nagano T.;
secretory isoform of SGISF/TSLC-1.";
I-2002) to the EMBL/GenBank/DBJ databases.
6; BAC66178.1; -.
003599; IG.
007110; IG-like.
003598; IG_c2.
; IG; 3.
9; IG; 3.
8; IGC2; 3.
835; IG LIKE; 3.
3 AA; 36915 MW; D7C1102F46D08492 CRC64;

1.7%; Score 9; DB 4; Length 333;
arity 100.0%; Pred.No. 25;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 120 AAAAAAAPP 128
Db 14 AAAAAAAPP 22

RESULT 149
Q84J51 PRELIMINARY; PRT; 333 AA.
AC Q84J51; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative peroxisomal Ca-dependent solute carrier protein (Hypothe
protein QJAI364E02.4).
GN QJAI364E02.15 OR QJAI364E02.4.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
SEQUENCE FROM N.A.
RP Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K.;
RT "Rice Genomic Sequence.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135208; AAP06887.1; -.
DR EMBL; AC139168; AAP06894.1; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Hypothetical protein.
SQ SEQUENCE 333 AA; 36347 MW; F6E1EEA3E08D45C CRC64;

Query Match 1.7%; Score 9; DB 10; Length 333;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 222 QQQQPPPPQ 230
Db 18 QQQQPPPPQ 26

RESULT 150
Q8C4L5 PRELIMINARY; PRT; 333 AA.
AC Q8C4L5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical SNF2 related domain containing protein.
GN BC004701 OR D330021P09RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotati
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK081756; BAC38321.1; -.
DR MGI; MGI:2384292; BC004701.
DR InterPro; IPR008941; TPR-like.

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11:33:42 2004

us-09-976-740-43.olig.rspt

EW

protein.

13 AA; 36271 MW; 2B3B61EF7E32CBD1 CRC64;

1.7%; Score 9; DB 11; Length 333;

arity 100.0%; Pred.No. 25;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

DEDED 342

|||||

DEDED 123

DE

Se

March 30, 2004, 15:02:09

JO

s

11:33:41 2004

us-09-976-740-43.olig.rsp

GenCore version 5.1.6
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in search, using sw model

sch 30, 2004, 14:54:51 ; Search time 18 Seconds
(without alignments)

1556.319 Million cell updates/sec

-09-976-740-43

3

MAGPPALPPETATAAATAA.....HIKVLQGHFEDDDPDGFLG 538

IGO

pop 60.0 , Gapext 60.0

1681 seqs, 52070155 residues

cs satisfying chosen parameters: 141681

eth: 0

eth: 2000000000

isting first 150 summaries

wissProt_42:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

seq	length	DB	ID	Description
2.0	239	1	CENB_SHEEP	P49451 ovis aries
2.0	808	1	Y066 NPVAC	P41467 autographa
2.0	892	1	ATX7 HUMAN	O15265 homo sapien
1.9	75	1	MSDA DROME	Q9VB16 drosophila
1.9	260	1	A32E MOUSE	P97822 mus musculus
1.9	275	1	HXA5 HETER	Q9JA23 heterodontu
1.9	403	1	FXQ1 HUMAN	Q9C009 homo sapien
1.9	469	1	FXGA HUMAN	P55316 homo sapien
1.9	557	1	ACH1 SCHGR	P23414 schistocerc
1.9	579	1	Z384 RAT	Q9eqj4 rattus norv
1.9	613	1	RPSD ECOLI	P00579 escherichia
1.9	615	1	RPSD SALTY	P07336 salmonella
1.9	621	1	VP40 HSVBC	P54817 bovine herp
1.9	678	1	GARP PLAFB	P13816 plasmodium
1.9	1054	1	RDGB DROME	P43125 drosophila
1.9	1362	1	BRD4 HUMAN	O60885 homo sapien
1.9	1461	1	TOP2 CANAL	P87078 candida alb
1.9	1887	1	FAS2 YEAST	P19077 s fatty aci
1.7	109	1	RLA1 MAIZE	P52855 zea mays (m
1.7	109	1	RLA1 TRYCR	P28643 trypanosoma
1.7	158	1	RK12 ORYSA	O22386 oryza sativ
1.7	178	1	RPOE LISMO	Q8Y494 listeria mo
1.7	228	1	V33P ADE02	P24939 human adeno
1.7	229	1	V33P ADE05	P24940 human adeno
1.7	254	1	BRX1 MOUSE	Q9er42 mus musculu
1.7	272	1	TRPC MYCTU	O06129 mycobacteri
1.7	282	1	RK4 ARATH	O50061 arabidopsis
1.7	288	1	SDC CAEL	P50605 caenorhabdi
1.7	376	1	HMEV DROME	P06602 drosophila
1.7	415	1	RL3 DROME	O16797 drosophila
1.7	416	1	EVX1 MOUSE	P23683 mus musculu
1.7	440	1	Y77A STRCO	Q9f1y6 streptomyce
1.7	482	1	BHB3 HUMAN	Q9c0j9 homo sapien

HLX1_HUMAN	1	488	1.7	9	34
MOT3_YEAST	1	490	1.7	9	35
PIAG_MOUSE	1	507	1.7	9	36
SIS2_YEAST	1	562	1.7	9	37
FXJ2_MOUSE	1	565	1.7	9	38
FXJ2_HUMAN	1	574	1.7	9	39
ZIC5_HUMAN	1	639	1.7	9	40
ELS_RAT	1	864	1.7	9	41
A180_MOUSE	1	901	1.7	9	42
A180_RAT	1	915	1.7	9	43
MCR_HUMAN	1	984	1.7	9	44
IF3A_ARATH	1	987	1.7	9	45
KOG1_HUMAN	1	1065	1.7	9	46
IFH1_YEAST	1	1085	1.7	9	47
MSH3_HUMAN	1	1137	1.7	9	48
NRDC_HUMAN	1	1150	1.7	9	49
IE18_PRIVIF	1	1461	1.7	9	50
MTS3_HUMAN	1	2004	1.7	9	51
NCO6_MOUSE	1	2063	1.7	9	52
MLL4_HUMAN	1	2715	1.7	9	53
DY1B_CHLRE	1	4513	1.7	9	54
ANP3_PSEAM	1	37	1.5	8	55
ANPA_PSEAM	1	82	1.5	8	56
ANP4_PSEAM	1	85	1.5	8	57
ANPX_PSEAM	1	91	1.5	8	58
ANPY_PSEAM	1	91	1.5	8	59
ANP_IIMFE	1	97	1.5	8	60
CU02_BLACK	1	99	1.5	8	61
RL12_METVA	1	99	1.5	8	62
HSP3_RAT	1	104	1.5	8	63
RLA2_DICDI	1	105	1.5	8	64
RL12_ARCFU	1	106	1.5	8	65
RLA1_CABEL	1	111	1.5	8	66
RLA1_DROME	1	112	1.5	8	67
RLA2_EINTE	1	114	1.5	8	68
ASF2_HELAN	1	121	1.5	8	69
SECR_PIG	1	131	1.5	8	70
RS16_BRUME	1	134	1.5	8	71
SR14_HUMAN	1	136	1.5	8	72
HEX9_ADE07	1	138	1.5	8	73
RL34_AETR	1	138	1.5	8	74
RNS3_STRAU	1	141	1.5	8	75
WHM1_WHEAT	1	146	1.5	8	76
WHW2_WHEAT	1	148	1.5	8	77
HMGL_VICFA	1	149	1.5	8	78
RS16_CAUCR	1	165	1.5	8	79
OM19_BRUME	1	177	1.5	8	80
REMS_CHICK	1	200	1.5	8	81
PSAD_HORVU	1	205	1.5	8	82
YNP2_CABEL	1	205	1.5	8	83
HS27_CANFA	1	209	1.5	8	84
HM1X_HUMAN	1	211	1.5	8	85
RS5_CORGL	1	211	1.5	8	86
RSMB_RAT	1	214	1.5	8	87
HANI_HUMAN	1	215	1.5	8	88
RSMB_MOUSE	1	231	1.5	8	89
UCRI_NEUCR	1	231	1.5	8	90
RSMB_CHICK	1	240	1.5	8	91
RSMB_ERIEU	1	240	1.5	8	92
RSMB_MONDO	1	240	1.5	8	93
YPBE_BACSU	1	240	1.5	8	94
AX28_SOYBN	1	243	1.5	8	95
PEA_MYCLE	1	249	1.5	8	96
RPC8_YEAST	1	251	1.5	8	97
YU95_MYCTU	1	255	1.5	8	98
GSHI_MOUSE	1	261	1.5	8	99
GSHI_HUMAN	1	264	1.5	8	100
HXA9_MOUSE	1	271	1.5	8	101
HXA9_HUMAN	1	272	1.5	8	102
ASF1_YEAST	1	279	1.5	8	103
CEBE_RAT	1	281	1.5	8	104

Q14774 homo	1	488	1.7	9	34
P54785 sacc	1	490	1.7	9	35
Q9Jm05 mus	1	507	1.7	9	36
P36024 sacc	1	562	1.7	9	37
Q9es18 mus	1	565	1.7	9	38
Q9p0x8 homo	1	574	1.7	9	39
Q9et25 homo	1	639	1.7	9	40
Q99372 ratt	1	864	1.7	9	41
Q61548 mus	1	901	1.7	9	42
Q05140 ratt	1	915	1.7	9	43
P08235 homo	1	984	1.7	9	44
Q9ld55 arab	1	987	1.7	9	45
O75912 homc	1	1065	1.7	9	46
P39520 sacc	1	1085	1.7	9	47
P20585 homo	1	1137	1.7	9	48
O43847 homo	1	1150	1.7	9	49
P11675 pseu	1	1461	1.7	9	50
Q92794 homc	1	2004	1.7	9	51
Q14686 h nu	1	2063	1.7	9	52
Q9J119 m nu	1	2715	1.7	9	53
Q9umf6 homc	1	4513	1.7	9	54
Q9mbf8 chla	1	37	1.5	8	55
P02733 pseu	1	82	1.5	8	56
P04002 pseu	1	85	1.5	8	57
P07835 pseu	1	91	1.5	8	58
P23699 pseu	1	91	1.5	8	59
P09031 lima	1	97	1.5	8	60
P08076 blat	1	99	1.5	8	61
P10623 meth	1	99	1.5	8	62
Q84256 ratt	1	104	1.5	8	63
P22683 dict	1	105	1.5	8	64
Q28780 arch	1	106	1.5	8	65
P91913 caer	1	111	1.5	8	66
P08570 droe	1	112	1.5	8	67
Q967y3 eime	1	114	1.5	8	68
P22184 heli	1	121	1.5	8	69
P01279 sus	1	131	1.5	8	70
Q8YJ59 bruc	1	134	1.5	8	71
P37108 homc	1	136	1.5	8	72
P03283 huma	1	138	1.5	8	73
Q9nb34 aede	1	138	1.5	8	74
P30289 stre	1	141	1.5	8	75
O64392 trit	1	146	1.5	8	76
O64393 trit	1	148	1.5	8	77
O40620 vici	1	149	1.5	8	78
P58122 caul	1	165	1.5	8	79
Q44663 bruc	1	177	1.5	8	80
Q9w611 gall	1	200	1.5	8	81
P36213 horc	1	205	1.5	8	82
P34555 caer	1	205	1.5	8	83
P42929 cani	1	209	1.5	8	84
Q9ugv6 homc	1	211	1.5	8	85
Q8nsx5 corl	1	211	1.5	8	86
P17136 ratt	1	214	1.5	8	87
O96004 homc	1	215	1.5	8	88
P27048 mus	1	231	1.5	8	89
P07056 neur	1	231	1.5	8	90
Q9pv94 gall	1	240	1.5	8	91
Q8tu67 erir	1	240	1.5	8	92
P14678 homc	1	240	1.5	8	93
Q9tu66 homc	1	240	1.5	8	94
P50731 baci	1	240	1.5	8	95
P13089 glyc	1	243	1.5	8	96
P41484 mycc	1	249	1.5	8	97
P17890 sacc	1	251	1.5	8	98
Q10863 mycc	1	255	1.5	8	99
P31315 mus	1	261	1.5	8	100
Q9H4B2 homc	1	264	1.5	8	101
P09631 mus	1	271	1.5	8	102
P31269 homc	1	272	1.5	8	103
P32447 sacc	1	279	1.5	8	104
P56261 ratt	1	281	1.5	8	105

1.5 294 1 NPM_CHICK
 1.5 299 1 PP3D HUMAN
 1.5 303 1 ALB3 HUMAN
 1.5 304 1 RIP9 MAIZE
 1.5 311 1 CDX2 MOUSE
 1.5 313 1 HEM3 PREPK
 1.5 317 1 RLAO MOUSE
 1.5 320 1 TTP RAT
 1.5 322 1 KHSE XANCP
 1.5 323 1 OLG2 HUMAN
 1.5 323 1 OLG2 MOUSE
 1.5 335 1 HKDD HUMAN
 1.5 337 1 INGS HUMAN
 1.5 340 1 LIMA PSEAE
 1.5 341 1 MENL MOUSE
 1.5 347 1 RLAO METAC
 1.5 353 1 NK24 HUMAN
 1.5 354 1 ATH1 HUMAN
 1.5 354 1 SXL DRONE
 1.5 357 1 IF35 HUMAN
 1.5 359 1 WN9B MOUSE
 1.5 372 1 GDF1 HUMAN
 1.5 376 1 HXA2 HUMAN
 1.5 377 1 CX10 CHICK
 1.5 387 1 SOX1 HUMAN
 1.5 388 1 MENL HUMAN
 1.5 391 1 SOX1 MOUSE
 1.5 392 1 HME1 HUMAN
 1.5 394 1 HGH1 YEAST
 1.5 394 1 K1M4 HUMAN
 1.5 395 1 IF5 SCHPO
 1.5 396 1 ARRS XENLA
 1.5 396 1 SX11 CHICK
 1.5 399 1 HXAA MOUSE
 1.5 401 1 HME1 MOUSE
 1.5 405 1 GDFB MOUSE
 1.5 407 1 GDFB HUMAN
 1.5 407 1 YOI4 CAEEL
 1.5 410 1 BHB3 MOUSE
 1.5 410 1 BHB3 RAT
 1.5 410 1 HME2 DROME
 1.5 412 1 FK34 SPOFR
 1.5 416 1 CRTC MOUSE
 1.5 416 1 CRTC RAT

ALIGNMENTS

STANDARD; PRT; 239 AA.

(Rel. 33, Created)
 (Rel. 33, Last sequence update)
 (Rel. 41, Last annotation update)
 mere autoantigen B (Centromere protein B) (CENP-B)

Sheep).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 rinae; Ovis.
 940;
 M N.A.

9078; PubMed=8893808;
 Jones C.A., Burkin H.R., McGrew J.A., Broad T.E.;
 and CENP genes show a high level of sequence similarity
 d synteny with their human homologs.;
 ell Genet. 74:86-89(1996).
 ; Interacts with centromeric heterochromatin in

CC chromosomes and binds to a specific subunit of alphoid satell
 CC DNA, called the CENP-B box. May organize arrays of centromer
 CC satellite DNA into a higher order structure which then direc
 CC centromere formation and kinetochore assembly in mammalian
 CC chromosomes (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 CENPB domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a col
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 CC -----
 CC EMBL: U35655; AAA79098.1; -;
 CC InterPro: IPR004875; CENP-B.
 CC Pfam: PF03184; DDE; 1.
 CC Chromosomal protein; Nuclear protein; DNA-binding; Centromere.
 FT NON TER 1 1
 SQ SEQUENCE 239 AA; 26436 MW; 259C6C72E7D9C135 CRC64;

Query Match 2.0%; Score 11; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0;
 Matches 11; Conservative 0; Mismatches 0;

QY 329 EEEEDDEDED 339
 DB 158 EEEEDDEDED 168

RESULT 2

Y066 NPVAC
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 AC P41457;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE Hypothetical 94.0 kDa protein in POL-LEF3 intergenic region.
 OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=46015;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6;
 RX MEDLINE=94303173; PubMed=8030224;
 RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
 RT "The complete DNA sequence of Autographa californica nuclear
 RT polyhedrosis virus.";
 RL Virology 202:586-605(1994).
 CC -!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV AND LDMNPV.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L22859; AAA66696.1; -;
 CC PIR: C72858; C72858.
 CC Hypothetical protein.
 FT DOMAIN 106 117
 SQ SEQUENCE 808 AA; 93973 MW; 76A871D2B6633F8A CRC64;

Query Match 2.0%; Score 11; DB 1; Length 808;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 11; Conservative 0; Mismatches 0; Indels 0;


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/FTid=VAR_011823.
P -> S (in dbSNP:1053340).
/FTid=VAR_011824.
P -> H (IN REF. 2; AAC19162).
C -> S (IN REF. 2; AAC19162).
V -> M (IN REF. 2).
PKARP -> VGNGL (IN REF. 2;
AAC39765/AAC19163).
2 AA; 95451 MW; 9AEAF7D771035F CRC64;
arity 2.0%; Score 11; DB 1; Length 892;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
PPPPQQ 232
PPPPQQ 46
STANDARD; PRT; 75 AA.
0; Q6MSH9;
Rel. 42, Created
Rel. 42, Last sequence update)
nd-specific peptide 57Da precursor (Male accessory gland
tein 57Da)
DNA:GH19893 OR CG9074.
lanogaster (Fruit fly).
taxoa; Arthropoda; Hexapoda; Insecta; Pterygota;
opterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
27;
[N.A., AND TISSUE SPECIFICITY.
188; PubMed=7711745;
chaefer M., Schaefer U.;
d regulation of a gene cluster for male accessory gland
n Drosophila melanogaster."
m. Mol. Biol. 25:127-137(1995).
[N.A.
ey;
1006; PubMed=10731132;
leiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
le C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
ghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cawley S., Dahlke C., Davenport L.B., Davies P.,
Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
ibriel A.E., Garg N.S., Gelbart W.M., Glasser K.,
ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
uston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
ilush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
i Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
ai B., McIntosh T.C., McLeod M.P., McPherson D.,
Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
oy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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```

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[3]
SEQUENCE OF 2-75 FROM N.A.
STRAIN=Berkeley; TISSUE=Head;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Wan
RA George R.A., Guarin H., Kronmiller B., Pacleeb J.M., Park S., Wan
RA Rubin G.M., Celniker S.E.;
RA "A Drosophila full-length cDNA resource.";
RT Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
RL
CC -!- FUNCTION: Transferred from male to female during mating and it
CC affect egg laying and behavior after mating.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Lumen fluid of male accessory glands, bec
CC seminal fluid.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z33647; CAA83925.1; -
CC EMBL; AE003753; AAF56515.1; -
CC EMBL; AY118802; AAM50662.1; -
CC FlyBase; FBgn0011668; Mst57Da.
KW Signal; Behavior.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 75 ACCESSORY GLAND-SPECIFIC PEPTIDE 57I
FT DOMAIN 39 64 ALA/PRO-RICH DOMAIN.
FT CONFLICT 39 46 MISSING (IN REF. 1).
FT CONFLICT 64 75 MISSING (IN REF. 1).
SQ SEQUENCE 75 AA; 7106 MW; BCD3D70817C98E14 CRC64;
Query Match 1.9%; Score 10; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C
QY 118 APAAATAAAP 127
Db 40 APAAATAAAP 49
RESULT 5
A32E MOUSE STANDARD; PRT; 260 AA.
AC P97822; Q8BPR8; Q8C2L4; Q8C7Q8; Q9CZD2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Acidic leucine-rich nuclear phosphoprotein 32 family member E (lf
DE like protein) (LAMP-L) (Cerebellar postnatal development protein-
GN ANP32E OR CPDI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, SUBCELLULAR LOCATION, 1
RP SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

```

74; PubMed=11430900;
 Villa-Ortiz G., Cafferata E.G.A., Di Tella M.C.,
 Ico A., Perandones C., Pivetta O.H., Carminatti H.,
 V.P., Santa-Coloma T.A.;
 expression of CPD during postnatal development in the
 hm.;
 :162-174 (2001).
 N.A. (ISOFORM 1).
 ; TISSUE=Brain;
 -2000) to the EMBL/GenBank/DBJ databases.
 N.A. (ISOFORMS 1 AND 2).
 J, and NOD; TISSUE=Embryo, Spinal cord, and Thymus;
 83; PubMed=12466851;
 runo M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 ato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 u Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
 Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 adt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 ani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gariboldi M., Gissi C., Godzik A., Gough J.,
 ustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 ji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 urochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Malcais L., Marchionni L., McKenzie L., Miki H.,
 Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 d J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 chenider C., Simple C.A., Setou M., Shimada K.,
 kenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 gner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 Wynchaw-Boris A., Yanoisawa M., Yang I., Yang L.,
 an M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 kawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 ki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 zume Y., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 akai K., Sasaki D., Shibata K., Shingawa A.,
 Yoshino M., Waterston R., Lander E.S., Rogers J.,
 ashizaki Y.;
 he mouse transcriptome based on functional annotation of
 ngth cDNAs.;
 -573 (2002).
 N.A. (ISOFORM 1).
 57; PubMed=12477932;
 ., Feingold E.A., Grouse L.H., Derge J.G.,
 Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 ., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 uellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Ewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 orley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 on E., Ketterman W., Madan A., Rodrigues S., Sanchez A.,
 dan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 , Touchman J.W., Green E.D., Dickson M.C.,
 , Grimwood J., Schmutz J., Myers R.M.,
 S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
 chein J.E., Jones S.J.M., Marra M.A.;
 d initial analysis of more than 15,000 full-length human
 sequences.;
 ad. Sci. U.S.A. 99:16899-16903 (2002).
 Inhibits activity of protein phosphatase 2A. Does not
 otein phosphatase 1. May play a role in cerebellar
 r. LOCATION: Nuclear and cytoplasmic.

CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P97822-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P97822-2; Sequence=VSP_007373;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Expressed at highest levels in cerebellum
 CC spleen. In the cerebellum, expressed mainly in granule cells a
 CC to a lesser extent, in Purkinje cells.
 CC -!- DEVELOPMENTAL STAGE: Low levels are found at postnatal day 4.
 CC Levels increase from postnatal day 7 to postnatal day 17. Leve
 CC decrease and remain low in the adult.
 CC -!- SIMILARITY: Belongs to the ANP32 family.
 CC -!- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U9345; AAB49462.2; -;
 CC EMBL; AB037685; BAB03507.1; -;
 CC EMBL; AK012759; BAB28449.1; -;
 CC EMBL; AK049647; BAC33858.1; -;
 CC EMBL; AK076049; BAC36147.1; -;
 CC EMBL; AK088401; BAC40331.1; -;
 CC EMBL; BC005690; AAB05690.1; -;
 CC MGD; MGI:1913721; Amp32e.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:0019212; P:phosphatase inhibitor activity; IDA.
 CC InterPro; IPR001611; LRR.
 CC Pfam; PF00560; LRR; 3.
 CC SMART; SM00446; LRRcap; 1.
 CC Leucine-rich repeat; Repeat; Nuclear protein; Alternative splicing
 FT REPEAT 41 63
 FT REPEAT 64 86
 FT REPEAT 87 111
 FT REPEAT 115 138
 FT VARSPLIC 208 219
 FT CONFLICT 98 98 N -> D (IN REF. 3; BAB28449).
 FT CONFLICT 199 199 S -> T (IN REF. 3; BAC33858).
 SQ SEQUENCE 260 AA; 29622 MW; 7F94E46D72A04780 CRC64;
 Query Match 1.9%; Score 10; DB 1; Length 260;
 Best Local Similarity 100.0%; Pred.No.1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga
 QY 329 EEEEDDEDE 338
 Db 187 EEEEDDEDE 196
 RESULT 6
 HXAS_HETFR
 ID HXAS_HETFR STANDARD; PRT; 275 AA.
 AC Q91A23;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A5.
 GN HOXA5.
 OS Heterodontus francisci (Horn shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes
 OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
 OC Heterodontidae; Heterodontus.
 OC NCBI_TaxID=7792;

[N.A.
 096; PubMed=10677514;
 miya C., Bailey W., Kawasaki K., Mezey J., Miller W.,
 Shimizu N., Wagner G., Ruddle F.;
 genomics in the horn shark, *Heterodontus francisci*.;
 Acad. Sci. U.S.A. 97:1653-1660(2000).
 Sequence-specific transcription factor which is part of
 mental regulatory system that provides cells with
 positional identities on the anterior-posterior axis (By
 Y).
 AR LOCATION: Nuclear (By similarity).
 Y: Belongs to the Antp homeobox family.

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 ail to license@isb-sib.ch).

 2; AAF44643.1; -
 1SAN.
 476; -
 001827; Antennapedia.
 001356; Homeobox.
 ; homeobox; 1.
 25; ANTENNAPEDIA.
 24; HOMEBOX.
 010; Homeobox; 1.
 9; HOX; 1.
 032; ANTENNAPEDIA; 1.
 027; HOMEBOX; 1.
 071; HOMEBOX; 2; 1.
 -binding; Developmental protein; Nuclear protein;
 regulation.
 81 186 ANTP-TYPE HEXAPEPTIDE.
 00 259 HOMEBOX.
 75 78 POLY-ALA.
 81 84 POLY-ALA.
 34 142 POLY-SER.
 27 230 POLY-ARG.
 5 AA; 30214 MW; 51BC2720808A31B6 CRC64;
 1.9%; Score 10; DB 1; Length 275;
 arity 100.0%; Pred. No. 1.1;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TTA AAA 22
 |||||
 TTA AAA 84
 STANDARD; PRT; 403 AA.
 6;
 Rel. 41, Created
 Rel. 41, Last sequence update
 Rel. 42, Last annotation update
 Protein Q1 (Hepatocyte nuclear factor 3 forkhead homolog
 'head-like protein 1) (HNF-1).
 ..
 (Human).
 Taxa: Chordata; Craniata; Vertebrata; Euteleostomi;
 Heria; Primates; Catarrhini; Hominidae; Homo.
 .06;
 [N.A., AND TISSUE SPECIFICITY.
 .676; PubMed=11747606;
 asche B., Frank S., Glaeser B., Kunz J., Witt K.,

RT "Isolation and characterization of the human forkhead gene FOXQ1.
 RL DNA Cell Biol. 20:555-561(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21207067; PubMed=11309849;
 RA Hong H.-K., Noveroske J.K., Headon D.J., Liu T., Sy M.S.,
 RA Justice M.J., Chakravarti A.;
 RT "The winged helix/forkhead transcription factor Foxq1 regulates
 RT differentiation of hair in satin mice.";
 RL Genesis 29:163-171(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Schenker C.M., Schuler G.I
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz J
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madañ A., Rodrigues S., Sanchez
 RA Whiting M., Madañ A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the stomach,
 CC trachea, bladder and salivary gland.
 CC -!- SIMILARITY: Contains 1 fork-head domain.

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 CC EMBL; AF225950; AAK00639.1; -
 CC EMBL; AF153341; AAF75586.1; -
 CC EMBL; BC053850; AAH53850.1; -
 CC HSP; Q63245; 2HFH.
 CC Genew; HGNC:20951; FOXQ1.
 CC InterPro; IPR001766; TF_Fork_head.
 CC Pfam; PF00250; Fork_head; 1.
 CC PRINTS; PR00053; FORKHEAD.
 CC ProDom; PDO00425; TF_Fork_head; 1.
 CC SMART; SMO0339; FH; 1.
 CC PROSITE; PS00657; FORK_HEAD_1; 1.
 CC PROSITE; PS00658; FORK_HEAD_2; 1.
 CC PROSITE; PS00039; FORK_HEAD_3; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 FT DNA BIND 119 214 FORK-HEAD.
 FT DOMAIN 13 103 ALA/GLY-RICH.
 FT DOMAIN 221 397 PRO-RICH.
 FT CONFLICT 49 52 NSPA -> KPS (IN REF. 2).
 FT CONFLICT 60 61 PP -> TQ (IN REF. 2).
 FT CONFLICT 386 386 S -> L (IN REF. 2).
 FT CONFLICT 395 395 P -> S (IN REF. 2).
 SQ SEQUENCE 403 AA; 41491 MW; EB52255A8AC6929B CRC64;
 Query Match 1.9%; Score 10; DB 1; Length 403;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; C

JAPAAP 187
 |||||
 JAPAAP 246

STANDARD; PRT; 469 AA.
 Rel. 34, Created
 Rel. 34, Last sequence update)
 Rel. 40, Last annotation update)
 protein G1A (forkhead-related protein FKHL2)
 1 factor BF-2) (Brain factor 2) (BF2) (HFK2).
 2.
 Human).
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Metazoa; Primates; Catarrhini; Hominiidae; Homo.
 6;
 N.A.
 132; PubMed=7959731;
 Niese S., Burfeind P., Schmundt D., Mattei M.-G.,
 et al., Thies U.;
 factor 1, a new member of the fork head gene family.";
 51-557(1994).
 N.A.
 150; PubMed=759184;
 My D.B., Schling A., Burfeind P., Schmundt D.,
 Mattei M.-G., Thies U.;
 human brain factor 1 and 2, members of the fork head
 are clustered on chromosome 14q.";
 WS. Acta 1262:105-112(1995)
 Plays an important role in the establishment of the
 subdivision of the developing brain and in the
 it of the telencephalon. Sequence-specific DNA-binding
 with a distinct binding specificity (By similarity).
 NR LOCATION: Nuclear (potential).
 1. Contains 1 fork-head domain.
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 CAA55038.1; -;
 CAA52240.1; -;
 37451.
 2HFH.
 192;
 111; FOXG1A.
 F: DNA binding; TAS.
 P: brain development; TAS.
 101766; TF_Fork_head.
 Fork_head; 1.
 125; TF_Fork_head; 1.
 157; FORK_HEAD_1; 1.
 158; FORK_HEAD_2; 1.
 159; FORK_HEAD_3; 1.
 regulation; DNA-binding; Nuclear protein;
 protein.
 13 56 HIS-RICH.
 17 79 PRO-RICH.
 0 73 POLY-GLN.

FT DOMAIN 83 88 POLY-ARG.
 FT DNA_BIND 161 252 FORK-HEAD.
 SQ SEQUENCE 469 AA; 50539 MW; 943B8BDB90008EDC CRC64;
 Query Match 1.9%; Score 10; DB 1; Length 469;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 220 PQQQQQPPPP 229
 |||||
 Db 68 PQQQQQPPPP 77

RESULT 9
 ACHI SCHGR STANDARD; PRT; 557 AA.
 ID ACHI SCHGR STANDARD; PRT; 557 AA.
 AC P23414;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-L1 chain precursor.
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
 OX NCBI_TaxID=7010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91032263; PubMed=1702381;
 RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
 Darlison M.G., Sattelle D.B., Barnard E.A.;
 RT "Sequence and functional expression of a single alpha subunit of
 RT insect nicotinic acetylcholine receptor.";
 RL EMBO J. 9:4391-4398(1990).
 CC -i- FUNCTION: After binding acetylcholine, the AChR responds by a
 CC extensive change in conformation that affects all subunits an
 CC leads to opening of an ion-conducting channel across the plas
 CC membrane.
 CC -i- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -i- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC -----
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 DR EMBL; X55439; CAA39081.1; -;
 DR FIR; S12359; S12359.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neu_chan_LBD.
 DR InterPro; IPR006201; Neu_chan_memb.
 DR Pfam; PF02931; Neu_chan_LBD; 1.
 DR Pfam; PF02932; Neu_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Sig
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPH
 FT CHAIN EXTRACELLULAR.
 FT DOMAIN 24 244
 FT TRANSMEM 245 286
 FT TRANSMEM 274 294
 FT TRANSMEM 308 329
 FT DOMAIN 330 500
 FT TRANSMEM 501 523
 FT TRANSMEM 501 523
 FT DISULFID 151 165
 FT DISULFID 224 225
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).

```

47 47 N-LINKED (GLNAC. . .) (POTENTIAL).
135 235 N-LINKED (GLNAC. . .) (POTENTIAL).
182 400 ALA/SER-RICH.
106 422 HIS-RICH.
17 AA; 63026 MW; 168389C887DFDF3E CRC64;
1.9%; Score 10; DB 1; Length 557;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ASSSAAS 28
|||||
ASSSAAS 399

STANDARD; PRT; 579 AA.
I2; Q9EQJ3; Q9JWJ5;
(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
protein 384 (Nuclear matrix transcription factor 4)
ded zinc finger protein).
A OR CIZ.
Ricus (Rat).
azao; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1116;

1 N.A. (ISOFORM 1), SUBCELLULAR LOCATION, DNA-BINDING, AND
WITH CAS.
1045; PubMed=10669742;
Yamagata T., Sakai R., Ogawa S., Honda H., Ueno H.,
izaki Y., Hirai H.;
finger protein that interacts with p130cas and activates
n of matrix metalloproteinases."
.OL. 20:1649-1658(2000).

1 N.A. (ISOFORMS 1; 2 AND 3).
ie-Dawley;
193; PubMed=11149472;
l P., Alvarez M., Tokunaga K., Onyia J.E., Hock J.,
ister H., Rhodes S.J., Bidwell J.P.;
functional analysis of a family of nuclear matrix
; factors (NP/NMP4) that regulate type I collagen
t osteoblasts."
. Res. 16:10-23(2001).
Transcription factor that binds the consensus DNA
[GC]AAAAA. Seems to bind and regulate the promoters of
3, MMP7 and COL1A1.
Interacts with Cas.
AR LOCATION: Nuclear.
VE PRODUCTS;
ernative splicing: Named isoforms=3;
Additional isoforms seem to exist;

9EQJ4-1; Sequence=Displayed;
9EQJ4-2; Sequence=VSP_006921;
9EQJ4-3; Sequence=VSP_006922;
ECIFCIYV; Expressed in osteocytes, osteoblasts, and
tes in bone.
Y; BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
TEINS.
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CC -----
DR EMBL; AB019281; BAA89664.1; -
DR EMBL; AF216804; AAG40582.1; -
DR EMBL; AF216805; AAG40583.1; -
DR EMBL; AF216806; AAG40584.1; -
DR HSSP; P08153; 1ZFD.
DR TRANSFAC; T05136; -
DR TRANSFAC; T05137; -
DR TRANSFAC; T05138; -
DR TRANSFAC; T05141; -
DR TRANSFAC; T05142; -
DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PF00096; zf-C2H2; 8.
DR ProDom; PD000003; Znf C2H2; 4.
DR SMART; SM00355; Znf C2H2; 8.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 8.
KW Transcription regulation; Zinc-finger; Metal-binding; Nuclear pr
KW DNA-binding; Repeat; Alternative splicing.
FT ZN_FING 229 251
C2H2-TYPE 1.
FT ZN_FING 257 279
C2H2-TYPE 2.
FT ZN_FING 285 307
C2H2-TYPE 3.
FT ZN_FING 318 340
C2H2-TYPE 4.
FT ZN_FING 346 368
C2H2-TYPE 5.
FT ZN_FING 374 398
C2H2-TYPE 6.
FT ZN_FING 404 426
C2H2-TYPE 7.
FT ZN_FING 434 456
C2H2-TYPE 8.
FT DOMAIN 462 524
GLN-RICH.
FT DOMAIN 467 506
ALA-RICH.
FT VARSPPLIC 103 118
Missing (in isoform 2).
FT VARSPPLIC 301 361
/FTID=VSP_006921.
FT VARSPPLIC 178 179
Missing (in isoform 3).
FT CONFLICT 576 577
GG -> RS (IN REF. 1).
FT CONFLICT 579 579
LA -> WP (IN REF. 1).
SQ SEQUENCE 579 AA; 63139 MW; FBC242E0D1050C45 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 222 QQQQPPPPPP P31
Db 511 QQQQPPPPPP P20

RESULT 11
RPSD_ECOLI
ID RPSD_ECOLI STANDARD; PRT; 613 AA.
AC P00579;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase sigma factor rpoD (Sigma-70).
GN RPOD OR ALT OR B3067.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=82014879; PubMed=6269063;
RA Burton Z.F., Burgess R.R., Lin J., Moore D., Holder S., Gross C.F
RT "The nucleotide sequence of the cloned rpoD gene for the RNA
RL Nucleic Acids Res. 9:2889-2903(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;

```

Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Lado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
his N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
genome sequence of *Escherichia coli* K-12.;
153-1474 (1997).

LOGRAPHY (2.6 ANGSTROMS) OF 113-446.

145; PubMed=8858155;

Severinova E., Darst S.A.;

ture of a sigma 70 subunit fragment from *E. coli* RNA

36 (1996).

The sigma factor is an initiation factor that promotes
of the RNA polymerase to specific initiation sites and
eleased. This is the primary sigma-factor of this

f: Belongs to the sigma-70 factor family.

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AAA24601.1; -

AAA89147.1; -

}; AAC76103.1; -

UNES

MAY-97.

12:0; 6TH EDITION.

196; rpoD.

09043; RNA_pol sigma.

07631; Sigma70 ner.

07127; Sigma70_r1_1.

09042; Sigma70_r1_2.

07627; Sigma70_r2.

07624; Sigma70_r3.

07630; Sigma70_r4.

00943; Sigma 70.

sigma70_ner; 1.

sigma70_r1_1; 1.

sigma70_r1_2; 1.

sigma70_r2; 1.

sigma70_r3; 1.

sigma70_r4; 1.

16; SIGMA70FCT.

15; SIGMA70_1; 1.

16; SIGMA70_2; 1.

regulation; Sigma factor; DNA-directed RNA polymerase;

1D-structure; Complete proteome.

13 416 POLYMERASE CORE BINDING (POTENTIAL).

13 592 H-T-H MOTIF (BY SIMILARITY).

13 149 D -> N (IN REF. 1).

13 115

13 134

13 136

13 148

13 154

13 160

13 161

13 165

13 182

13 190

13 234

13 236

13 256

13 258

13 261

13 292

13 294

FT HELIX 299 306
FT TURN 307 309
FT HELIX 313 315
FT TURN 316 316
FT HELIX 317 320
FT TURN 321 322
FT HELIX 325 329
FT TURN 330 332
FT HELIX 333 333
FT TURN 334 351
FT HELIX 352 352
FT TURN 355 382
FT TURN 383 383
FT HELIX 384 391
FT TURN 392 393
FT TURN 395 396
FT HELIX 401 418
FT HELIX 421 423
FT HELIX 427 445
SQ SEQUENCE 613 AA; 70263 MW; CA4FOE30DEC1703D CRC64;

Query Match 1.9%; Score 10; DB 1; Length 613;

Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; G

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 333 DDEDEDEED 342

Db 191 DDEDEDEED 200

RESULT 12

RPSD SALTY

ID RPSD SALTY STANDARD; PRT; 615 AA.

AC P07336; Q823M4;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE RNA polymerase sigma factor rpoD (Sigma-70).

GN RPOD OR STM3211 OR STY3390 OR T3131.

OS Salmonella typhimurium, and

OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602, 601;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium;

RX MEDLINE=86137422; PubMed=3005129;

RA Erickson B.D., Burton Z.F., Watanabe K.K., Burgess R.R.;

RT "Nucleotide sequence of the rpoD-dnaG-rpoD operon from Salmonella

RT typhimurium and a comparison of this sequence with the homologous

RT operon of *Escherichia coli*.";

RL Gene 40:67-78 (1985).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille

RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RT "Complete genome sequence of *Salmonella enterica* serovar Typhimur:

RT LT2.";

RL Nature 413:852-856 (2001).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=CT18;

RX MEDLINE=21534947; PubMed=11677608;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wair

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia I

RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
sen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
utherford K., Simmonds M., Skelton J., Stevens K.,
Barrell B.G.;
ome sequence of a multiple drug resistant *Salmonella*
var Typhi CT18.";
8-852(2001)).

N.A.
hi; STRAIN=Ty2 / ATCC 700931;
367; PubMed=12644504;
S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
odoyanni V., Schwartz D.C., Blattner F.R.;
Genomics of *Salmonella enterica* serovar Typhi strains Ty2
185:2330-2337(2003).

The sigma factor is an initiation factor that promotes
t of the RNA polymerase to specific initiation sites and
released. This is the primary sigma-factor of this
Y: Belongs to the sigma-70 factor family.

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ail to license@isb-sib.ch).

AAA27242.1; -
7; AAL22085.1; ALT INIT.
8; CAD07736.1; ALT INIT.
4; AAO70674.1; ALT INIT.
RNEB5T.
1SIG.
369; rpoD.
009043; RNA pol sigma.
007631; Sigma70 ner.
007127; Sigma70 r1 1.
009042; Sigma70 r1 2.
007627; Sigma70 r2.
007624; Sigma70 r3.
007630; Sigma70 r4.
009943; Sigma70.
; sigma70 ner; 1.
; sigma70 r1 1; 1.
; sigma70 r1 2; 1.
; sigma70 r2; 1.
; sigma70 r3; 1.
; sigma70 r4; 1.
46; SIGMA70FCT.
715; SIGMA70 1; 1.
716; SIGMA70 2; 1.
regulation; Sigma factor; DNA-directed RNA polymerase;
Complete proteome.
05 418 POLYMERASE CORE BINDING (POTENTIAL).
73 592 H-T-H MOTIF (BY SIMILARITY).
5 AA; 70530 MW; 114E8D4236A3D59A CRC64;
1.9%; Score 10; DB 1; Length 615;
arity 100.0%; Pred.No.2.2;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
DEDEED 342
|||||
DEDEED 202

STANDARD; PRT; 621 AA.
5;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid protein P40 [Contains: Assemblin (Protease) (EC 3.4.21.97);
DE Capsid assembly protein].
GN UL26.
OS Bovine herpesvirus type 1 (strain Cooper).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10323;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96013856; PubMed=7474173;
RA Haanes E.J., Thomsen D.R., Martin S., Homa F.L., Lowery D.E.;
RT "The bovine herpesvirus 1 maturational proteinase and scaffold
RT proteins can substitute for the homologous herpes simplex virus 1
RT proteins in the formation of hybrid type B capsids.";
RL J. Virol. 69:7375-7379(1995).
CC -!- FUNCTION: THE CAPSID ASSEMBLY PROTEIN IS COMPONENT OF THE CAI
CC CORE INVOLVED IN PROCESSING AND PACKAGING OF PROGENY DNA.
CC -!- FUNCTION: ASSEMBLIN IS A PROTEASE WHICH CAN PROTEOLYTICALLY (C
CC ITSELF AND THE CAPSID ASSEMBLY PROTEIN AT THE C-TERMINUS.
CC -!- CATALYTIC ACTIVITY: Cleaves -Ala-|-Ser- and -Ala-|-Ala- bonds;
CC the scaffold protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, UL26 (shown here) and UL26.5, are produ
CC by alternative initiation;
CC -!- SIMILARITY: Belongs to peptidase family S21.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40.
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CC between the Swiss Institute of Bioinformatics and the EMBL out
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CC use by non-profit institutions as long as its content is ir
CC modified and this statement is not removed. Usage by and for c
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EMBL; U31809; AAA91999.1; -
EMBL; U31809; AAA92000.1; -
EMBL; Z78205; CAB01599.1; -
EMBL; AJ004801; CAA06107.1; -
HSSP; P16753; 1CMV.
MEROPS; S21.001; -
DR InterPro: IPR001847; Peptidase S21.
DR Pfam: PF00716; Peptidase S21; 1.
DR PRINTS; PR00236; HSVCAPSIDP40.
KW Capsid assembly; Hydrolase; Serine protease; Coat protein;
KW Alternative initiation.
FT CHAIN 1 621 CAPSID PROTEIN P40, ISOFORM UL26.
FT CHAIN 314 621 FOR ISOFORM UL26.5.
FT INIT MET 314 314 ASSEMBLIN (PROTEASE).
FT CHAIN 1 254 CAPSID ASSEMBLY PROTEIN.
FT CHAIN 255 621 CLEAVAGE (BY THE PROTEASE) (PROBABLE
FT SITE 254 255 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 68 68 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 136 136 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 155 155 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 621 AA; 63711 MW; AEF6D7C9DEB69003 CRC64;
Query Match 1.9%; Score 10; DB 1; Length 621;
Best Local Similarity 100.0%; Pred.No.2.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 120 AAAAAAAAAPPP 129
|||||
Db 368 AAAAAAAAAPPP 377

RESULT 14
GARP_PLAFF STANDARD; PRT; 678 AA.
ID_GARP_PLAFF

el. 13, Created)
 el. 13, Last sequence update)
 el. 38, Last annotation update)
 rich protein precursor.

ciparum (isolate FC27 / Papua New Guinea).
 eolata; Apicomplexa; Haemosporida; Plasmodium.
 7;

N.A.
 48; PubMed-2903445;
 ahl H.-D., Crewther P.E., Silva A., Anders R.F.,
 a Plasmodium falciparum gene that encodes a glutamic
 ein (GARP).";
 Parasitol. 31:199-202(1988).

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AAJ29605.1; -.
 54514.
 a; Antigen; Signal.
 1 25
 6 678 GLUTAMIC ACID-RICH PROTEIN.
 0 164 15 X 3 AA TANDEM REPEATS OF K-K-X.
 2 416 9 X APPROXIMATE TANDEM REPEATS.
 7 441 5 X APPROXIMATE TANDEM REPEATS.
 6 604 POLY-GLU.
 5 653 7 X APPROXIMATE TANDEM REPEATS.
 4 663 POLY-GLU.
 AA; 80551 MW; 2ABF85606496EA9E CRC64;
 1.9%; Score 10; DB 1; Length 678;
 rity 100.0%; Pred. No. 2.4;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 EDEDE 340
 EDEDE 649

STANDARD; PRT; 1054 AA.
 el. 32, Created)
 el. 32, Last sequence update)
 el. 32, Last annotation update)
 ration B protein (Probable calcium transporter RDGB).
 anogaster (Fruit fly).
 azoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 pterygota; Diptera; Brachycera; Muscomorpha;
 rosophilidae; Drosophila.
 7;

N.A.
 R; TISSUE=Head;
 70; PubMed=1903119;
 Hyde D.R., O'Tousa J.E.;
 Characterization of the Drosophila retinal
 (rdgB) gene."
 51-768(1991).
 RDGB mutants undergo rapid light-induced retinal
 on. May control phosphatidylinositol concentration in
 vesicles from the subrhabdomeric cisternae (SRC) to the

CC rhabdomere. May function as a calcium transporter.
 CC -!- TISSUE SPECIFICITY: Expressed in adult heads, not detected in
 CC bodies.
 CC -!- SIMILARITY: THE N-TERMINAL IS SIMILAR TO MAMMALIAN
 CC PHOSPHATIDYLINOSITOL (PTDINS) TRANSFER PROTEINS.
 CC
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CC EMBL; X57978; CAA41044.1; -.
 CC PIR; A61221; A61221.
 CC FlyBase; FBgn0003218; rdgB.
 CC GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
 CC GO; GO:0008525; F:phosphatidylcholine transporter activity; IDA.
 CC GO; GO:0008526; F:phosphatidylinositol transporter activity; IDA.
 CC GO; GO:0016059; P:deactivation of rhodopsin mediated signaling; IN
 CC GO; GO:0007608; P:olfaction; IMP.
 CC GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
 CC InterPro; IPR004177; DDHD_dom.
 CC InterPro; IPR001666; PI_transfer.
 CC Pfam; PF02862; DDHD; 1.
 CC PRINTS; PR00391; PITRANSFER.
 KW Transmembrane, Vision.
 FT DOMAIN 321 332 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT TRANSMEM 501 519 POTENTIAL.
 FT TRANSMEM 734 750 POTENTIAL.
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 658 658 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 852 852 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 928 928 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 1054 AA; 116560 MW; 87F26EB871003CA8 CRC64;
 Query Match 1.9%; Score 10; DB 1; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 329 EEEEDDEDE 338
 Dd 324 EEEEDDEDE 333

RESULT 16
 BRD4_HUMAN
 ID BRD4_HUMAN STANDARD; PRT; 1362 AA.
 AC O60885; Q96PD3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bromodomain-containing protein 4 (HUNK1 protein).
 GN BRD4 OR HUNK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21590020; PubMed=11733348;
 RA French C.A., Miyoshi I., Aster J.C., Kubonishi I., Kroll T.G.,
 RA Dal Cin P., Vargas S.O., Perez-Atayde A.R., Fletcher J.A.;
 RT "BRD4 bromodomain gene rearrangement in aggressive carcinoma with
 RT translocation t(15;19).";
 RL Am. J. Pathol. 159:1987-1992 (2001).
 RN [2]
 RP SEQUENCE OF 1-722 FROM N.A.
 RC TISSUE=Placenta;

R-1997) to the EMBL/GenBank/DBJ databases.
 AR LOCATION: Nuclear (Potential).
 Y: Contains 2 bromodomains.

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9; AAL26987.1; -;
 CAA72780.1; -;
 1B91.
 3575; BRD4.
 001487; Bromodomain.
 ; bromodomain; 2.
 03; BROMODOMAIN.
 7; BROMO; 2.
 633; BROMODOMAIN 1; 1.
 014; BROMODOMAIN 2; 2.
 Repeat; Nuclear Protein.
 75 147 BROMODOMAIN 1.
 68 440 BROMODOMAIN 2.
 35 594 LYS-RICH.
 92 717 SER-RICH.
 93 714 POLY-SER.
 38 743 POLY-HIS.
 57 761 POLY-PRO.
 64 770 POLY-PRO.
 71 775 POLY-GLN.
 76 783 POLY-PRO.
 54 964 POLY-PRO.
 74 986 POLY-PRO.
 11 1014 POLY-PRO.
 28 1033 POLY-PRO.
 83 1300 POLY-GLN.
 01 1308 POLY-ALA.
 35 1338 POLY-ARG.
 20 721 EM -> GP (IN REF. 2).
 62 AA; 152219 MW; D52EFCF9960907 CRC64;
 arity 1.9%; Score 10; DB 1; Length 1362;
 conservative 0; Pred.No. 4.2;
 0; Mismatches 0; Indels 0; Gaps 0;
 QPQPPP 235
 |||||
 QPQPPP 986

STANDARD; PRT; 1461 AA.
 Rel. 35, Created)
 Rel. 35, Last sequence update)
 Rel. 39, Last annotation update)
 rase II (EC 5.99.1.3).
 ans (Yeast).
 ngi; Ascomycota; Saccharomycotina; Saccharomycetes;
 ales; mitosporic Saccharomycetales; Candida.
 76;
 N.A.
 gton 2402E;
 233; PubMed=9164874;
 Patel S., Fisher L.M.;
 oning and expression of the Candida albicans TOP2 gene
 of fungal DNA topoisomerase II inhibitors in yeast."

Biochem. J. 324:329-339(1997).
 -!- FUNCTION: Control of topological states of DNA by transient
 breakage and subsequent rejoining of DNA strands. Topoisomerase
 makes double-strand breaks.
 -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoin
 of double-stranded DNA.
 -!- SUBUNIT: Homodimer (By similarity).
 -!- SUBCELLULAR LOCATION: Nuclear.
 -!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax bc
 negative and positive supercoils, whereas prokaryotic enzymes
 relax only negative supercoils.
 -!- SIMILARITY: Belongs to the type II topoisomerase family.

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EMBL; Y10177; CAA71405.1; -;
 HSSP; P06786; LSGW.
 InterPro; IPR003594; ATPbind_ATPase.
 InterPro; IPR003957; CBFA_NFYB_topis.
 InterPro; IPR001241; DNA_topoisomII.
 InterPro; IPR002205; DNA_topoisomIV.
 Pfam; PF00204; DNA_gyraseB; 1.
 Pfam; PF00521; DNA_topoisomIV; 1.
 Pfam; PF02518; HATFase_C; 1.
 PRINTS; PR00615; CCAATSUBUNTA.
 PRINTS; PR00418; TPI2FAMILY.
 ProDom; PD000742; DNA_topoisomIV; 1.
 SMART; SM00387; HATPase_C; 1.
 SMART; SM00433; TOP2C; 1.
 SMART; SM00434; TOP4C; 1.
 PROSITE; PS00177; TOPOISOMERASE_II; FALSE NEG.
 Isomerase; Topoisomerase; DNA-binding; ATP-binding; Phosphorylati
 Nuclear protein.
 NP_BIND 190 195 ATP (POTENTIAL).
 ACT_SITE 842 842 DNA_CLEAVAGE (BY SIMILARITY).
 SEQUENCE 1461 AA; 165386 MW; B2F7933B05804E36 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 1461;
 Best Local Similarity 100.0%; Pred.No. 4.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 334 DDEDEDEDD 343
 |||||
 DB 1436 DDEDEDEDD 1445

RESULT 18
 FAS2_YEAST
 ID_FAS2_YEAST STANDARD; PRT; 1887 AA.
 AC P19097; Q12533;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fatty acid synthase subunit alpha (EC 2.3.1.86) [Includes: Acyl
 carrier; 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100
 (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier protein] synth
 (EC 2.3.1.41) (Beta-ketoacyl synthase)].
 GN FAS2 OR YPL231W OR P1409.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCB1_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88315020; PubMed=2900835;
 RA Mohamed A.H., Chirala S.S., Mody N.H., Huang W.Y., Wakil S.J.;
 RT "Primary structure of the multifunctional alpha subunit protein o

id synthase derived from FAS2 gene sequence.";
263:12315-12325(1988).
N.A.
A;
(-1994) to the EMBL/GenBank/DBJ databases.
N.A.
AB972;
71; PubMed=9169875;
rms R.K., Ahmed A., Albermann K., Allen E., Ansonge W.,
Riccio A., Bartell B.G., Badcock K., Benes V.,
Iowman S., Bruckner M., Carpenter J., Cherry J.M.,
Cher C.M., Coster F., Davis K., Davis R.W.,
Delius H., Dipaolo T., Dubois E., Dueterhoeft A.,
eth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
ng U., Heumann K., Hilbert H., Hillier L.W.,
S., Hyman R., Johnston M., Kalman S., Klein K.,
O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
ssenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
Namath A., Nentwich U., Oefner P., Pearson D.,
hi T.M., Purnelle D., Schafer M., Scharfe M.,
chramm S., Schroeder M., Sdicu A.M., Tettelin H.,
A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
mbutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
lilner A., Vo D.H., Hani J.;
e sequence of Saccharomyces cerevisiae chromosome XVI.";
-105(1997).
GLY-1250.
98; PubMed=8041367;
omoda H., Hashimoto H., Watanabe A., Takeshima H.,
instant mutants of Saccharomyces cerevisiae with an
acid synthase gene.";
t. 244:90-96(1994).
Fatty acid synthetase catalyzes the formation of
fatty acids from acetyl-CoA, malonyl-CoA and NADPH.
subunit contains domains for: acyl carrier protein,
[acyl-carrier protein] reductase, and 3-oxoacyl-[acyl-
oate] synthase. This subunit coordinates the binding
beta subunits to the enzyme complex.
ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
acyl-CoA + N CoA + N CO(2) + 2N NADP(+).
ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
oate] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
ier protein]
ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
3-oxoacyl-[acyl-carrier protein] + NADPH.
Alpha(6)beta(6)] hexamers of two multifunctional
alpha and beta].
: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
I.
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AAA34601.1; -
CAA54218.1; -
CAA64256.1; -
CAA97947.1; -
CAA97948.1; -
61703.
4213; -
FAS2.
08278; 4-PPT_transf.

DR InterPro; IPR000794; Ketoacyl synth.
DR InterPro; IPR004568; Pantethn trn.
DR Pfam; PF01648; ACPS; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt C; 1.
DR TIGRFAM; TIGR00556; pantethn trn; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
DR PROSITE; PS00606; B KETOACYL SYNTHASE; 1.
KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
KW Transferase; NADP; Phosphopantetheine.
FT DOMAIN 1 ? ACYL CARRIER (ACP).
FT DOMAIN 675 874 BETA-KETOACYL REDUCTASE.
FT DOMAIN 1149 1363 BETA-KETOACYL SYNTHASE.
FT BINDING 180 180 PHOSPHOPANTHETHEINE (BY SIMILARITY).
FT ACT_SITE 1305 1305 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT MUTAGEN 1250 1250 G->S: CEREULIN-RESISTANCE.
FT CONFLICT 310 310 G -> GTTGTGG (IN REF. 1).
FT CONFLICT 594 594 T -> I (IN REF. 1).
FT CONFLICT 941 1019 AKIRKELVETSEVRKAVSTALEHKKVNGNSADA;
FT IOPRANIQDFFELPKYKQVQIAPAELEGGLDLER;
FT CINCVKSWLKLLKLEPFKSKLLMSRLSMAIMLI;
FT XNQLTFTWTSQNRNHTNLKLLPLSLRVCWIKI
(IN REF. 1).
FT CONFLICT 1036 1041 RWMEA -> KMGNGS (IN REF. 1).
FT CONFLICT 1408 1408 A -> S (IN REF. 1).
FT CONFLICT 1671 1671 N -> T (IN REF. 1).
SQ SEQUENCE 1887 AA; 206946 MW; 08B872734CF3AEEA CRC64;
Query Match 1.9%; Score 10; DB 1; Length 1887;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gc
QY 137 PAPVAAAPPA 146
Db 125 PAPVAAAPPA 134
|||||
RESULT 19
RLAI MAIZE
ID FLAI MAIZE STANDARD; PRT; 109 AA.
AC P52855; O24414;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 60S acidic ribosomal protein P1 (L12).
GN RPL1A.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W22;
RA Hamilton D.A., Turcich M.P., Bokhari-Riza A., Mascarenhas J.P.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 18-21.
RC STRAIN=cv. B73; TISSUE=Ear;
RX MEDLINE=97422884; PubMed=9276949;
RA Bailey-Serres J., Vargala S., Szick K., Lee C.H.;
RT "Acidic phosphoprotein complex of the 60S ribosomal subunit of mai
seedling roots. Components and changes in response to flooding.";
RL Plant Physiol. 114:1293-1305(1997).
CC -!- FUNCTION: Plays an important role in the elongation step of
protein synthesis (By similarity).
CC -!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subu
(By similarity).
CC -!- PTM: Phosphorylated.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the L12p family of ribosomal proteins.

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AA91168.1; -
 AAB71079.1; -
 T02039.
 T02716.
 1; -
 001813; Ribosomal 60S.
 001859; Ribosomal_P2.
 ; 60s ribosomal; 1.
 56; RIBOSOMALP2.
 tein.
 9
 9 AA; 11096 MW; 18FC8E34391F080 CRC64;
 1.7%; Score 9; DB 1; Length 109;
 arity 100.0%; Pred. No. 3.4;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
 |||||
 AAAPA 77

STANDARD; PRT; 109 AA.

Rel. 23, Created)
 Rel. 23, Last sequence update)
 Rel. 34, Last annotation update)
 bosomal protein P1.
 ruzi.
 Glucosza; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 93;

N.A.
 148; PubMed=1598221;
 chijman A., Levin M.;
 equence of a cDNA encoding a Trypanosoma cruzi acidic
 type protein.";
 Res. 20:2599-2599(1992).
 Plays an important role in the elongation step of
 synthesis.
 P1 and P2 exist as dimers at the large ribosomal subunit.
 Y: Belongs to the L12P family of ribosomal proteins.

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CRA46159.1; -
 R6UTP1.
 001813; Ribosomal 60S.
 001859; Ribosomal_P2.
 ; 60s ribosomal; 1.
 56; RIBOSOMALP2.
 tein; Phosphorylation.
 9 AA; 10754 MW; D674D31C102F70AF CRC64;

1.7%; Score 9; DB 1; Length 109;
 arity 100.0%; Pred. No. 3.4;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 APAAAAAA 126
 |||||
 Db 77 APAAAAAA 85
 RESULT 21
 RK12_ORYSA
 ID RK12_ORYSA STANDARD; PRT; 158 AA.
 AC O22386;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 50S ribosomal protein L12, chloroplast precursor (CL12) (Fragment
 Oryza sativa (Rice).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ILPUM; TISSUE=Seedling;
 RA Lee J.S.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
 CC
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 or send an email to license@isb-sib.ch).

CC EMBL; AF010581; AAB66886.1; -
 DR HSSP; P02392; 1CTF.
 DR Gramene; O22386; -
 DR InterPro; IPR008932; Ribos_L12/7_olig.
 DR InterPro; IPR002026; Ribosomal_L12.
 DR Pfam; PF00542; Ribosomal_L12; 1.
 DR ProDom; PD001326; Ribosomal_L12; 1.
 KW Ribosomal protein; Chloroplast; Transit peptide.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN ? >158 50S RIBOSOMAL PROTEIN L12.
 FT NON_TER 158 158
 SQ SEQUENCE 158 AA; 16313 MW; BFD1733A6AF9372A CRC64;

Query Match 1.7%; Score 9; DB 1; Length 158;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 119 PAAAAAAP 127
 |||||
 Db 21 PAAAAAAP 29

RESULT 22

RPOE LISMO
 ID RPOE LISMO STANDARD; PRT; 178 AA.
 AC Q8Y494;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable DNA-directed RNA polymerase delta subunit (RNAP delta
 factor).
 DE factor).
 GN RPOE OR LMO2560.
 OS Listeria monocytogenes
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OC NCBI_TaxID=1639;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;

ID	BRX1 MOUSE	STANDARD;	PRT;	254 AA.
AC	Q9ER42;	O09066;	P70159;	Q9ERV2;
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-MAR-2004	(Rel. 43, Last annotation update)		

[illegible]

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CAB08905.1; -;
9; AAK45915.1; ALT_INIT.
3; CAD96305.1; -;
470557.
1P11.

RV1611; -;
34; -; 1.
003009; FNN enzyme.
001468; IGPS.
1; IGPS; 1.
511; IGPS; 1.
514; IGPS; 1.
0synthesis; Lyase; Decarboxylase; Complete proteome.
32 37 POLY-ALA.
34 164 T -> I (IN REF. 2).
2 AA; 28023 MW; 9CA29D0FOFAC76C2 CRC64;

1.7%; Score 9; DB 1; Length 272;
arity 100.0%; Pred. No. 7.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
VAPP 129
|||||
VAPP 40

STANDARD; PRT; 282 AA.
-; Q9LNV1;
rel. 37, Created
rel. 41, Last sequence update)
rel. 43, Last annotation update)
protein L4, chloroplast precursor (R-protein L4).
320 OR F22G5.34 OR F22G5.28.

ialiana (Mouse-ear cress).
diplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; rosids;
Brassicales; Brassicaceae; Arabidopsis.
12;

N.A.
umbia;
05; PubMed=9461586;
at I., Gagnon J., Baera L., Lerbs-Mache S.;
P4 gene encodes a chloroplast protein that co-purifies
the transcription complex as well as plastid

273:3980-3985(1998).

N.A.
umbia;
719; PubMed=11130712;
Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
iso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
ian A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
yun L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
demich A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
son J.K., Rizzo M., Rooney T., Rowley D.,
berg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
i L.J., Tambunga G., Toriumi M.J., Town C.D.,
Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana";
Nature 408:816-820(2000).

[3]
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
RC MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.
RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
Kaniya A., Meyers E., Nakajima M., Narusaka M., Seki M., Sakurai
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamur
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome";
Science 302:842-846(2003).

RL Science 302:842-846(2003).
CC -1- FUNCTION: This protein binds directly and specifically to 23S
CC (by similarity). May play a role in plastid transcriptional
CC regulation.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the L4P family of ribosomal proteins.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to errone
CC gene model prediction.

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CC EMBL; Y14565; CAA74894.1; -;
CC EMBL; Y14566; CAA74895.1; -;
CC EMBL; AC022464; AAF79563.1; ALT SEQ.
CC EMBL; AY063889; AAL36245.1; -;
CC InterPro; IPR002136; Ribosomal L4/L1E.
CC Pfam; PF00573; Ribosomal L4; 1.
CC Ribosomal protein; rRNA-Binding; Chloroplast; Transit peptide.
KW TRANSIT 1 49 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 50 282 50S RIBOSOMAL PROTEIN L4.
FT DOMAIN 267 282 ASP/GLU-RICH (ACIDIC).
FT CONFLICT 192 192 F -> L (IN REF. 1).
SQ SEQUENCE 282 AA; 30558 MW; 1479CCICEA75F29C CRC64;

Query Match 1.7%; Score 9; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G;

QY 330 EEEEDDEDE 338
Db 267 EEEEDDEDE 275

RESULT 28

ID SDC CAEEL STANDARD; PRT; 288 AA.
AC P50605;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable synecan precursor.
GN F57C7.3.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoid
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

N.A.
 1 N2;
 B-1996) to the EMBL/GenBank/DBJ databases.
 Cell surface proteoglycan that bears heparan sulfate
 arity).
 AR LOCATION: Type I membrane protein (Potential).
 Y: Belongs to the syndecan proteoglycan family.

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 CAA93474.1; -.
 T22846.
 .7.3; CE05996.
 .003585; Neurexin-like.
 .001050; Syndecan.
 ; Syndecan; 1.
 4; 4.1m; 1.
 964; SYNDECAN; 1.
 Heparan sulfate; Transmembrane; Glycoprotein; Signal.
 POTENTIAL.
 1 26
 PROBABLE SYNDECAN.
 27 288
 EXTRACELLULAR (POTENTIAL).
 32 231
 POTENTIAL.
 53 288
 CYTOPLASMIC (POTENTIAL).
 71 71
 N-LINKED (GLCNAc...) (POTENTIAL).
 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 14 214
 ASP/GLU-RICH (HIGHLY ACIDIC).
 42 161
 POLY-THR.
 75 181
 8 AA; 30979 MW; 10F14F119541341F CRC64;
 1.7%; Score 9; DB 1; Length 288;
 arity 100.0%; Pred. No. 7.6;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DEDEDE 340
 |||||
 DEDEDE 153
 STANDARD; PRT; 376 AA.
 7; Q9V5B6;
 Rel. 06, Created
 Rel. 40, Last sequence update
 Rel. 42, Last annotation update
 protein even-skipped.
 .
 .lanogaster (Fruit fly).
 .tazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 .pterygota; Diptera; Brachycera; Muscomorpha;
 .Drosophilidae; Drosophila.
 127;
 1 N.A.
 .744; PubMed=2877745;
 .Ingham P., Struhl G.;
 .structure, and expression of even-skipped: a second pair-
 .Drosophila containing a homeo box.";
 '34(1986).
 1 N.A.
 536; PubMed=2884106;
 1 N.A.
 Evans C.A., Gocayne J.D.,
 Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
 Amanatides P.G., Scher S.E., Richards S., Ashburner M., Henderson S.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.,
 Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers J.-H.C., Blazey R.G., Champe M., Pfeiffer B.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.N,
 Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Du
 Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dur
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmar
 Foster C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum
 Jalali M., Kalush C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.
 Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 Science 287:2185-2195(2000).
 [4]
 RN SEQUENCE OF 1-58 FROM N.A.
 RP STRAIN-OR-RC; WA-F, ZM56, AF-S, and FL-S;
 RC STRAIN-OR-RC; WA-F, ZM56, AF-S, and FL-S;
 RX MEDLINE=96038621; PubMed=8524036;
 Ludwig M.Z., Kreitman M.;
 "Evolutionary dynamics of the enhancer region of even-skipped in
 Drosophila.";
 Mol. Biol. Evol. 12:1002-1011(1995).
 [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 70-189.
 RX MEDLINE=96134926; PubMed=8557047;
 Hirsch J.A., Aggarwal A.K.;
 "Structure of the even-skipped homeodomain complexed to AT-rich I
 new perspectives on homeodomain specificity.";
 EMBO J. 14:6280-6291(1995).
 CC -!- FUNCTION: May play a role in determining neuronal identity. It
 CC directly involved in specifying identity of individual neuron
 CC pair-rule protein required for segmentation; involved in
 CC transforming the broad, spatial, aperiodic expression pattern
 CC the gap genes into a system of precise periodic expression
 CC patterns of the pair-rule and segmentary polarity genes.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the even-skipped homeobox family.
 CC -!- SIMILARITY: Contains 1 homeobox domain.
 CC -----
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AAA28522.1; -
CAA28784.1; -
; AAF59865.1; -
AAB05358.1; -
AAB05359.1; -
AAB05360.1; -
AAB05361.1; -
AAB05362.1; -
126066.
-JUL-01.
172; -.
000606; eve.
; P: determination of anterior/posterior axis, e. . . ; NAS.
01356; Homeobox.
homeobox; 1.
110; Homeobox; 1.
127; HOX; 1.
171; HOMEBOX_2; 1.
developmental protein; Embryo; Pair-rule protein;
regulation; Homeobox; Nuclear protein; 3D-structure.
0 129 HOMEBOX.
5 179 ALA-RICH.
10 300 L -> V (IN REF. 1).
; AA; 39970 MW; 59059E0634B1BED0 CRC64;
1.7%; Score 9; DB 1; Length 376;
urity 100.0%; Pred. No. 9.4;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
JAAA 126
||||
JAAA 173

STANDARD; PRT; 415 AA.
; Q9VGR5; Q9VGR6;
el. 36, Created
el. 36, Last sequence update)
el. 42, Last annotation update)
protein L3.

anogaster (Fruit fly).
azoa; Arthropoda; Hexapoda; Insecta; Pterygota;
pterygota; Diptera; Brachycera; Muscomorpha;
rosophilidae; Drosophila.
7;

N.A. (ISOFORM A).
17; PubMed=9661671;
hang Y., Hoheisel J.D., O'Kane C.J.;
n and characterization of the gene for Drosophila L3
ein".
25(1998).

N.A.
y;
06; PubMed=10731132;
liniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
i., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
ewis S.E., Richards S., Ashburner M., Henderson S.N.,
ortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
e C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

```

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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin
RA Ballw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M
RA Beeson K.Y., Berman P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000)
[3]
RN REVISIONS, AND ALTERNATIVE SPLICING.
RP MEDLINE=22426069; PubMed=12537572;
RX Misra S., Croesby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC -!- FUNCTION: The L3 protein is a component of the large subunit
CC cytoplasmic ribosomes.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=A; Synonyms=B, E;
CC IsoId=O16797-1; Sequence=Displayed;
CC Name=D;
CC IsoId=O16797-2; Sequence=VSP_005715, VSP_005717;
CC Name=C;
CC IsoId=O16797-3; Sequence=VSP_005714, VSP_005716;
CC -!- SIMILARITY: Belongs to the L3P family of ribosomal proteins.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL out
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```

0020910; RPL3.
000597; Ribosomal L3.
009000; Translat.Factor.
; Ribosomal L3; 1.
474; RIBOSOMAL L3; 1.
tein; Alternative splicing.
0
BY SIMILARITY.
21 137 WYKSKKAFKASKWT -> CSSISLLRELFKSLNV
(in isoform C).
/FTID-VSP 005714.
23 160 KSKKKAFTKASKWTDLDGKKSIENDFRMLRYCKVIR ->
VSEDHVVLPTEPVALFPAGVHTKMAADTCFLLES
(in isoform D).
/FTID-VSP 005715.
38 415 Missing (in isoform C).
/FTID-VSP 005716.
61 415 Missing (in isoform D).
/FTID-VSP 005717.
5 AA; 46784 MW; DE5964681FAF8A15 CRC64;
arity 1.7%; Score 9; DB 1; Length 415;
conservative 0; Pred.No.10;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
TAAAA 22
|||||
TAAAA 408
STANDARD; PRT; 416 AA.
Rel. 20, Created)
Rel. 20, Last sequence update)
Rel. 43, Last annotation update)
-skipped homolog protein 1 (EVX-1).
(Mouse).
; Chordata; Craniata; Vertebrata; Euteleostomi;
; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
090;
[N.A.
; TISSUE=Liver;
1218; PubMed=1971786;
; n-skipped homologue, Evx 1, is expressed during early
; and neurogenesis in a biphasic manner.";
9-1852(1990).
[N.A.
; 649; PubMed=1349539;
artin G.R.;
mouse Evx genes: Evx-1 displays graded expression in the
teak.";
1:273-287(1992).
May play a role in the specification of neuronal cell
ay play a role in the dorsoventral specification of
al cell fate.
AR LOCATION: Nuclear.
ENTRAL STAGE: Shows a graded distribution in the primitive
id in cells lateral to it. It is not detected in cells
; A-P axis of the embryo anterior to the primitive streak,
; E7.5 when there is transient expression in the head
The highest levels of expression are found within the
(posterior) portion of the primitive streak and cells
with expression levels decreasing more distally
ily).
CY: Belongs to the even-skipped homeobox family.
CY: Contains 1 homeobox domain.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X54239; CRA38145.1; -.
CC HSSP; P14653; 1B72.
CC TRANSFAC; T02023; -.
CC MGD; MGI:95461; Evx1.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Developmental protein; Homeobox; Nuclear protein.
FT DNA BIND 114 124 ASP/GLU-RICH (ACIDIC).
FT DNA BIND 183 242 HOMEBOX.
FT DOMAIN 289 297 ALA-RICH.
FT DOMAIN 341 349 ALA-RICH.
FT DOMAIN 369 375 ALA-RICH.
SQ SEQUENCE 416 AA; 43198 MW; 9F0EE4F3677CD3EE CRC64;
Query Match 1.7%; Score 9; DB 1; Length 416;
Best Local Similarity 100.0%; Pred.No.10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; C
QY 148 APRAAAAA 156
Db 366 APRAAAAA 374
|||||
RESULT 32
Y77A_STRCO
ID Y77A_STRCO STANDARD; PRT; 440 AA.
AC Q9FYI6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein SCO7700.
GN SCO7700 OR SCIA4.08 OR SCBAC12C8.01.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1147;
RA Watanabe M., Kawamoto S., Ochi K.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor
RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- SIMILARITY: Strong, to S.griseus 47.6 kDa protein in glk 3're
CC -----
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2; BAB20433.1; -;
2; CAD55534.1; -;
08949; Terpenoid synth.
protein; Complete proteome.
0 AA; 47792 MW; 0228C9B635F4CB2 CRC64;

1.7%; Score 9; DB 1; Length 440;
arity 100.0%; Pred. No. 11;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PPAP 139
|||||
PPAP 63

STANDARD; PRT; 482 AA.

rel. 41, Created)
rel. 41, Last sequence update)
rel. 42, Last annotation update)
helix-loop-helix protein 3 (bHLH3) (Differentially
chondrocytes protein 2) (hDEC2) (Enhancer-of-splc and
protein 1) (SHARP-1).
2 OR SHARP1.
(Human).
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
16;

N.A.
582; PubMed=1162494;
hen M., Noshiro M., Matsubara K., Shingu S., Honda K.,
ardica K., Matsuda Y., Kato Y.;
xing and characterization of DEC2, a new member of basic
ix proteins.";
ys. Res. Commun. 280:164-171(2001).

15; PubMed=11278948;
M., Roopra A., Buckley N.J.;
ix-loop-helix protein, SHARP-1, represses transcription
leacetylase-dependent and histone deacetylase-independent
276:14821-14828(2001).
May be a transcriptional repressor that represses both
activated transcription.
monodimerize.
R LOCATION: Nuclear (By similarity).
XIFITY: Highly expressed in skeletal muscle and brain,
, expressed in pancreas and heart, weakly expressed in
lung, liver and kidney.
(: Contains 1 basic helix-loop-helix (bHLH) domain.
(: Contains 1 orange domain.

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1; BAB21502.1; -;
1C7583.

DR Genew; HGNC:16617; BHLHB3.
DR MIM; 606200; -;
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0030154; P:cell differentiation; NAS.
DR GO; GO:0008283; P:cell proliferation; NAS.
DR GO; GO:0009887; P:organogenesis; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR003650; Orange.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00511; ORANGE; 1.
DR PROSITE; PS00888; HLH; 1.
KW Transcription regulation; Repressor; DNA-binding; Nuclear protein
FT DNA BIND 45 57 BASIC DOMAIN.
FT DOMAIN 58 100 HELIX-LOOP-HELIX MOTIF.
FT DOMAIN 129 175 ORANGE.
FT DOMAIN 297 431 ALA/GLY-RICH.
SQ SEQUENCE 482 AA; 50497 MW; 2BECDC2FDEB7CE14 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 482;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 118 APAAAAAAA 126
|||
Db 394 APAAAAAAA 402

RESULT 34

HLX1 HUMAN
ID HLX1 HUMAN STANDARD; PRT; 488 AA.
AC Q14774;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein HLX1 (Homeobox protein HB24).
GN HLX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=91291757; PubMed=1676597;
RA Deguchi Y., Moroney J.F., Wilson G.L., Fox C.H., Winter H.S.,
Kehrl J.H.;
RT "Cloning of a human homeobox gene that resembles a diverged
RT Drosophila homeobox gene and is expressed in activated lymphocyte
RL New Biol. 3:353-363(1991).
RN [2]
RP SEQUENCE OF 1-326 FROM N.A.
RX MEDLINE=95104845; PubMed=7806220;
RA Kennedy M.A., Rayner J.C., Morris C.M.;
RT "Genomic structure, promoter sequence, and revised translation of
RT human homeobox gene HLX1.";
RL Genomics 22:348-355(1994).
CC -I- FUNCTION: Putative transcription factor involved in embryogen
CC and hematopoiesis. May play an important role in lymphocytes
CC certain developing tissues.
CC -I- SUBCELLULAR LOCATION: Nuclear (potential).
CC -I- TISSUE SPECIFICITY: Low level expression seen in normal B and
CC lymphocytes, while a high level expression is seen in activat
CC lymphocytes and activated monocytes. Also found in the thymus
CC tonsil, bone marrow, developing vessels, and fetal brain.
CC -I- SIMILARITY: Belongs to the H2.0 homeobox family.
CC -I- SIMILARITY: Contains 1 homeobox domain.
CC -----
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: NOT_ANNOTATED_CDS.
: AAC51346.1; JOINED.
: AAC51346.1; JOINED.
: AAC51346.1; JOINED.
: AAC51346.1; JOINED.
: A55180.
: IPTT.
2051; -.
4978; HLX1.
-- P:development; TAS.
R001356; Homeobox.
R000047; HTH_lambrepresr.
5; homeobox; 1.
J24; HOMEBOX.
J31; HYHREPRESS.
J010; Homeobox; 1.
J9; HOX; 1.
J027; HOMEBOX 1; 1.
J071; HOMEBOX 2; 1.
1 regulation; DNA-binding; Homeobox; Nuclear protein.
120 123 POLY-HIS.
125 137 POLY-GLN.
138 142 POLY-PRO.
276 335 HOMEBOX.
428 431 POLY-GLY.
437 448 POLY-SER.
456 459 POLY-GLY.
63 63 MISSING (IN REF. 1).
69 116 AAATAHLSVHPHAFQAAARSPRLRPTVPAPSEVPAGFP
CRLSPLP -> PPPSPRTWARFRTLPSKRDPDPDPQW
WRPKSLASRSCRLRL (IN REF. 1).
QQQ -> RRE (IN REF. 1).
SGRVVFNPHSGSA -> RDAGSEPPPPQWLC (IN
REF. 1).
38 AA; 50799 MW; ACEIA91ADA9C851A CRC64;
1.7%; Score 9; DB 1; Length 488;
larity 100.0%; Pred. No. 12;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QPPPPP 229
|||||
QPPPPP 141

STANDARD; PRT; 490 AA.

(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
protein MOT3/HMS1.
OR YMR070W OR YMR916.09.
s cerevisiae (Baker's Yeast).
ungi; Ascomycota; Saccharomycotina; Saccharomycetes;
cales; Saccharomycetaceae; Saccharomycetes.
932;

N.A.
Winston F.;
PR-1995) to the EMBL/GenBank/DBJ databases.

N.A.
/ AB972;
3268; PubMed-9169872;

RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII.";
RL Nature 387:90-93 (1997).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 2 C2H2-type zinc fingers.
CC -----
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CC -----
CC EMBL; U25279; AAC49982.1; -.
DR EMBL; Z48952; CAA88795.1; -.
DR PIR; S52830; S52830.
DR GerMOnline; 142736; -.
DR TRANSFAC; T03448; -.
DR TRANSFAC; T03500; -.
DR SGD; S0004674; MOT3.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0003677; F:DNA binding; IPI.
DR GO; GO:0016564; F:transcriptional repressor activity; IDA.
DR GO; GO:0006350; P:transcription; IGI.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.
KW Nuclear protein; Zinc-finger; Metal-binding; Repeat.
FT ZN_FING 346 368 C2H2-TYPE 1.
FT ZN_FING 374 397 C2H2-TYPE 2.
FT DOMAIN 8 35 POLY-GLN.
FT DOMAIN 98 104 POLY-ASN.
FT DOMAIN 143 157 POLY-ASN.
FT DOMAIN 173 177 POLY-ALA.
FT DOMAIN 240 245 POLY-HIS.
FT DOMAIN 417 420 POLY-SER.
FT DOMAIN 421 433 POLY-ASN.
FT DOMAIN 441 450 POLY-ALA.
SQ SEQUENCE 490 AA; 54382 MW; 4D0DASDE43F171ED CRC64;

Query Match 1.7%; Score 9; DB 1; Length 490;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAAATAP 159
|||||
DB 443 AAAAAATAP 451

RESULT 36
PIAG_MOUSE
ID PIAG_MOUSE STANDARD; PRT; 507 AA.
AC Q9JMO5; Q8R165;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein gamma (PIAS-gamma)
DE (PIASy).
GN PIASG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE=Brain;

089; PubMed=10854042;
 h M., White F.A.;
 analysis of a murine Pias family member, Pias-gamma, in
 in and neurons.";
 sci. 14:107-121(2000).
 N.A.
 257; PubMed=12477932;
 L., Feingold B.A., Grouse L.H., Derge J.G.,
 Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
 J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Quallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Ewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Con E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 Adan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Touchman J.W., Green E.D., Dickson M.C.,
 Greenwood J., Schmutz J., Myers R.M.,
 S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 Schein J.E., Jones S.J.M., Marra M.A.;
 and initial analysis of more than 15,000 full-length
 se cDNA sequences.";
 cad. Sci. U.S.A. 99:16899-16903(2002).
 CELLULAR LOCATION, AND MUTAGENESIS OF CYS-330; CYS-335;
 340 AND 470-SER-SER-474.
 340; PubMed=11731474; 474.
 cuhn L., Sieber H., Pichler A., Melchior F.,
 lear matrix-associated SUMO E3 ligase, represses LEF1
 sequestration into nuclear bodies.";
 :3088-3103(2001).
 Specifically inhibits activated STAT signaling and acts
 as a transcriptional corepressor of STAT1, without blocking its
 activity. Represses the activity of a Wnt-responsive
 transcription factor, LEF1, by stimulating sumoylation and
 sequestration into nuclear bodies. Also interacts with the C-
 region of tumor suppressor protein p53 and inhibits p53-
 mediated transcriptional activity.
 AR LOCATION: Nuclear.
 ICIFICITY: During embryo development, expressed in the
 part of the neural tube (E8.5), neuroepithelium of the
 and hindbrain (E10.5), neural tube, eye, limb buds and
 arches (E11.5), hindlimbs, forelimbs and forebrain
 developing limb buds and single cells of the mesenchyme
 of future digit structures (E13.5), inner root sheath of
 hair follicle (E15.5) and epithelium of olfactory and the
 (E6.5). In adult mice, expressed in most major organs, but
 liver and lung.
 TIAL STAGE: In the embryo, expressed from day 7.5 and
 throughout development. Also expressed in the adult.
 : Contains 1 SAP domain.
 : Contains 1 MIZ-type zinc finger.

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 mail to license@isb-sib.ch).

 i; AAF72040.1; -;
 i; AAH25159.1; -;
 i; 340; Piasg.
 i; C:nuclear matrix; IDA.

DR GO; GO:0003677; F:DNA binding; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0019789; F:SUMO ligase activity; IDA.
 DR GO; GO:0003714; F:transcription co-repressor activity; IDA.
 DR GO; GO:0016564; F:transcriptional repressor activity; IDA.
 DR GO; GO:0008270; F:zinc ion binding; NAS.
 DR GO; GO:0007275; P:development; NAS.
 DR GO; GO:0001122; P:negative regulation of transcription from P.
 DR GO; GO:0016481; P:negative regulation of transcription; ISS.
 DR GO; GO:0016925; P:protein sumoylation; IDA.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 KW Transcription regulation; Repressor; Developmental protein;
 KW DNA-binding; Ub1 conjugation pathway; Nuclear protein; Zinc-finger
 KW Metal-binding; Zinc.
 FT DOMAIN 12 46
 FT ZN_FING 315 367
 FT MUTAGEN 330 330
 FT MUTAGEN 335 335
 FT MUTAGEN 337 337
 FT MUTAGEN 340 340
 FT MUTAGEN 470 474
 FT CONFLICT 230 230 K -> N (IN REF. 1).
 FT CONFLICT 417 417 L -> H (IN REF. 1).
 FT CONFLICT 494 494 K -> N (IN REF. 1).
 SQ SEQUENCE 507 AA; 55569 MW; A83E6E3BAC76426 CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 507;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 Qy 332 EDDEDEDE 340
 Db 481 EDDEDEDE 489
 RESULT 37
 SIS2 YEAST
 ID -SIS2 YEAST STANDARD; PRT; 562 AA.
 AC P36024;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SIS2 protein (Halotolerance protein HAL3).
 GN SIS2 OR HAL3 OR YKR072C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95220693; PubMed=7705654;
 RA di Como C.J., Bose R., Arndt K.T.;
 RT "Overexpression of SIS2, which contains an extremely acidic regio-
 increases the expression of SWI4, CLN1 and CLN2 in sit4 mutants."
 RL Genetics 139:95-107(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pohl T.M., Pohl F.M.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=96009574; PubMed=7565698;
 RA Ferrando A., Kron S.J., Rios G., Fink G.R., Serrano R.;
 RT "Regulation of cation transport in Saccharomyces cerevisiae by the
 salt tolerance gene HAL3.";
 RL Mol. Cell. Biol. 15:5470-5481(1995).
 RN [4]
 RP IDENTIFICATION AS INHIBITORY SUBUNIT OF PP21.

1578; PubMed=9636153;
 Clotet J., Fosas R., Serrano R., Gomez N., Arino J.;
 tolerance determinant Halp3 is an inhibitory subunit of
 r/thr protein phosphatase.";
 Acad. Sci. U.S.A. 95:7357-7362(1998).
 : May stimulate expression of certain genes that are
 ally expressed during late G1. Also modulates the
 on of the enal ATPase. Interacts with the C-terminal
 f the serine-threonine protein phosphatase PP21 and acts
 inhibitory subunit of PP21.
 AR LOCATION: NUCLEAR OR CYTOPLASMIC.
 TY: TO C.TROPICALIS SIS2/HAL3 AND TO YEAST YKL088W. SOME,
 JIANA HAL3A AND HAL3B.
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 ail to license@isb-sib.ch).
 : AAA80000.1; -;
 : CAAG2151.1; -;
 S38149.
 : LE20.
 140051; -;
 : SIS2.
 37; C:cytoplasm; IC.
 34; C:nucleus; IDA.
 54; F:protein phosphatase inhibitor activity; IDA.
 32; P:G1/S transition of mitotic cell cycle; IGI.
 46; P:regulation of mitotic cell cycle; IGI.
 51; P:salinity response; IGI.
 003382; Flavoprotein.
 1; Flavoprotein; 1.
 196 553 ASP/GLU-RICH (HIGHLY ACIDIC).
 52 AA; 62478 MW; 19A9A75154DA7AB CRC64;
 1.7%; Score 9; DB 1; Length 562;
 arity 100.0%; Pred. No. 13;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DDEDE 338
 |||||
 DDEDE 504
 STANDARD; PRT; 565 AA.
 (Rel. 40, Created)
 (Rel. 40, Last sequence update)
 (Rel. 43, Last annotation update)
 protein J2 (Fork head homologous X).
 (Mouse).
 stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 0090;
 N.A.
 0369; PubMed=11025217;
 , Arias-de-la-Fuente C., Perez-Sanchez C., Parraga M.,
 dez L.A., del Mazo J., Rey-Campos J.;
 expression is activated during spermatogenesis and very
 rnyonic development.";
 7:157-160(2000).
 N.A.
 ; TISSUE=Salivary gland;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
 Brownstein M.J., Udwin T.B., Toshlyuki S., Carninci P., Prange C
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanche
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL -!- FUNCTION: Transcriptional activator. Able to bind to two dif
 CC -!- TYPE OF DNA binding sites.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 fork-head domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a col
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 CC
 CC EMBL; AF253052; AAG30406.1; -;
 DR EMBL; BC040395; AAH40395.1; -;
 DR HSP; O63245; 2HFH.
 DR TRANSFAC; T04170; -;
 DR MGD; MGI:1526805; Foxj2.
 DR InterPro; IPR001766; TF Fork head.
 DR Pfam; PF00250; Fork head; 1.
 DR PRINTS; PR00053; FORKHEAD.
 DR ProDom; PD000425; TF_Fork_head; 1.
 DR SMART; SM00339; FH; 1.
 DR PROSITE; PS00657; FORK_HEAD_1; FALSE NEG.
 DR PROSITE; PS00658; FORK_HEAD_2; 1.
 DR PROSITE; PS00659; FORK_HEAD_3; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein; Activato
 FT DNA_BIND 66 143 FORK-HEAD.
 FT DOMAIN 266 269 POLY-SER.
 FT DOMAIN 290 296 POLY-GLN.
 FT DOMAIN 306 314 POLY-GLN.
 SQ SEQUENCE 565 AA; 61569 MW; 9178AFF3F9227AD4 CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 565;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 227 PPPQPPPP 235
 Db 297 PPPQPPPP 305
 RESULT 39
 FXJ2 HUMAN
 ID FXJ2 HUMAN STANDARD; PRT; 574 AA.
 AC Q9P0K8; Q9P0K8; Q9NSN5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Forkhead box protein J2 (Fork head homologous X).
 GN FOXJ2 OR FOX.
 OS Homo sapiens (Human).

Chordata; Craniata; Vertebrata; Euteleostomi;
 Seria; Primates; Catarrhini; Homiidae; Homo.
 36;
 N.A. (ISOFORM FOXJ2.L).
 944; PubMed=10777590;
 C., Gomez-Ferrera M.A., de la Fuente C.A.,
 Velasco G., Esteban A., Rey-Campos J.,
 fork factor with a dual DNA binding specificity.";
 . 275:12909-12916(2000).
 N.A. (ISOFORM FOXJ2.S).
 082; PubMed=10966786;
 C., de la Fuente C.A., Gomez-Ferrera M.A.,
 Key-Campos J.;
 X.S., two isoforms of the human fork-head factor FOX
 differential activity.";
 301:795-806(2000).
 58-574 FROM N.A. (ISOFORM FOXJ2.L).
 na;
 Irkner U., Mewes H.-W., Weil B., Wiemann S.;
 2-2000) to the EMBL/GenBank/DBJ databases.
 Transcriptional activator. Able to bind to two different
 NA binding sites. Isoform FOXJ2.L behaves as a more
 inactivator than FOXJ2.S.
 IR LOCATION: Nuclear.
 IE PRODUCTS:
 ernative splicing; Named isoforms=2;
 2.L; Synonyms=FXH.L;
 3POK8-1; Sequence=Displayed;
 2.S; Synonyms=FXH.S;
 3POK8-2; Sequence=VSP_001544;
 3CIFICITY: Widely expressed.
 1; Contains 1 fork-head domain.
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 ail to license@isb-sib.ch).
 ; AAF65927.1; -
 ; AAK49016.1; -
 ; CAB82315.1; -
 47161.
 2HFH.
 69; -
 71; -
 01766; TF Fork head.
 Fork head; 1.
 3; FORKHEAD.
 25; TF Fork head; 1.
 3; FH; 1.
 57; FORK HEAD 1; FALSE_NEG.
 58; FORK HEAD 2; 1.
 39; FORK HEAD 3; 1.
 regulation; DNA-binding; Nuclear protein; Activator;
 splicing.
 6 143 FORK-HEAD.
 6 270 POLY-SER.
 1 294 POLY-GLN.
 5 298 POLY-PRO.
 9 306 POLY-GLN.
 13 321 POLY-GLN.
 30 395 POLY-PRO.
 13 574 VNSVGHQAELHVPSPMTPIPTQDSAGYNRPAAHVMVPRP
 SVPPPGANEIPDDFDWLLT -> GTAPSPWRRLC
 (in isoform FOXJ2.S).
 /FTid=VSP_001544.
 1 AA; 62394 MW; 258120EDAE4B11EB CRC64;

Query Match 1.7%; Score 9; DB 1; Length 574;
 Best Local Similarity 100.0%; Pred.No. 13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 222 QQQQPPPPQ 230
 Db 291 QQQQPPPPQ 299

RESULT 40
 ZICS HUMAN
 ID_ZICS_HUMAN STANDARD; PRT; 639 AA.
 AC Q96T25;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein ZIC 5 (Zinc finger protein of the cerebellum
 ZIC5.
 GN Homo sapiens (Human).
 OS
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gou D.M., Li W.X., Gao L., Sun Y.;
 RT "A novel human zinc finger gene, hZic5.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
 CC PROTEINS.
 CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.
 CC
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 CC
 CC EMBL; AF378304; AAK55418.1; -
 CC Genew; HGNC:20322; ZIC5.
 CC InterPro; IPR007087; Znf_C2H2.
 CC Pfam; PF00096; zf-C2H2; 4.
 CC ProDom; PD000003; Znf_C2H2; 1.
 CC SMART; SM00355; Znf_C2H2; 5.
 CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 CC PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
 CC Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein.
 KW DOMAIN 82 400 PRO-RICH.
 FT DOMAIN 262 321 ALA-RICH.
 FT ZN_FING 434 461 C2H2-TYPE 1.
 FT ZN_FING 467 491 C2H2-TYPE 2.
 FT ZN_FING 497 521 C2H2-TYPE 3.
 FT ZN_FING 527 551 C2H2-TYPE 4.
 SQ SEQUENCE 639 AA; 65849 MW; FB1E966ED28D38BF CRC64;

Query Match 1.7%; Score 9; DB 1; Length 639;
 Best Local Similarity 100.0%; Pred.No. 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 131 PAPPAPPAP 139
 Db 334 PAPPAPPAP 342

RESULT 41
 ELS RAT
 ID_ELS_RAT STANDARD; PRT; 864 AA.
 AC Q99372;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

```

InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Structural protein; Connective tissue; Repeat; Signal;
Alternative splicing.
NON_TER 1
SIGNAL <1 21 BY SIMILARITY.
CHAIN 22 864 ELASTIN.
DISULFID 854 859 BY SIMILARITY.
VARSPPLIC 263 307 Missing (in isoform 2, isoform 5, i
7 and isoform 8).
/FTId=VSP_004244.
VARSPPLIC 308 308 Missing (in isoform 3, isoform 5, i
6 and isoform 8).
/FTId=VSP_004245.
VARSPPLIC 809 823 Missing (in isoform 4, isoform 6, i
7 and isoform 8).
/FTId=VSP_004246.
SEQUENCE 864 AA; 72786 MW; 456894BB09E79FD4 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 864;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

OY 117 GAPAAAAAA 125
|||||
Db 715 GAPAAAAAA 723

RESULT 42
A180 MOUSE STANDARD; PRT; 901 AA.
IID A180 MOUSE
AC Q61548; Q61547;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Clathrin coat assembly protein APL80 (Clathrin coat associated p
APL80) (91 kDa synaptosomal-associated protein) (Phosphoprotein
201).
DE DE 201.
DE SNAP91.
OS Mus musculus (Mouse).
GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT) .
MEDLINE=92300439; PubMed=1607933;
Zhou S., Sousa R., Tannery N.H., Lafer E.M.;
"Characterization of a novel synapse-specific protein. II. cDNA
cloning and sequence analysis of the F1-20 protein.";
J. Neurosci. 12:2144-2155(1992).
-!- FUNCTION: Adaptins are components of the adaptor complexes w
link clathrin to receptors in coated vesicles. Clathrin-asso
protein complexes are believed to interact with the cytoplasi
tails of membrane proteins, leading to their selection and
concentration. Binding of APL80 to clathrin triskelia induce
their assembly into 60-70 nm coats.
-!- SUBCELLULAR LOCATION: Component of the coat surrounding the
cytoplasmic face of coated vesicles in the plasma membrane.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Long;
IsoId=Q61548-1; Sequence=Displayed;
Name=Short;
IsoId=Q61548-2; Sequence=VSP_000172;
-!- TISSUE SPECIFICITY: Brain. Associated with the synapses.
-!- DEVELOPMENTAL STAGE: Developmentally regulated in a pattern
coincident with active synaptogenesis and synaptic maturati
-!- DOMAIN: Possesses a three domain structure: the N-terminal 30
residues harbor a clathrin binding site, an acidic middle do
450 residues, interrupted by an Ala-rich segment, and the C-
terminal domain (166 residues).
-!- PTM: Phosphorylated.
-!- SIMILARITY: Contains 1 ensin N-terminal homolog (ENTH) doma

```

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 AAA37587.1; -;
 AAA37586.1; -;
 14825.
 12; Snap91.
 01026; ENTH.
 08943; PI_bind_N.
 1; ENTH; 1.
 142; ENTH; 1.
 Alternative splicing; Phosphorylation.
 4 145 ENTH.
 0 413 POLY-THR.
 5 539 POLY-ALA.
 7 550 POLY-ALA.
 9 664 POLY-SER.
 14 710 POLY-SER.
 5 719 Missing (in isoform Short).
 /FTid=VSP_000172.
 . AA; 91851 MW; 2498FBACE8DB8B1 CRC64;
 1.7%; Score 9; DB 1; Length 901;
 identity 100.0%; Pred. No. 20;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TAAA 21
 |||||
 TAAA 555

STANDARD; PRT; 915 AA.

Rel. 35, Created)
 Rel. 35, Last sequence update)
 Rel. 43, Last annotation update)
 assembly protein AP180 (Clathrin coat associated protein
 synaptosomal-associated protein).
 cus (Rat).
 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 16;
 N.A. (ISOFORMS LONG AND SHORT).

42; PubMed=8440257;
 Schroeder S.; Plesmann U., Weber K., Ungewickell E.;
 mly protein AP180: Primary structure, domain
 and identification of a clathrin binding site.";
 "-675(1993).
 Adaptins are components of the adaptor complexes which
 rin to receptors in coated vesicles. Clathrin-associated
 mplexes are believed to interact with the cytoplasmic
 membrane proteins, leading to their selection and
 ion. Binding of AP180 to clathrin triskelia induces
 mly into 60-70 nm coats.
 AR LOCATION: Component of the coat surrounding the
 c face of coated vesicles in the plasma membrane.
 E PRODUCTS:
 nnative splicing; Named isoforms=2;
 5140-1; Sequence=Displayed;

 IsoId=Q05140-2; Sequence=VSP_000173;
 -1- DOMAIN: Possesses a three domain structure: the N-terminal 30
 residues harbor a clathrin binding site, an acidic middle dom
 450 residues, interrupted by an Ala-rich segment, and the C-
 terminal domain (166 residues).
 -1- PTM: Phosphorylated (By similarity).
 -1- SIMILARITY: Contains 1 epsin N-terminal homology (ENTH) domai

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 or send an email to license@isb-sib.ch).

 EMBL; X68877; CAA48748.1; -;
 EMBL; X68878; CAA48749.1; -;
 PIR; S36326; S36326.
 PIR; S36327; S36327.
 DR InterPro; IPR001026; ENTH.
 DR InterPro; IPR008943; PI_bind_N.
 DR Pfam; PF01417; ENTH; 1.
 DR SMART; SM00273; ENTH; 1.
 DR PROSITE; PS00942; ENTH; 1.
 KW Coated pits; Alternative splicing; Phosphorylation.
 FT DOMAIN 14 145 ENTH.
 FT DOMAIN 410 413 POLY-THR.
 FT DOMAIN 535 539 POLY-ALA.
 FT DOMAIN 547 550 POLY-ALA.
 FT DOMAIN 678 683 POLY-SER.
 FT DOMAIN 723 729 POLY-SER.
 FT VARSPLIC 614 632 Missing (in isoform Short).
 /FTid=VSP_000173.
 SQ SEQUENCE 915 AA; 93518 MW; 32EC1B38EC5DF8C0 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 915;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 13 AAAATTAAA 21
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 Db 547 AAAATTAAA 555

RESULT 44
 ID_MCR_HUMAN STANDARD; PRT; 984 AA.
 AC P08235; Q96KQ8; Q96KQ9;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mineralocorticoid receptor (MR).
 GN NR3C2 OR MLR OR MCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
 RC TISSUE=Kidney;
 RX MEDLINE=87263386; PubMed=3037703;
 RA Arriaza J.L., Weinberger C., Cerelli G., Glaser T.M., Handelin B.L.
 RA Housman D.E., Evans R.M.;
 RT "Cloning of human mineralocorticoid receptor complementary DNA:
 RT structural and functional kinship with the glucocorticoid receptor;
 RL Science 237:268-275(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4), TISSUE SPECIFICITY,
 RP INTERACTIONS WITH NCOAL1, TIF1 AND NR1F1, AND VARIANTS VAL-180 AND
 RP VAL-241.
 RC TISSUE=Heart;
 RX MEDLINE=21410115; PubMed=11518808;

Souque A., Viengchareun S., Poisson E., Lombes M.;
MR splice variant is a ligand-independent transactivator
of glucocorticoid action.";
Mol. 15:1586-1598(2001).

445-984 FROM N.A., AND DISEASE.
1781; PubMed=962404;
Rodriguez-Soriano J., Vallo Boado A., Schifter S.,
ing S.S., Lifton R.P.;
The mineralocorticoid receptor gene cause autosomal
recessive hypokalemia type 1.";
Am. J. Hum. Genet. 59:279-281(1998).

OCATION, AND PHOSPHORYLATION.
1536; PubMed=1655735;
Makymowych A.B., Robertson N.M., Litwack G.;
Isolation and characterization of the human mineralocorticoid
receptor cDNA.
Mol. Cell. Biochem. 166:180-188(1997).

IN OF ISOFORM 3.
1549; PubMed=7495694;
Luo C., Pratt J.H.;
Cloning of a splice variant of the rat and human
mineralocorticoid receptor genes.";
Mol. Cell. Biochem. 166:180-188(1997).

1. 266:18072-18081(1991).

EX WITH HSP90; HSP70 AND FKBP4, AND DISSOCIATION UPON
BINDING.
1330; PubMed=9332437;
Derfoul A., Robertson N.M., Guerriero G.,
Iemmi T., Alnemri E.S., Litwack G.;
The mineralocorticoid receptor is associated with heat
shock protein 90 and the immunophilin FKBP-52.";
Mol. Cell. Biochem. 166:180-188(1997).

OF CYS-808; CYS-849 AND CYS-942.
1467; PubMed=9724527;
Luo C., Pratt J.H.;
Cloning of a splice variant of the rat and human
mineralocorticoid receptor genes.";
Mol. Cell. Biochem. 166:180-188(1997).

OF ASN-770; GLN-776; ARG-817 AND THR-945.
1548; PubMed=10760050;
Luo C., Pratt J.H.;
Cloning of a splice variant of the rat and human
mineralocorticoid receptor genes.";
Mol. Cell. Biochem. 166:180-188(1997).

WITH NCOAL1, TIF1 AND NR1P1, AND MUTAGENESIS OF LEU-952;
-954; PHE-956 AND PRO-957.
1588; PubMed=10935545;
Luo C., Pratt J.H.;
Cloning of a splice variant of the rat and human
mineralocorticoid receptor genes.";
Mol. Cell. Biochem. 166:180-188(1997).

OCATION, AND INTERACTION WITH HSD11B2.
1362; PubMed=11350956;
Arnold P., Frey F.J.;
The mineralocorticoid receptor is
located in the nucleus of the mineralocorticoid receptor is
11beta-hydroxysteroid dehydrogenase type 2.";
Mol. Cell. Biochem. 166:180-188(1997).

RN VARIANTS VAL-180; THR-444; GLN-537 AND SER-554.
RX MEDLINE=99318094; PubMed=10391210;
RA Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.
Cooper R., Lipshutz R., Chakravarti A.;
Patterns of single-nucleotide polymorphisms in candidate genes:
blood-pressure homeostasis.";
Nat. Genet. 22:239-247(1999).

[13]
RN CHARACTERIZATION OF VARIANT PHA1 PRO-924.
RX MEDLINE=20576523; PubMed=11134129;
RA Tajima T., Kitagawa H., Yokoyama S., Tachibana K., Adachi M., Nakai
Suwa S., Katoh S., Fujieda K.;
A novel missense mutation of mineralocorticoid receptor gene in
Japanese family with a renal form of pseudohypoaldosteronism type
1. Clin. Endocrinol. Metab. 85:4690-4694(2000).

[14]
RN VARIANT EARLY ONSET HYPERTENSION LEU-810, AND MUTAGENESIS OF SER-
MEDLINE=20342438; PubMed=10842226;
RA Geller D.S., Farhi A., Pinkerton N., Fradley M., Moritz M.,
Spitzer A., Meinke G., Tsai F.T.F., Sigler P.B., Lifton R.P.;
Activating mineralocorticoid receptor mutation in hypertension
exacerbated by pregnancy.";
Science 289:119-123(2000).

[15]
RN CHARACTERIZATION OF VARIANTS VAL-180 AND VAL-241.
RX MEDLINE=22370905; PubMed=12483305;
RA Arai K., Nakagami Y., Iketani M., Shimura Y., Amemiya S., Ohyama
Shibasaki T.;
Functional polymorphisms in the mineralocorticoid receptor and
amiloride-sensitive sodium channel genes in a patient with sporadic
pseudohypoaldosteronism.";
Hum. Genet. 112:91-97(2003).

CC -!- FUNCTION: Receptor for both mineralocorticoids (MC) such as
aldosterone and glucocorticoids (GC) such as corticosterone (CORT).
Binds to mineralocorticoid response elements (MRE)
and water transport and thus raise extracellular fluid volume
and blood pressure and lower potassium levels.

CC -!- SUBUNIT: Heteromultimeric cytoplasmic complex with HSP90, HSP
and FKBP4. In the absence of ligand. After ligand binding, it
translocates to the nucleus and binds to DNA as a homodimer (or
a heterodimer with NR3C1). Binds the coactivator NCOA2 (By
similarity). May interact with HSD11B2 in the absence of ligand.
Binds the coactivators NCOA1, TIF1 and NR1P1.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear in the absence
of ligand; nuclear after ligand-binding. When bound to HSD11B2,
found associated with the endoplasmic reticulum membrane.

CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=P08235-1; Sequence=Displayed;
Name=2;
IsoId=P08235-2; Sequence=VSP_007358, VSP_007359;
Note=Lacks steroid-binding activity and acts as
ligand-independent transactivator;
Name=3;
IsoId=P08235-3; Sequence=VSP_007357;
Name=4; Synonyms=Delta;
IsoId=P08235-4; Sequence=VSP_007360;
TISSUE SPECIFICITY: Ubiquitous. Highly expressed in distal
tubules, convoluted tubules and cortical collecting duct in
kidney, and in sweat glands. Detected at lower levels in
cardiomyocytes, in epidermis and in colon enterocytes.

CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
a DNA-binding domain and a C-terminal steroid-binding domain.
PTM: Phosphorylated.

CC -!- DISEASE: Defects in NR3C2 are a cause of autosomal dominant
pseudohypoaldosteronism type 1 (PHA1) [MIM:177735]. PHA1 is
characterized by urinary salt wasting, resulting from target
unresponsiveness to mineralocorticoids. There are 2 forms of
the autosomal dominant form that is mild, and the recessive form

more severe and due to defects in any of the epithelial inner subunits. In autosomal dominant PHAI the target act is confined to kidney. Clinical expression can vary from asymptomatic to moderate. It may be severe at birth, but remit with age. Familial and sporadic cases have been reported.

Defects in NR3C2 are a cause of early onset hypertension (SH), with severe exacerbation in pregnancy. Inheritance is autosomal recessive. The disease is characterized by the onset of hypertension before the age of 20, and by suppression of aldosterone secretion.

NR3C2 belongs to the nuclear hormone receptor family. NR3C2

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1.7%; Score 9; DB 1; Length 984;
Identity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

pppp 229
|||||
pppp 697

STANDARD; PRT; 987 AA.

rel. 41, Created)
rel. 41, Last sequence update)
rel. 42, Last annotation update)
translation initiation factor 3 subunit 10 (eIF-3 theta)
translation initiation factor 3 large subunit (eIF3a)

H1420 OR F35E4.40.
Maliana (Mouse-ear cross).
Maliplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; rosids;
brassicales; Brassicaceae; Arabidopsis.
12;

N.A.
umbia;
76; PubMed=11042177;
zerra P.P., Le H., Gallie D.R., Browning K.S.;
ion factor 3 subunit composition resembles mammalian
For 3 and has a novel subunit.";
276:2122-2131 (2001).

N.A.
umbia;
88; PubMed=10617198;
Schueller C., Wambutt R., Murphy G., Volckaert G.,
erhoeft A., Stiekema W., Entian K.-D., Terryn N.,
orge W., Brandt P., Grivell L.A., Rieger M.,
r M., de Simone V., Obermaier B., Mache R., Mueller M.,
eny M., Puigdomenech P., Watson M., Schmidtheini T.,
ortetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
el J., Zimmermann W., Wedler M., Ridley P.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E
RA Weitzenecker T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Bael
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Maye
RA Pettitt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Blocker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandjean K., Dauner D., Herzl
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedford P., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K
RA Parnell L., Dedhia N., Gao J., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Bernghoff A., Jones K., Drone K., Cotton M., Joshi
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
CC -1- FUNCTION: Binds to the 40S ribosome and promotes the binding
CC -1- methionyl-tRNA and mRNA.
CC -1- SUBUNIT: eIF-3 is composed of at least 12 different subunits.
CC -1- SIMILARITY: Contains 1 PCI domain.
CC -1- SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
CC -----
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CC -----
CC EMBL; AF291711; AAC53635.1; -;
CC EMBL; AL050399; CAB82147.1; -;
CC EMBL; AL161531; CAB81243.1; -;
CC FIR; T10562; T10562.
CC InterPro; IPR000717; PCI.
CC Pfam; PF01399; PCI; 1.
CC SMART; SM00088; PINT; 1.
KW Initiation factor; Protein biosynthesis.
FT DOMAIN 436 510 PCI.
SQ SEQUENCE 987 AA; 114298 MW; F38BA715209D55FB CRC64;

Query Match 1.7%; Score 9; DB 1; Length 987;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 APAAAAAAA 126
Db 881 APAAAAAAA 889

STANDARD; PRT; 1065 AA.
 19; (Rel. 40, Created)
 (Rel. 40, Last sequence update)
 (Rel. 42, Last annotation update)
 21 kinase, iota (EC 2.7.1.107) (Diglyceride kinase) (DGK-
 inase iota).
 (Human).
 stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Theria; Primates; Catarrhini; Hominidae; Homo.
 506;
 4 N.A.
 7655; PubMed=9830018;
 ar E., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
 and characterization of a novel human diacylglycerol
 iota.";
 n. 273:32746-32752(1998).
 135-1065 FROM N.A., AND VARIANT PHE-153.
 3854; PubMed=10706894;
 Sullivan L.S., Ding L., Traer E., Prescott S.M.,
 Keman A., Humphries P., Daiger S.P.;
 of human diacylglycerol kinase iota, DGKI, a homolog of
 39A, in inherited retinopathy mapping to 7q.";
 5:6-9(2000).
 2 ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
 ycerol 3-phosphate.
 IAR LOCATION: Nuclear and cytoplasmic.
 FY: Belongs to the eukaryotic diacylglycerol kinase
 domain.
 FY: Contains 2 zinc-dependent phorbol-ester and DAG
 domains.
 FY: Contains 2 ANK repeats.
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product interacts with a fork head protein in cerevisiae.";
[70(1995)].

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AB972;
PubMed=9169871;
fillier L., Riles L., Albermann K., Andre B., Ansoerge W.,
Kner M., Delius H., Dubois E., Dueterhoeft A.,
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Urrestarazu L.A., Vandenbol M., Verhasselt P.,
Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
mermann F.K., Zollner A., Hani J., Hoheisel J.D.;
le sequence of Saccharomyces cerevisiae chromosome XII.";
90(1997).
Controls the pre-rRNA processing machinery in
n with PHL1. Could convert PHL1 from a repressor
vator.

AR LOCATION: Nuclear (Probable).

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CRA82624.1; -;
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S5352.
1285; -;
IFHL.

; P:chromatin silencing at telomere; IMP.
; P:RNA processing; IGI.
in; Transcription regulation.
22 163 ASP/GLU-RICH (HIGHLY ACIDIC).
15 AA; 122491 MW; BEIC7DEF06213FE0 CRC64;

1.7%; Score 9; DB 1; Length 1085;
arity 100.0%; Pred.No.23;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DDDED 337
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DDDED 141

STANDARD; PRT; 1137 AA.

rel. 17, Created)
rel. 17, Last sequence update)
rel. 42, Last annotation update)
repair protein Men3 (Divergent upstream protein) (DUP)
r protein 1) (MRP1).
r DUC1.
(Human).
:azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
6;

N.A.
190; PubMed=2722860;
ada T.;

i characterization of cDNA clones derived from the
anscribed gene in the region upstream from the human

RT dihydrofolate reductase gene.";
RL J. Biol. Chem. 264:10057-10064(1989).
RN [2]
RX SEQUENCE FROM N.A., AND VARIANT ALA-1045.
RA MEDLINE=97098445; PubMed=8942985;
RA Acharya S., Wilson T., Gradia S., Kane M.F., Guerrette S.,
RA Marsischky G.T., Kolodner R., Fishel R.;
RT "hMSH2 forms specific mismatch-binding complexes with hMSH3 and
RT hMSH6.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13629-13634(1996).
CC -1- FUNCTION: NOT KNOWN. PROBABLE DNA-REPAIR PROTEIN
CC -1- DISEASE: Defects in MSH3 are a cause of susceptibility to
CC endometrial cancer [MIM:608089].
CC -1- SIMILARITY: Belongs to the DNA mismatch repair mutS family.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).

CC
DR EMBL; J04810; BAB47281.1; -;
DR EMBL; U61981; AAB6045.1; -;
DR PIR; A33507; A33507.
DR Genew; HGNC:7326; MSH3.
DR MIM; 600887; -;
DR MIM; 608089; -;

DR GO; GO:0006298; P:mismatch repair; TAS.
DR InterPro; IPR000432; MutS_C.
DR InterPro; IPR007860; MutS_I.
DR InterPro; IPR007696; MutS_III.
DR InterPro; IPR007695; MutS_N.
DR Pfam; PF01624; MutS_I_1.
DR Pfam; PF05188; MutS_II_1.
DR Pfam; PF05192; MutS_III_1.
DR Pfam; PF00488; MutS_V_1.
DR ProDom; PD001263; MutS_C_1.
DR SMART; SM00534; MUTSAC; 1.
DR SMART; SM00533; MUTSD; 1.
DR PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
KW DNA repair; ATP-binding; DNA-binding; Polymorphism.
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FT NP BIND 896 903 ATP POTENTIAL).
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FT VARIANT 949 949 R -> Q (in dbSNP:184967).
FT VARIANT 1045 1045 /FTID=VAR_016161.
FT VARIANT 1054 1054 /FTID=VAR_016162.
FT VARIANT 1054 1054 /FTID=VAR_016163.
FT CONFLICT 57 65 MISSING (IN REF. 2).
FT CONFLICT 622 622 G -> E (IN REF. 2).
SQ SEQUENCE 1137 AA; 127383 MW; 704D1194E336848E CRC64;

Query Match 1.7%; Score 9; DB 1; Length 1137;
Best Local Similarity 100.0%; Pred.No.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G.

QY 120 AAAAAAAPP 128
Db 56 AAAAAAAPP 64

RESULT 49

NRDC HUMAN
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AC 043847; O15241; O15242; Q96HB2; Q9NU57;
DT 15-DEC-1998 (Rel. 37, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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recurso (EC 3.4.24.61) (N-arginine dibasic convertase)
(see) (NRD-C).
(Human).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominidae; Homo.
06;
1 N.A. (ISOFORM 1).
123; PubMed=9479496;
Accarino M., Egeo A., Scartezzini P., Rappazzo G.,
vvanaggiato V., Simeone A., Arrigo G., Zuffardi O.,
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nterbase: a highly conserved metalloendopeptidase
specific sites during development and in adult
138-245(1998).
1 N.A. (ISOFORMS 1 AND 2).
1;
1057; PubMed=9581555;
Prat A., Joulie C., Cherif D., Day R., Cohen P.;
at testis express two mRNA species encoding variants of
se, a metalloendopeptidase of the insulinase family.;
127:773-779(1997).
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ita;
1257; PubMed=12477932;
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Zeberg B., Suec K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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and initial analysis of more than 15,000 full-length
ise cDNA sequences";
Acad. Sci. U.S.A. 99:16899-16903(2002).
1-107 FROM N.A.
3757; PubMed=11042131;
Pierotti A.R.;
sion of the dibasic-pair cleaving enzyme NRD convertase
ibasic convertase) is differentially regulated in the
/ and Mat-Lu prostate cell lines.";
151:755-764(2000).
289-1150 FROM N.A.
EB-2000) to the EMBL/GenBank/DBJ databases.
: Cleaves peptide substrates on the N-terminus of arginine
in dibasic pairs.
: ACTIVITY: Hydrolysis of polypeptides, preferably at
f-Lys, and less commonly at Arg-|-Arg-Xaa, in which Xaa is
or Lys.
: Binds 1 zinc ion per subunit (By similarity).
IVE PRODUCTS:
ternative splicing; Named isoforms=2;
Synonyms=NRD1;
343847-1; Sequence=Displayed;
Synonyms=NRD2;

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Isoid=O43847-2; Sequence=VSP 007114;
 TISSUE SPECIFICITY: Primarily in adult heart, skeletal muscle
 testis and at much lower levels in other tissues.
 SIMILARITY: Belongs to peptidase family M16.
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 entities requires a license agreement (See http://www.isb-sib.ch
 or send an email to license@isb-sib.ch).
 EMBL; U64898; AAC39597.1; -
 EMBL; X93209; CAA63698.1; -
 EMBL; X93207; CAA63694.1; -
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 EMBL; AL050343; CAB72328.1; -
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 MIM; 602651; -
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 GO; GO:0007528; P:neuromuscular junction development; TAS.
 GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 InterPro; IPR001431; Peptidase_M16.
 InterPro; IPR007863; Peptidase_M16_C.
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 Pfam; PF05193; Peptidase_M16_C; 2.
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 Hydrolase; Metalloprotease; Zinc; Signal; Alternative splicing.
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 isoform 2).
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 E -> EE (IN REF. 2).
 Q -> L (IN REF. 2).
 A -> G (IN REF. 1).
 V -> A (IN REF. 2).
 V -> A (IN REF. 1).
 T -> S (IN REF. 2).
 DCIIPITDIRAFTTTLNLLPYHKIVK -> SVSSP.
 SQHSTFSPFTIK (IN REF. 1).
 SQHSTFSPFTIK; 3846DAD898E038B CRC64;
 SEQUENCE 1150 AA; 131571 MW; 3846DAD898E038B CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 1150;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; (

QY 329 EEEEDDED 337
 Db 150 EEEEDDED 158
 RESULT 50
 IE18_PRVIF
 ID IE18_PRVIF STANDARD; PRT; 1461 AA.
 AC P11675;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Immediate-early protein IE180.
 IE.
 OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
 QS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC

ciniae; Varicellovirus.

123;

N.A.

207; PubMed-2546124;

ie sequence analysis of the immediate-early gene of

virus.";

Res. 17:4637-4646(1989).

1-1989) to the EMBL/GenBank/DBJ databases.

THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
ING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
AL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.

AR LOCATION: Nucleus of infected cells.

g stretch of serine residues may be a major site of
ation.

tion: BELONGS TO THE ICP4/IE140/IE180 FAMILY.

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al to license@isb-sib.ch).

CAA33214.1; -.

JBIEIF.

105205; Herpes_ICP4_C.

105206; Herpes_ICP4_N.

Herpes_ICP4_C; 1.

Herpes_ICP4_N; 1.

Transcription regulation: Trans-acting factor;

phosphorylation; Nuclear protein.

0 405 POLY-SER.

8 966 POLY-SER.

1 AA: 149833 MW; 7F31E7ABE403B208 CRC64;

1.7%; Score 9; DB 1; Length 1461;

idity 100.0%; Pred. No. 29;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126

|||||

AAAA 385

STANDARD; PRT; 2004 AA.

el. 36, Created)

el. 36, Last sequence update)

el. 42, Last annotation update)

cetyltransferase 3 (Runt-related transcription factor
n 2) (Monocytic leukemia zinc finger protein) (Zinc
.220).

P2 OR ZNF220 OR MOZ.

Human).

azoa; Chordata; Craniata; Vertebrata; Euteleostomi;

eria; Primates; Catarrhini; Hominidae; Homo.

6;

N.A.

68; PubMed-8782817;

nton V.P. Jr., Andresen J.M., Becher R., Behm F.G.,

.., Civin C.I., Distèche C., Dube I., Frischauf A.M.,

telman F., Volinia S., Watmore A.E., Housman D.E.,

tion t(8;16)(p11;p13) of acute myeloid leukaemia fuses

tyltransferase to the CREB-binding protein.";

RL Nat. Genet. 14:33-41(1996).

CC -I- FUNCTION: May represent a chromatin-associated acetyltransfer

CC -I- SUBCELLULAR LOCATION: Nuclear.

CC -I- DISEASE: Involved in acute myeloid leukemias through a chromo

CC translocation t(8;16)(p11;p13) involving MYST3 and CREBBP.

CC -I- SIMILARITY: Contains 2 PHD-type zinc fingers.

CC -I- SIMILARITY: Belongs to the MYST (SAS/MOZ) family.

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modified and this statement is not removed. Usage by and for c
entities requires a license agreement (See <http://www.isb-sib.ch/>
or send an email to license@isb-sib.ch).

DR EMBL; UA7742; AAC50662.1; -.

DR Genew; HGNC:13013; MYST3.

DR MIM; 601408; -.

DR GO; GO:0006323; P:DNA packaging; TAS.

DR InterPro; IPR005818; Histone H1/H5.

DR InterPro; IPR002717; MOZ SAS.

DR InterPro; IPR001965; Znf_PHD.

DR Pfam; PF01853; MOZ_SAS; 1.

DR Pfam; PF00628; PHD; 2.

DR SMART; SM00526; H15; 1.

DR SMART; SM00249; PHD; 2.

DR PROSITE; PS01359; ZF_PHD_1; 1.

DR PROSITE; PS50016; ZF_PHD_2; 2.

KW Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;

KW Nuclear protein.

FT ZN FING 206 265 PHD-TYPE 1.

FT ZN FING 259 313 PHD-TYPE 2.

FT DOMAIN 371 379 POLY-SER.

FT ZN FING 538 560 C2HC-TYPE.

FT DOMAIN 788 801 POLY-GLU.

FT DOMAIN 989 995 POLY-GLU.

FT DOMAIN 1019 1026 POLY-ARG.

FT DOMAIN 1069 1078 POLY-GLU.

FT DOMAIN 1147 1150 POLY-LYS.

FT DOMAIN 1221 1242 GLU-RICH.

FT DOMAIN 1267 1302 GLU-RICH.

FT DOMAIN 1411 1414 POLY-SER.

FT DOMAIN 1593 1597 POLY-SER.

FT DOMAIN 1643 1704 GLN/PRO-RICH.

FT DOMAIN 1897 1977 MET-RICH.

FT SITE 1546 1547 BREAKPOINT FOR TRANSLOCATION TO FORM

MOZ-CBP.

SQ SEQUENCE 2004 AA; 225054 MW; 9FFBAC3792854BA CRC64;

Query Match 1.7%; Score 9; DB 1; Length 2004;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G;

OY 225 QPPPPQPPQ 233

|||||

Db 1660 QPPPPQPPQ 1668

RESULT 52

NC06_HUMAN

ID NC06_HUMAN STANDARD; PRT; 2063 AA.

AC Q14686; Q9NTZ9; Q9UH74; Q9UK86;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Nuclear receptor coactivator 6 (Amplified in breast cancer-3 prote

DE (Cancer-amplified transcriptional coactivator ASC-2) (Activating

DE signal cointegrator-2) (ASC-2) (Peroxisome proliferator-activated

DE receptor-interacting protein) (PPAR-interacting protein) (PRIP)

DE (Nuclear receptor-activating protein, 250 kDa) (Nuclear receptor

DE coactivator RAP250) (NRC RAP250) (Thyroid hormone receptor-binding

DE protein).

OR RAP250 OR TRBP OR KIAA0181.
(Human).
tazoo; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominidae; Homo.
06;
[N.A., AND INTERACTION WITH CREBBP; NCOA1; GTF2A; TBP;
ARA AND THRA.
574; PubMed=10567404;
Wick S.L., Choi J.-E., Bubendorf L., Guan X.-Y.,
Gallionieri O.P., Kononen J., Trent J.M., Azorsa D.,
Heong J.H., Lee Y.C., Meltzer P.S., Lee J.W.;
ector ASC-2, as a cancer-amplified transcriptional
essential for ligand-dependent transactivation by nuclear
vivo.";
l. 274:34283-34293 (1999).
[N.A., HOMODIMERIZATION, AND INTERACTION WITH CREBBP;
R3C1; RARA; VDR AND THRA.
329; PubMed=10866662;
Samuels H.H.;
of nuclear receptor coregulators that integrates nuclear
aling through CBP.";
ol. 20:5048-5063 (2000).
[N.A., AND INTERACTION WITH PPARA; PPARG; ESR1; ESR2 AND
3;
724; PubMed=10681503;
onson P., Palto-Huikko M., Treuter E., Gustafsson J.-A.;
Characterization of RAP250, a nuclear receptor
";
n. 275:5308-5317 (2000).
[N.A., PHOSPHORYLATION BY PRKDC, AND INTERACTION WITH
300 AND CRSP3.
ocytes;
3976; PubMed=10823961;
na G.R., Chin W.W.;
none receptor-binding protein, an LXXLL motif-containing
ctions as a general coactivator.";
Acad. Sci. U.S.A. 97:6212-6217 (2000).
[N.A.
narrow;
1124; PubMed=8724849;
eki N., Iihikawa K.-I., Tanaka A., Nomura N.;
of the coding sequences of unidentified human genes. V.
quences of 40 new genes (KIAA0161-KIAA0200) deduced by
cDNA clones from human cell line KG-1.";
7-24 (1996).
M N.A.
8749; PubMed=11780052;
Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
avrides G., Almeida J.P., Babage A.K., Bagguley C.L.,
arlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
rill W.D., Butler A.P., Carder C., Carter N.P.,
Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
bley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coville G.J., Deadman R., Dhani P.D., Dunn M.,
G., Frankland J.A., Fraser A., French L., Garner P.,
Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
unt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
mberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
arker A., Patel R., Pearce T.A.V., Peck A.I.,
J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
oss M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe J.
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 2(
RL Nature 414:865-871 (2001).
RN [7]
RP INTERACTION WITH NCOA6IP.
RX MEDLINE=21417756; PubMed=11517327;
RA Zhu Y.-J., Qi C., Cao W.-Q., Yeldandi A.V., Rao M.S., Reddy J.K.
RT "Cloning and characterization of PIMT, a protein with a
methyltransferase domain, which interacts with and enhances nuclei
receptor coactivator PRIP function.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:10380-10385 (2001).
RN [8]
RP INTERACTION WITH RBM14.
RX MEDLINE=21423995; PubMed=11443112;
RA Iwasaki T., Chin W.W., Ko L.;
RT "Identification and characterization of RRM-containing coactivat
activator (CoA) as TRBP-interacting protein, and its splice var
as a coactivator modulator (CoAM).";
RL J. Biol. Chem. 276:33375-33383 (2001).
RN [9]
RP INTERACTION WITH HRMT1L.
RX MEDLINE=22151129; PubMed=12039952;
RA Qi C., Chang J., Zhu Y., Yeldandi A.V., Rao S.M., Zhu Y.-J.;
RT "Identification of protein arginine methyltransferase 2 as a
coactivator for estrogen receptor alpha.";
RL J. Biol. Chem. 277:28624-28630 (2002).
RN [10]
RP INTERACTION WITH MLL3 AND THE ASCOM COMPLEX.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=22371496; PubMed=12482968;
RA Goo Y.-H., Sohn Y.C., Kim D.-H., Kim S.-W., Kang M.-J., Jung D.-
RA Kwak E., Barlev N.A., Berger S.L., Chow V.T., Roeder R.G.,
RA Azorsa D.O., Meltzer P.S., Suh P.-G., Song E.J., Lee K.-J., Lee
Lee J.W.;
RT "Activating signal cointegrator 2 belongs to a novel steady-stat
complex that contains a subset of trithorax group proteins.";
Mol. Cell. Biol. 23:140-149 (2003).
RN [11]
RP MUTAGENESIS OF 883-THR-GLU-894, AND PHOSPHORYLATION.
RX MEDLINE=21635582; PubMed=11773444;
RA Ko L., Cardona G.R., Iwasaki T., Bramlett K.S., Burris T.P.,
RA Chin W.W.;
RT "Ser-884 adjacent to the LXXLL motif of coactivator TRBP defines
selectivity for ERS and TRs.";
RL Mol. Endocrinol. 16:128-140 (2002).
CC -I- FUNCTION: Nuclear receptor coactivator that directly binds n
receptors and stimulates the transcriptional activities in a
hormone-dependent fashion. Coactivates expression in an agon
and AF2-dependent manner. Involved in the coactivation of
different nuclear receptors, such as for steroids (GR and ER
retinoids (RARs and RXRs), thyroid hormone (TRs), vitamin D3
and prostanoids (PPARs). Probably functions as a general
coactivator, rather than just a nuclear receptor coactivator
also be involved in the coactivation of the NF-kappa-B pathw
May coactivate expression via a remodeling of chromatin and
interaction with histone acetyltransferase proteins.
CC -I- SUBUNIT: Monomer and homodimer. Interacts with RNP2. (By
similarity). Interacts in vitro with the basal transcription
factors GTF2A and TBP, suggesting an autonomous transactivat
function. Interacts with NCOA1, CRSP3, RBM14, the histone
acetyltransferases EP300 and CREBBP, and with the
methyltransferases NCOA6IP and HRMT1L/PRMT2. Belongs to the
ASC-2/NCOA6 complex (ASCOM), which contains ASC-2/NCOA6, the
retinoblastoma-binding protein RBQ-3/RBP5, alpha- and beta
tubulins, the trithorax group proteins MLL2 and MLL3, and
ASH2/ASCL2.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain,

testis and ovary; weakly expressed in lung, thymus and
 uterine.
 contains two Leu-Xaa-Leu-Leu (LXXLL) motifs. Only
 essential for the association with nuclear receptors,
 cent Ser-884 displays selectivity for nuclear receptors.
 horylated by PRKDC.
 horylation on Ser-884 leads to a strong decrease in
 ESR1 and ESR2.
 XOUS: Frequently amplified or overexpressed in colon,
 lung cancers.
 ref.1 (AA16403) sequence differs from that shown due to
 ft in position 88.

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 ail to license@isb-sib.ch).

 ; AA13595.1; -
 ; AA16403.1; ALT_FRAME.
 ; AA178480.1; -
 ; AA137003.1; -
 ; AA171829.1; -
 ; BAA11498.2; ALT_INIT.
 ; CAB92721.1; -
 ; 9336; NCOA6.
 ; C:nucleus; IDA.
 ; C:transcription factor complex; TAS.
 ; F:chromatin binding; ISS.
 ; F:estrogen receptor binding; TAS.
 ; F:retinoid X receptor binding; TAS.
 ; F:thyroid hormone receptor binding; IDA.
 ; F:transcription co-activator activity; IDA.
 ; F:transcriptional activator activity; TAS.
 ; P:brain development; ISS.
 ; P:embryonic development (sensu Mammalia); ISS.
 ; P:heart development; ISS.
 ; P:myeloid blood cell differentiation; IDA.

1.7%; Score 9; DB 1; Length 2063;
 100.0%; Pred.No. 39;
 0; Mismatches 0; Indels 0; Gaps 0;
 229
 1018

STANDARD; PRT; 2067 AA.
 ;
 rel. 41, Created)
 rel. 41, Last sequence update)
 rel. 42, Last annotation update)
 or coactivator 6 (Amplified in breast cancer-3 protein)
 fied transcriptional coactivator ASC-2) (Activating
 rator-2) (ASC-2) (Peroxisome proliferator-activated
 acting protein) (PPAR-interacting protein) (Nuclear
 ating protein, 250 kDa) (Nuclear receptor coactivator
 (Thyroid hormone receptor binding protein).
 OR RAP250 OR PRIP OR TRBP.
 (Mouse).

Coxa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 090;

N.A. (ISOFORMS 1 AND 2), AND INTERACTION WITH
 RARA; RXRA; ESR1; ESR2 AND THR3.

RC TISSUE=Liver;
 RX MEDLINE=20250907; PubMed=10788465;
 RA Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
 RA Reddy J.K.,
 RT "Isolation and characterization of peroxisome proliferator-activa
 RT receptor (PPAR) interacting protein (PRIP) as a coactivator for
 RL PPAR.";
 RL J. Biol. Chem. 275:13510-13516(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Breast;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 786-1142 FROM N.A. (ISOFORM 1), INTERACTION WITH PPAR
 RP PARG; ESR1; ESR2; THRA AND THR3, AND MUTAGENESIS OF LEU-831 AND
 RP LEU-894.
 RC TISSUE=Embryo;
 RX MEDLINE=20148724; PubMed=10681503;
 RA Cairn F., Antonson P., Pelto-Huikko M., Treuter E., Gustafsson J.
 RT "Cloning and characterization of RAP250, a nuclear receptor
 RT coactivator.";
 RL J. Biol. Chem. 275:5308-5317(2000).
 RN [4]
 RP INTERACTION WITH RNPC2.
 RX MEDLINE=21638469; PubMed=11704680;
 RA Jung D.-J., Na S.-Y., Na D.S., Lee J.W.;
 RT "Molecular cloning and characterization of CAPER, a novel coactiv
 RT of activating protein-1 and estrogen receptors.";
 RL J. Biol. Chem. 277:1229-1234(2002).
 CC -1- FUNCTION: Nuclear receptor coactivator that directly binds nu
 CC receptors and stimulates the transcriptional activities in a
 CC hormone-dependent manner. Coactivates expression in an agoni
 CC and AP2-dependent fashion. Involved in the coactivation of
 CC different nuclear receptors, such as for steroids (GR and ERs
 CC retinoids (RARs and RXRs), thyroid hormone (TRs), vitamin D3
 CC and prostanooids (PPARs). Probably functions as a general
 CC coactivator, rather than just a nuclear receptor coactivator.
 CC also be involved in the coactivation of the NF-kappa-B pathwa
 CC May coactivate expression via a remodeling of chromatin and i
 CC interaction with histone acetyltransferase proteins. Involved
 CC placental, cardiac, hepatic and embryonic development.
 CC -1- SUBUNIT: Monomer and homodimer. Interacts in vitro with the b
 CC transcription factors GTF2A and TBP, suggesting an autonomous
 CC transactivation function. Interacts with NCOA1, CREBBP, RBM14,
 CC histone acetyltransferase proteins EP300 and CREBBP, and with
 CC methyltransferase proteins NCOA6IP and HMT111 (By similarity
 CC interacts with RNPC2. Belongs to the ASC-2/NCOA6 complex (ASC
 CC which contains ASC-2/NCOA6, the retinoblastoma-binding protei
 CC RBQ-3/ RBBP5, alpha- and beta-tubulins, the triothorax group
 CC proteins MLL2 and MLL3, and ASH2/ASCL2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;

19UL19-1; Sequence=VSP 003410;
 its as a dominant negative repressor;
 ECIFICITY: Widely expressed. High expression in testis
 expression in small intestine.
 INTAL STAGE: Expressed at E9 in placenta and at weaker
 uterus. High expression in sensory ganglia and
 at development. High expression in olfactory epithelium
 som E11. In the alimentary tract and olfactory epithelium
 y, from E11 and E13 respectively, and then expression
 i at later stages of development. Moderate expression in
 n E13, while it decreases during postnatal life. Strong
 on in thymus from E15 onwards, and in spleen from E17 and
 arly postnatal life. then, the expression decreases.
 contains two Leu-Xaa-Xaa-Leu-Leu (LXXLL) motifs. Only
 is essential for the association with nuclear receptors.
 phosphorylated (by similarity).

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 16; RAFP35860.1; -;
 13; AAF31113.1; -;
 39; AAF35973.1; -;
 3915; NCOA6.
 14; C:nucleus; IDA.
 57; C:transcription factor complex; IDA.
 32; F:chromatin binding; IDA.
 31; F:estrogen receptor binding; ISS.
 35; F:retinoid X receptor binding; ISS.
 56; F:thyroid hormone receptor binding; ISS.
 13; F:transcription co-activator activity; ISS.
 53; F:transcriptional activator activity; IDA.
 20; P:brain development; IMP.
 21; P:embryonic development; IMP.
 37; P:heart development; IMP.
 39; P:myeloid blood cell differentiation; ISS.
 57; P:transcription initiation from Pol II promoter; IDA.
 a regulation; Activator; Nuclear protein; Repeat;
 splicing.
 1 1060 CREBBP-BINDING REGION (BY SIMILARITY).
 1 932 TBP/GTF2A-BINDING REGION (BY SIMILARITY).
 1 1314 NCOA1-BINDING REGION (BY SIMILARITY).
 777 931 NCOA6IP-BINDING REGION (BY SIMILARITY).
 544 2067 EP300/CRSP3-BINDING REGION
 (BY SIMILARITY).
 227 1044 GLN-RICH.
 376 381 POLY-PRO.
 917 922 POLY-LYS.
 543 1592 SER-RICH.
 891 895 LXXLL MOTIF 1.
 495 1499 LXXLL MOTIF 2.
 458 2067 Missing (in isoform 2).
 /FTID=VSP_003410.
 891 894 LVNL->AVNA: ABOLISHES INTERACTION WITH
 NUCLEAR RECEPTORS.
 39 39 G -> S (IN REF. 2).
 109 109 W -> R (IN REF. 2).
 194 194 M -> I (IN REF. 2).
 290 290 Q -> QQ (IN REF. 2).
 014 1014 P -> L (IN REF. 3).
 141 1142 SE -> RS (IN REF. 3).
 067 AA; 219663 MW; C855F877167AD48 CRC64;
 1.7*; Score 9; DB 1; Length 2067;

Best Local Similarity 100.0%; Pred. No. 39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 221 PQQQQPPPP 229
 DB 1014 PQQQQPPPP 1022
 RESULT 54
 MLL4 HUMAN
 ID MLL4 HUMAN STANDARD; PRT: 2715 AA.
 AC Q9UNW6: O15022; Q95836; Q96IP2; Q96IP3; Q9UK25; Q9Y668; Q9Y669;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Myeloid/lymphoid or mixed-lineage leukemia protein 4 (Trithorax
 DE homolog 2).
 GN MLL4 OR TRX2 OR HRX2 OR MLL2 OR KIAA0304.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Angrand P.O., Valvatne H., Jeanmougin F., Adamson A.,
 van der Hoeven F., Olsen L., Tekotte H., Huang N., Poch O.,
 Lamerdin J., Chambon P., Lossos R., Stewart A., Asland R.;
 RA "Mammalian trithorax- and ASH1-like proteins: putative chromatin
 RT regulators which contain PHD fingers and SET domains";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
 Garcia E., Kyle A., Ramirez M., Stillwagen S., Garnes J., Dangana
 RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O
 RA Carrano A.V.;
 RT "Sequence analysis of a 1 Mb region in human 19q13.1";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 111-2715 FROM N.A. (ISOFORM 1).
 RC TISSUE=Leukocyte, and Testis;
 MEDLINE=20105772; PubMed=10637508;
 RX Huntsman D.G., Chin S.-F., Muleris M., Batley S.J., Collins V.P.
 RA Wiedemann L.M., Aparicio S., Caldas C.;
 RA "MLL2, the second human homolog of the Drosophila trithorax gene
 RT to 19q13.1 and is amplified in solid tumor cell lines";
 RL Oncogene 18:7975-7984(1999).
 RN [4]
 RP SEQUENCE OF 816-2715 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain, and Skin;
 MEDLINE=97349994; PubMed=9205841;
 RX Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RA "Prediction of the coding sequences of unidentified human genes.
 RT The complete sequences of 100 new cDNA clones from brain which c
 RT code for large proteins in vitro";
 RL DNA Res. 4:141-150(1997).
 RN [5]
 RP SEQUENCE OF 1918-2715 FROM N.A.
 RC TISSUE=Brain, and Skin;
 MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen P.
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanche

idan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Touchman J.W., Green E.D., Dickson M.C.,
 Grimwood J., Schmutz J., Myers R.M.,
 S.N., Krzywinski M.I., Skalska U., Skallus D.E.,
 Schein J.E., Jones S.J.M., Marra M.A.,
 and initial analysis of more than 15,000 full-length
 cDNA sequences.";
 Acad. Sci. U.S.A. 99:16999-16993(2002).

ICE FROM N.A. (ISOFORMS 1 AND 2).
 arrow, and Placenta;
 183; PubMed=10409430;
 ...; Diaz M.O.;
 mammalian member of the trx/MLL family of genes.";
 17-192(1999).
 Possibly acts as a transcriptional regulatory factor.
 AR LOCATION: Nuclear (By similarity).
 PE PRODUCTS:
 alternative splicing; Named isoforms=2;
 /nonys=long;
 /UNN6-1; Sequence=Displayed;
 /nonys=truncated;
 /UNN6-2; Sequence=VSP_006668, VSP_006669;
 SPECIFICITY: Widely expressed. Highest levels in testis,
 i in brain, bone marrow, heart, muscle, kidney, pancreas,
 ymus, prostate, and placenta.
 often amplified in pancreatic carcinomas.
 f: Belongs to the TRX/MLL family.
 f: Contains 1 bromodomain.
 f: Contains 1 SET domain.
 f: Contains 3 PHD-type zinc fingers.
 f: Contains 1 CXXC-type zinc finger.
 f: Contains 1 post-SET domain.
 This protein was first named MLL2 by Ref.3 and Ref.6.
 asponds to another protein located on chromosome 12 (see

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 ail to license@isb-sib.ch).

l; CAB45385.1; -;
 l; -; NOT_ANNOTATED_CDS.

l; BAA20763.2; -;
 l; AAD56420.1; -;
 l; AAD17932.1; -;
 l; AAD26113.1; -;
 l; AAH09337.1; -;
 l; AAH07353.1; -;
 l; AAD26112.1; -;

l; C:nucleus; NAS.
 l; F:transcription factor activity; NAS.
 l; F:zinc ion binding; NAS.
 l; P:chromatin-mediated maintenance of transcrip. . . ; NAS.
 03889; Fvrich C.
 03888; Fvrich N.
 03616; PostSET.
 01214; SET.
 02857; Znf_CXXC.
 01965; Znf_PHD.
 l; PHD; 3.
 l; SET; 1.
 l; zf_CXXC; 1.
 l; FYRC; 1.
 l; FYRN; 1.
 l; PHD; 4.
 l; PostSET; 1.

DR SMART; SM00317; SET; 1.
 DR PROSITE; PS00868; POST SET; 1.
 DR PROSITE; PS0280; SET; 1.
 DR PROSITE; PS01359; ZF_PHD_1; 3.
 DR PROSITE; PS00016; ZF_PHD_2; 3.
 KW DNA-binding; Bromodomain; Nuclear protein; Zinc-finger; Metal-bin
 KW Transcription regulation; Alternative splicing; Repeat.
 FT DNA_BIND 37 44 A.T HOOK (BY SIMILARITY).
 FT DNA_BIND 110 117 A.T HOOK (BY SIMILARITY).
 FT DNA_BIND 357 365 A.T HOOK (BY SIMILARITY).
 FT ZN_FING 959 1005 CXXC-TYPE.
 FT ZN_FING 1201 1252 PHD-TYPE 1.
 FT ZN_FING 1249 1303 PHD-TYPE 2.
 FT ZN_FING 1335 1396 PHD-TYPE 3.
 FT DOMAIN 1449 1471 BROMODOMAIN (DIVERGENT).
 FT DOMAIN 2574 2695 SET.
 FT DOMAIN 2699 2715 POST-SET.
 FT DOMAIN 26 37 POLY-GLY.
 FT DOMAIN 248 255 POLY-PRO.
 FT DOMAIN 362 398 ASP-/GLU-RICH (ACIDIC).
 FT DOMAIN 402 771 PRO-RICH.
 FT DOMAIN 808 812 POLY-GLN.
 FT DOMAIN 1963 1970 POLY-PRO.
 FT DOMAIN 2251 2259 POLY-PRO.
 FT VARSPIC 532 582 VSARSRVKTPRRFMDEPPKPKVSVLPVPP
 FT VQEPAPVPS -> PLSQSLMLPTQLSLGQWA
 FT ACIDSLPMSPLLRPRCLTGLQL (in isoform
 /FTid=VSP_006668.
 FT Missing (in isoform 2).
 FT /FTid=VSP_006669.
 FT K -> E (IN REF. 6).
 FT S -> Y (IN REF. 6).
 FT E -> Q (IN REF. 6).
 FT H -> Y (IN REF. 6).
 FT D -> N (IN REF. 6).
 FT PLA -> GTR (IN REF. 5; AAH09337).
 FT DEE -> ARG (IN REF. 5; AAH07353).
 FT D -> H (IN REF. 6).
 SQ SEQUENCE 2715 AA; 293511 MW; C0615B981BBE7BF CRC64;

Query Match 1.7%; Score 9; DB 1; Length 2715;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 131 PAPPVPPAP 139
 Db 623 PAPPVPPAP 631

RESULT 55

DY1B CHLRE
 ID DY1B CHLRE STANDARD; PRT; 4513 AA.
 AC Q9MBF8; Q9ZPC2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dynein 1-beta heavy chain, flagellar inner arm 11 complex (l-beta
 DHC) (Dynein 1, subspecies f).
 GN DHC10 OR IDA2.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A., CHARACTERIZATION, MUTAGENESIS, AND EXPRESSION
 RC STRAIN=219T;
 RX MEDLINE=20346958; PubMed=10888669;
 RA Perrone C.A., Myster S.H., Bower R., O'Toole E.T., Porter M.E.;
 RT "Insights into the structural organization of the 11 inner arm dy
 RL from a domain analysis of the 1 beta dynein heavy chain.";
 RL Mol. Biol. Cell 11:2297-2313(2000).
 RN [2]
 RP SEQUENCE OF 1820-1901 FROM N.A.

015; PubMed=1069912;
Bower R., Knott J.A., Byrd P., Dentler W.L.;
dynein heavy chain lb is required for flagellar assembly
nas.";
11 10:693-712(1999).
X ELECTRON MICROSCOPY.
722; PubMed=2957507;
W., Gebhart B., Mermall V., Mitchell D.R., Heuser J.E.;
e liquid chromatography fractionation of Chlamydomonas
ts and characterization of inner-arm dynein subunits.";
194:481-494(1987).
IPTON AND LOCALIZATION.
628; PubMed=2137128;
amanis Z., Smith E.F., Sale W.S.;
ct inner dynein arms in Chlamydomonas flagella: molecular
nd location in the axoneme.";
110:379-389(1990).
F I1 DYNEIN COMPLEX FOR PHOTOTAXIS.
457; PubMed=9008712;
tcher S.K.;
ation of an inner dynein arm complex in Chlamydomonas
s altered in phototactic mutant strains.";
136:177-191(1997).
Force generating protein of eukaryotic cilia and
roduces force towards the minus ends of microtubules.
s ATPase activity; the force-producing power stroke is
o occur on release of ADP. Required for assembly of the
arm complex and its targeting to the appropriate axoneme
Also required for phototaxis. Mutants swim slowly with
waveforms, and are unable to phototax.
The I1 inner arm complex (also known as the f dynein
is a two-headed isoform composed of two heavy chains (1-
1-beta), three intermediate chains and three light
1 occupies a specific position proximal to the first
oke and repeats every 96 nm along the length of the
AR LOCATION: Flagellar.
f; By deflagellation.
dynein heavy chains probably consist of an N-terminal stem
nds cargo and interacts with other dynein components),
ead or motor domain. The motor contains six tandemly-
A domains in the head, which form a ring. A stalk-like
; formed by two of the coiled coil domains) protrudes
AA 4 and AAA 5 and terminates in a microtubule-binding
eventh domain may also contribute to this ring; it is not
ther the N-terminus or the C-terminus forms this extra
here are four well-conserved and two non-conserved ATPase
e per AAA domain. Probably only one of these (within AAA
ly hydrolyzes ATP, the others may serve a regulatory
construct encoding the first 989 amino acids but lacking
domain is able to assemble I1 complexes and target them
correct location on the axoneme, partially restores
and fully rescue phototaxis.
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3; CAB99316.1; --
4; CAB99316.1; JOINED.
5; CAB99316.1; JOINED.
9; CAB39160.1; --
003593; AAA_ATPase.

DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
DR SMART; SM00362; AAA; 3.
KW Motor protein; Dynein; Flagellum; Microtubule; ATP-binding; Repetitive
KW Coiled coil.
FT DOMAIN 1 1806 STEM (BY SIMILARITY).
FT DOMAIN 1807 2028 AAA 1 (BY SIMILARITY).
FT DOMAIN 2089 2350 AAA 2 (BY SIMILARITY).
FT DOMAIN 2458 2706 AAA 3 (BY SIMILARITY).
FT DOMAIN 2808 3059 AAA 4 (BY SIMILARITY).
FT DOMAIN 3107 3384 STALK (BY SIMILARITY).
FT DOMAIN 3443 3674 AAA 5 (BY SIMILARITY).
FT DOMAIN 3890 4109 AAA 6 (BY SIMILARITY).
FT DOMAIN 192 223 COILED COIL (POTENTIAL).
FT DOMAIN 1544 1577 COILED COIL (POTENTIAL).
FT DOMAIN 1704 1727 COILED COIL (POTENTIAL).
FT DOMAIN 3107 3193 COILED COIL (POTENTIAL).
FT DOMAIN 3301 3384 COILED COIL (POTENTIAL).
FT DOMAIN 3499 3519 COILED COIL (POTENTIAL).
FT NP_BIND 1845 1852 ATP (POTENTIAL).
FT NP_BIND 2127 2134 ATP (POTENTIAL).
FT NP_BIND 2497 2504 ATP (POTENTIAL).
FT NP_BIND 2848 2855 ATP (POTENTIAL).
SQ SEQUENCE 4513 AA; 510655 MW; F2A3E10767FD6719 CRC64;
Query Match 1.7%; Score 9; DB 1; Length 4513;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 120 AAAAAAAP 128
DB 2374 AAAAAAAP 2382
RESULT 56
ANP3_PSEAM
ID ANP3_PSEAM STANDARD; PRT; 37 AA.
AC P02733;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antifreeze peptide 3.
OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes americanus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; OC Pleuronectoidae; Pleuronectidae; Pseudopleuronectes.
OX NCBI_TaxID=8265;
RN [1]
RP SEQUENCE.
RX MEDLINE=78060969; PubMed=588591;
RA Devries A.L., Lin Y.;
RT "Structure of a peptide antifreeze and mechanism of adsorption to ice.";
RL Biochim. Biophys. Acta 495:388-392(1977).
CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.
CC -!- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE I AFP ARE ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
DR PIR; A03192; FDFL3W.
DR InterPro; IPR000104; Antifreeze_1.
DR PRINTS; PR00308; ANTIFREEZE1.
KW Antifreeze protein; Repeat; Multigene family.
SQ SEQUENCE 37 AA; 3144 MW; 46AA951A962DECA9 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
DB 29 AAAAAATA 36

STANDARD; PRT; 82 AA.

rel. 02, Created)

rel. 02, Last sequence update)

rel. 40, Last annotation update)

stein A/B precursor.

ectus americanus (Winter flounder) (Pleuronectes

zozoa; Chordata; Craniata; Vertebrata; Euteleostomi;

i; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

i; Acanthopterygii; Percomorpha; Pleuronectiformes;

ei; Pleuronectidae; Pseudopleuronectes.

55;

N.A. (PROTEIN A).

190; PubMed=6952188;

osch A.H., Hew C.-L.;

coding for an antifreeze protein precursor from winter

ad. Sci. U.S.A. 79:335-339(1982).

N.A. (PROTEIN A).

136; PubMed=3133486;

ivies P.L., Kao M.H., Fletcher G.L.;

amplification of antifreeze protein genes in the

,";

27:29-35(1988).

N.A. (PROTEIN B).

159; PubMed=6086629;

ough C., Scott G.K., Ng N., White B.N., Hew C.-L.;

rotein genes of the winter flounder.;"

. 259:9241-9247(1984).

N.A.

195; PubMed=1555765;

of antifreeze protein-encoding genes in tandem

.70(1992).

MODELING OF 45-81.

133; PubMed=1738160;

zed structure of antifreeze protein and its binding

223:509-517(1992).

OGRAPHY (1.5 ANGSTROMS) OF 45-81.

160; PubMed=7760940;

structure and mechanism of an antifreeze protein from

er.;"

7-431(1995).

Antifreeze proteins lower the blood freezing point.

OUS: The sequence shown is that of protein A.

ELONG TO THE TYPE-1 APP FAMILY. TYPE 1 APP ARE

[CH, AMPHIPHILIC AND ALPHA-HELICAL.

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AAB59964.1; --

AAB59964.1; JOINED.

AAA49469.1; --

DR EMBL; X07506; CAA30389.1; --

DR EMBL; M62416; AAA49471.1; --

DR EMBL; M62417; AAA49472.1; --

DR PIR; A05161; A05161.

DR PIR; JS0704; FDFLAW.

DR PIR; JS0706; JS0706.

DR PIR; S02326; S02326.

DR PDB; 1ATP; 15-OCT-94.

DR PDB; 1WFA; 03-JUN-95.

DR PDB; 1WFB; 03-JUN-95.

DR InterPro; IPR000104; Antifreeze_1.

DR PRINTS; PR00308; ANTIFREEZE1.

KW Antifreeze protein; Repeat; Multigene family; Signal; 3D-structur

FT SIGNAL 1 21

FT PROPEL 22 44

FT CHAIN 45 82

FT VARIAT 36 36

FT VARIAT 70 70

FT CONFLIC 24 24

FT HELIX 46 80

SQ SEQUENCE 82 AA; 7711 MW; C2AE7B74COD46CC1 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 82;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAATA 158

DB 73 AAAAATA 80

|||||

RESULT 58

ANP4_PSEAM STANDARD; PRT; 85 AA.

AC P02734;

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Antifreeze peptide 4 precursor.

OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes

OS americanus).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

OC Pleuronectidae; Pleuronectidae; Pseudopleuronectes.

OX NCBI_TaxID=8265;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81247379; PubMed=6265915;

RA Lin Y., Gross J.K.;

RT "Molecular cloning and characterization of winter flounder antifr

RT cDNA.;"

RL Proc. Natl. Acad. Sci. U.S.A. 78:2825-2829(1981).

CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.

CC -!- SIMILARITY: BELONGS TO THE TYPE-1 APP FAMILY. TYPE 1 APP ARE

CC ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.

CC

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CC

DR EMBL; J00930; AAA49467.1; --

DR PIR; A03193; FDFLAW.

DR InterPro; IPR000104; Antifreeze_1.

DR PRINTS; PR00308; ANTIFREEZE1.

KW Antifreeze protein; Repeat; Multigene family; Signal.

FT SIGNAL 1 21

FT CHAIN 22 85

ANTIFREEZE PEPTIDE 4.

```

SQ      1; AA: 7215 MW; 8862E1D2B44117BC CRC64;
        1.5%; Score 8; DB 1; Length 85;
        arity 100.0%; Pred. No. 18;
        conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      AATA 158
        |||||
        AATA 35

        STANDARD; PRT; 91 AA.
        (Rel. 08, Created)
        (Rel. 32, Last sequence update)
        (Rel. 40, Last annotation update)
        cotein IIA7 precursor (AFP)
        ictes americanus (Winter flounder) (Pleuronectes
        traxosa; Chordata; Craniata; Vertebrata; Euteleostomi;
        ii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
        a; Acanthopterygii; Percomorpha; Pleuronectiformes;
        lei; Pleuronectidae; Pseudopleuronectes.
        165;

        1 N.A.
        1993; PubMed=6548752;
        Jin Y., Price J., Devries A.L., Powers D., Huang R.C.C.;
        nder antifreeze proteins: a multigene family.";
        1. 259;14960-14965(1984).
        Antifreeze proteins lower the blood freezing point.
        Y: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
        RICH, AMPHIPHILIC AND ALPHA-HELICAL.

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        mail to license@isb-sib.ch).

        AAA49465.1; -.
        A22592.
        000104; Antifreeze_1.
        08; ANTIFREEZE1.
        cotein; Repeat; Multigene family; Signal.
        1 21 POTENTIAL.
        22 39 REMOVED BY A DIPEPTIDYLPEPTIDASE
        (PROBABLE).
        40 91 ANTIFREEZE PROTEIN IIA7.
        AA: 8326 MW; DIFC542FD865012C CRC64;
        1.5%; Score 8; DB 1; Length 91;
        arity 100.0%; Pred. No. 19;
        conservative 0; Mismatches 0; Indels 0; Gaps 0;

        AATA 158
        |||||
        AATA 52

        STANDARD; PRT; 91 AA.
        (Rel. 20, Created)
        (Rel. 20, Last sequence update)
        (Rel. 40, Last annotation update)
        cotein precursor (AFP)
        ictes americanus (Winter flounder) (Pleuronectes

```

```

OS      americanus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC      Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC      Pleuronectoidae; Pleuronectidae; Pseudopleuronectes.
OX      NCBI_TaxID=8285;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90384854; PubMed=2402466;
RA      Gauthier S., Wu Y., Davies P.L.;
RT      "Nucleotide sequence of a variant antifreeze protein gene.";
RL      Nucleic Acids Res. 18:5303-5303(1990).
CC      -!- FUNCTION: Antifreeze proteins lower the blood freezing point
CC      -!- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
CC      ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
CC      This SWISS-PROT entry is copyright. It is produced through a col-
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CC      modified and this statement is not removed. Usage by and for
CC      entities requires a license agreement (See http://www.isb-sib.ch
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X53718; CAA37754.1; -.
DR      InterPro; IPR000104; Antifreeze_1.
DR      PRINTS; PRO0308; ANTIFREEZE1.
KW      Antifreeze protein; Repeat; Multigene family; Signal.
FT      SIGNAL 1 21 POTENTIAL.
FT      PROPEP 22 39 REMOVED BY A DIPEPTIDYLPEPTIDASE
        (PROBABLE).
FT      CHAIN 40 91 ANTIFREEZE PROTEIN.
        SEQUENCE 91 AA; 8354 MW; DIFC5439A902012C CRC64;

        Query Match 1.5%; Score 8; DB 1; Length 91;
        Best Local Similarity 100.0%; Pred. No. 19;
        Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY      151 AAAAAATA 158
        |||||
Db      45 AAAAAATA 52

        RESULT 61
        ANP LIMFE STANDARD; PRT; 97 AA.
        ID ANP LIMFE STANDARD; PRT; 97 AA.
        AC P09031;
        DT 01-NOV-1988 (Rel. 09, Created)
        DT 01-NOV-1988 (Rel. 09, Last sequence update)
        DT 01-AUG-1990 (Rel. 15, Last annotation update)
        DE Antifreeze protein precursor (AFP).
        OS Limanda ferruginea (Yellowtail flounder).
        OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
        OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
        OC Pleuronectoidae; Pleuronectidae; Limanda.
        OX NCBI_TaxID=8258;
        RN [1]
        RP SEQUENCE FROM N.A.
        RX MEDLINE=88029483; PubMed=3665937;
        RA Scott G.K., Davies P.L., Shears M.A., Fletcher G.L.;
        RT "Structural variations in the alanine-rich antifreeze proteins of
        RT pleuronectinae.";
        RL Eur. J. Biochem. 168:629-633(1987).
        CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.
        CC -!- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
        CC ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
        CC -----
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        between the Swiss Institute of Bioinformatics and the EMBL out-
        the European Bioinformatics Institute. There are no restrictio-
        use by non-profit institutions as long as its content is ir-
        modified and this statement is not removed. Usage by and for

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 all to license@isb-sib.ch).

 CAA29655.1; --

00104; Antifreeze_1.
 08; ANTIFREEZE1.
 1; Antifreeze; Signal.

1 23
 4 48
 9 97
 AA; 8865 MW; 62AD582DF8E459B6 CRC64;

REMOVED BY A DIPEPTIDYLPEPTIDASE
 (PROBABLE).

ANTIFREEZE PROTEIN.

1.5%; Score 8; DB 1; Length 97;
 identity 100.0%; Pred. No. 20;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 126
 ||||
 AAA 46

STANDARD; PRT; 99 AA.

1. 36, Created)

1. 36, Last sequence update)

1. 42, Last annotation update)

1. 2 (BC-NCP2).

1. 1 (Death's head cockroach).

1. 1 (Death's head cockroach).

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1. 1 (Death's head cockroach).

CTT

Caenorhabditis elegans
KFA-1 OK 13/E3.7.

Caenorhabditis elegans
KFA-1 OK 13/E3.7.

azoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Peleodierinae; Caenorhabditis.

39;

N.A.

1 N2;

Brodie J.;

3-1997) to the EMBL/GenBank/DBJ databases.

N.A.

1 N2;

R.; Doeber A.;

2-2000) to the EMBL/GenBank/DBJ databases.

2-2001) to the EMBL/GenBank/DBJ databases.

Plays an important role in the elongation step of

P1 and P2 exist as dimers at the large ribosomal subunit.

Belongs to the L12P family of ribosomal proteins.

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ail to license@isb-sib.ch).

AA048625.1; -

}; AA027864.1; -

1.7; CE26658.

001813; Ribosomal 60S.

001859; Ribosomal P2.

60S ribosomal; 1.

66; RIBOSOMALP2.

ein.

12 42 Y -> N (IN REF. 1).

. AA; 11283 MW; 6DB5B65BACFCC4A6 CRC64;

1.5%; Score 8; DB 1; Length 111;

urity 100.0%; Pred. No. 22;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 125

|||

AAA 79

STANDARD; PRT; 112 AA.

1; 08, Created)

rel. 33, Last sequence update)

rel. 43, Last annotation update)

osomal protein P1 (RP21C) (Acidic ribosomal protein

.C OR RPA2 OR RP21C OR CG4087.

anogaster (Fruit fly).

azoa; Arthropoda; Hexapoda; Insecta; Pterygota;

pterygota; Diptera; Brachycera; Muscomorpha;

Drosophilidae; Drosophila.

N.A.

10; PubMed-3122177;

iced amino acid sequence of Drosophila rp21C, another

omal protein."

Res. 15:10064-10064(1987).

SEQUENCE FROM N.A.

RP MEDLINE=93273819; PubMed=8501137;

RX Olson P.F., Salo T., Garrison K., Fessler J.H.;

RA "Drosophila acidic ribosomal protein rpA2: sequence and

RT characterization."

RL J. Cell. Biochem. 51:353-359 (1993).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.

RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley; TISSUE=Head;

RX MEDLINE=22426066; PubMed=12537569;

RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Wan

RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan

RA Rubin G.M., Celniker S.E.;

RT "A Drosophila full-length cDNA resource."

RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).

CC -1- FUNCTION: Plays an important role in the elongation step of

CC protein synthesis.

CC -1- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal sub

CC -1- SIMILARITY: Belongs to the L12P family of ribosomal proteins.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outst

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CC -----

CC EMBL; Y00504; CAA68557.1; -

DR EMBL; S62170; AAB26902.1; -

DR EMBL; AE003589; AAF51499.1; -

[illegible]

eria; Cetartiodactyla; Suina; Suidae; Sus.
3, 9913, 10141;

N.A.

95; PubMed-2315322;
eeler M.B., Leiter A.B.;
ucture of the precursor and tissue distribution of the
ad. Sci. U.S.A. 87:2299-2303(1990).

56.

ne;
89; PubMed-8618828;
ernvall H., Mutt V., Sillard R.;
ve processing pathways for a preprohormone: a bioactive
in.";
ad. Sci. U.S.A. 92:11985-11989(1995).

-56.

34; PubMed-5465996;
s J.B., Magnusson S.;
porine secretin. The amino acid sequence.";
m. 15:513-519(1970).

-59 AND 92-131.

67; PubMed-2395872;
oernvall H., Mutt V.;
prosecretin: isolation of a secretin precursor from
ine.";
ad. Sci. U.S.A. 87:6781-6785(1990).

0-131.

20; PubMed-5978238;
Ondetti M.A., Levine S.D., Narayanan V.L.,
Sheehan J.T., Williams N.J., Sabo E.F.;
a heptacosapeptide amide with the hormonal activity of
1757-1758(1966).

-56.

02; PubMed-7250377;
Joernvall H., Mutt V.;
amino acid sequence of bovine secretin.";
:71-74(1981).

-56.

ellus;
63; PubMed-2340294;
uvin A., Gourlet P., Gossen D., de Neef P., Rathe J.,
Vandermeers-piret M.-C., Vandermeers A., Christophe J.;
and amino acid sequence of vasoactive intestinal
de histidine isoleucineamide (1-27) and secretin from
stine of guinea pig.";
ys. Acta 1038:355-359(1990).

MR OF SECRETIN.

42; PubMed-2831051;
lges M., Bruenger A., Gronenborn A.M.;
of the backbone conformation of secretin by restrained
amics on the basis of interproton distance data.";
m. 171:479-484(1988).

MR OF SECRETIN.

117; PubMed-2883029;
I., Bovermann G., Clore G.M.;
ly of the solution conformation of secretin. Resonance
secondary structure.";

RL FEBS Lett. 215:88-94(1987).
CC -!- FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic ju.
CC and secretion of NaHCO(3)-rich bile and inhibits HCl producti
CC the stomach.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PHARMACEUTICAL: Available under the name Secretin-Perring (Fe
CC Pharmaceuticals).
CC -!- SIMILARITY: Belongs to the glucagon family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a colla
CC between the Swiss Institute of Bioinformatics and the EMBL out
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CC use by non-profit institutions as long as its content is in
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CC entities requires a license agreement (See <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC

DR EMBL; M31496; AAA31121.1; -.
DR PIR; B35094; SEFG.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation;
KW Cleavage on pair of basic residues; Signal; Pharmaceutical.
FT NON TER 1
FT SIGNAL <1 18
FT PEPTIDE 30 56
FT MOD_RES 56 56
SQ SEQUENCE 131 AA; 14277 MW; 1A24BDDA600E4E34 CRC64;
SECRETIN.
AMIDATION (G-57 PROVIDE AMIDE GROUP)

Query Match 1.5%; Score 8; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G;

QY 109 PAPPAPR 116

DB 22 PAPPAPR 29

RESULT 72

RS16_BRUME
ID RS16_BRUME STANDARD; PRT; 134 AA.
AC Q8YJ59;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S16.
GN RPSP OR BMEI0227 OR BR1824.
OS Brucella melitensis, and
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459, 29461;
RN [1]
SEQUENCE FROM N.A.
RP SPECIES=B.melitensis; STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Muej C., Lo
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsma
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
RN [2]
SEQUENCE FROM N.A.
RP SPECIES=B.suis; STRAIN=1330 / Biovar 1;
RX MEDLINE=2247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.I
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 Tettelin H., Gill S.R., White O., Salzberg S.L.,
 Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 suis genome reveals fundamental similarities between
 ant pathogens and symbionts";
 Cad. Sci. U.S.A. 99:13148-13153(2002).
 Y: Belongs to the S16P family of ribosomal proteins.

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 ail to license@isb-sib.ch).

 5; AAL51409.1; -;
 3; RAN30719.1; -;
 AF3280.

 85; -; 1.
 000307; Ribosomal S16.
 791; Ribosomal S16; 1.
 R00002; S16; 1.
 732; RIBOSOMAL S16; FALSE NEG.
 tein; Complete proteome.
 4 AA; 14529 MW; 5A716087E496C172 CRC64;

 1.5%; Score 8; DB 1; Length 134;
 arity 100.0%; Pred.No. 26;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

 AAAP 127
 |||||
 AAAP 127

 STANDARD; PRT; 136 AA.

 Rel. 30, Created)
 Rel. 30, Last sequence update)
 Rel. 42, Last annotation update)
 itation particle 14 kDa protein (SRP14) (18 kDa ALU RNA
 in).
 (Human).
 itaxoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Primates; Catarrhini; Hominidae; Homo.
 06;

 1 N.A.
 2854; PubMed-7542942;
 mallaz M., Jeffers H., Strub K.;
 subunit of the signal recognition particle (SRP) is
 re than 20-fold excess over SRP in primate cells and
 ily free but also in complex with small cytoplasmic Alu

 all 6:471-484(1995).

 4 N.A.
 1852; PubMed-8196634;
 Nelson B., Bilyeu T., Hsu K., Darlington G.J.,

 RNA-binding protein whose expression is associated with
 of small cytoplasmic Alu RNA";
 ol. 14:3949-3959(1994).
 ing secretory proteins to the rough endoplasmic reticulum
 . SRP9 together with SRP14 and the Alu portion of the SRP
 stitutes the elongation arrest domain of SRP. The complex

CC of SRP9 and SRP14 is required for SRP RNA binding.
 CC SUBUNIT: Signal recognition particle consists of a 7S RNA mo
 CC of 300 nucleotides and six protein subunits: SRP72, SRP68, SI
 CC SRP19, SRP14 and SRP9.
 CC SUBCELLULAR LOCATION: Cytoplasmic.
 CC SIMILARITY: Belongs to the SRP14 family.

 CC This SWISS-PROT entry is copyright. It is produced through a coll
 CC between the Swiss Institute of Bioinformatics and the EMBL out
 CC the European Bioinformatics Institute. There are no restriction
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 CC or send an email to license@isb-sib.ch).

 DR EMBL; X73459; CAA51838.1; -;
 DR EMBL; U07857; AAA59066.1; -;
 DR PIR; A56082; A56062.
 DR PIR; S34196; S34196.
 DR PDB; 1B80; 08-NOV-00.
 DR SWISS-2DPAGE; P37108; HUMAN.
 DR Genew; HGNC:11299; SRP14.
 DR MIM; 600708; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005786; C:signal recognition particle; TAS.
 DR GO; GO:0008312; F:7S RNA binding; TAS.
 DR GO; GO:0006613; P:cotranslational membrane targeting; TAS.
 DR InterPro; IPR003210; SRP14.
 DR InterPro; IPR009018; SRP9/14.
 DR Pfam; PF02290; SRP14; 1.
 DR ProDom; PD009170; SRP14; 1.
 KW Signal recognition particle; RNA-binding; 3D-structure.
 FT DOMAIN 108 136
 FT CONFLICT 124 124 A -> P (IN REF. 2).
 SQ SEQUENCE 136 AA; 14544 MW; 2B5B2D1D77BA5E8E CRC64;

 Query Match 1.5%; Score 8; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred.No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; (

QY 120 AAAAAAAP 127

Db 110 AAAAAAAP 117

RESULT 74

HEX9 ADE07

ID HEX9 ADE07 STANDARD; PRT; 138 AA.

AC P03283;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Hexon-associated protein (Protein IX).

GN PIX

OS Human adenovirus type 7, and

OS Human adenovirus type 3.

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenoviri

OX NCBI TaxID=10519, 45659;

[1] _TaxID=10519, 45659;

RN SEQUENCE FROM N.A.

RC SPECIES=Human adenovirus type 7; STRAIN=Gomen;

RX MEDLINE=81261948; PubMed=6266923;

RA Dijkema R., Maat J., Dekker B.M.M., van Ormondt H., Boyer H.W.;

RT "The gene for polypeptide IX of human adenovirus type 7.";

RL Gene 13:375-385(1981).

RN [2]

RC SEQUENCE FROM N.A.

RC SPECIES=Human adenovirus type 3;

RX MEDLINE=81261949; PubMed=7262560;

RA Engler J.A.;

RT "The nucleotide sequence of the polypeptide IX gene of human

adenovirus type 3.";

RL Gene 13:387-394(1981).

This protein is a structural component of the virion. It has an additional role during adenovirus multiplication.

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CAA26764.1; -
AAA42510.1; -
3XAD97.
005641; Adeno PTX.
; Adeno PTX; 1.
ed protein.
3 AA; 14107 MW; B45EFBD6F7933BF2 CRC64;

1.5%; Score 8; DB 1; Length 138;
arity 100.0%; Pred. No. 27;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158
|||||
ATA 68

STANDARD; PRT; 138 AA.
rel. 42, Created)
rel. 42, Last sequence update)
rel. 42, Last annotation update)
protein L34.

atus (Mosquito) (Ochlerotatus triseriatus).
; arzoa; Arthropoda; Hexapoda; Insecta; Pterygota;
; pterygota; Diptera; Nematocera; Culicoidea;
52;

284; PubMed=11328654;
; Rayms-Keller A., Blair C.D., Beatty B.J.;
ning and complete cDNA sequences of the ribosomal
1 and rpl44 from Aedes triseriatus mosquitoes.";
51-455(2000).
f; Belongs to the L34E family of ribosomal proteins.

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7; AAF87575.1; -
008195; Ribosomal L34E.
; Ribosomal L34e; 1.
50; RIBOSOMAL_L34.
145; RIBOSOMAL_L34E; 1.
tein.

8 AA; 15602 MW; 0232AECEPC95657 CRC64;
0
1.5%; Score 8; DB 1; Length 138;
arity 100.0%; Pred. No. 27;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 APAAAAA 125
|||||
Db 121 APAAAAA 128

RESULT 76
RNS3 STRAU STANDARD; PRT; 141 AA.
AC P30289;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Guanyl-specific ribonuclease Sa3 precursor (EC 3.1.27.3) (RNase S
GN RNAS3.
OS Streptomyces aureofaciens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10762 / CCM 3239;
RC MEDLINE=93012968; PubMed=1398084;
RA Homero D., Hollaenderova Z., Kormanec J., Sevcik J.;
RT "Cloning and sequencing of the gene encoding a ribonuclease from
RT Streptomyces aureofaciens CCM3239.";
RL Gene 119:147-148 (1992).
CC -|- CATALYTIC ACTIVITY: Two-stage endonucleolytic cleavage to
CC nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending
CC G-P with 2', 3'-cyclic phosphate intermediates.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the ribonuclease N1/T1 family.
CC -|- CAUTION: Ref.1 sequence differs from that shown due to
CC frameshifts.

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or send an email to license@isb-sib.ch).

EMBL; M82920; AAA26809.1; ALT_FRAME.
DR EIR; JCI287; JCI287.
DR PDB; 1MGR; 04-FEB-03.
DR InterPro; IPR000026; Ribonuc N1T1.
DR Pfam; PF00545; ribonuclease_1
KW Hydrolase; Nuclease; Endonuclease; Signal; 3D-structure.
FT SIGNAL 1 36 OR 43 (POTENTIAL).
FT CHAIN 37 141 GUANYL-SPECIFIC RIBONUCLEASE SA3.
FT ACT_SITE 99 99 BY SIMILARITY.
FT ACT_SITE 114 114 BY SIMILARITY.
FT ACT_SITE 130 130 BY SIMILARITY.
FT DISULFID 52 141 BY SIMILARITY.
SQ SEQUENCE 141 AA; 14819 MW; DB128BB3E60DFC6 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 139 PVAAPAA 146
|||||
Db 24 PVAAPAA 31

RESULT 77
WHW1 WHEAT STANDARD; PRT; 146 AA.
ID WHW1 WHEAT
AC O64392;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Wheatwin1 precursor (Pathogenesis-related protein 4a) (Protein 0.

14 86 BY SIMILARITY.
15 109 BY SIMILARITY.
16 146 BY SIMILARITY.
17 111 N -> D (IN REF. 2).
18 } AA; 15867 MW; 3D4EA32E085BCB1 CRC64;
19
20 1.5%; Score 8; DB 1; Length 148;
21 100.0%; Pred. No. 28;
22 nservative 0; Mismatches 0; Indels 0; Gaps 0;
23
24 DATA 158
25 |||||
26 DATA 23
27
28 STANDARD; PRT; 149 AA.
29
30 rel. 31, Created)
31 rel. 31, Last sequence update)
32 rel. 42, Last annotation update)
33
34 coin.
35 (oad bean).
36
37 diplantae; Streptophyta; Embryophyta; Tracheophyta;
38 : Magnoliophyta; eudicotyledons; core eudicots; rosids;
39 abales; Fabaceae; Papilionoideae; Viciaeae; Vicia.
40 }6;
41
42 N.A.
43
44 100; ISSUE=Cotyledon;
45 341; PubMed=8219095;
46 Chiffarth T., Baeumlein H., Feix G.;
47 analysis of chromosomal HMG proteins from monocotyledons
48 ons.";
49 ol. 23, 619-625 (1993).
50
51 AR LOCATION: Nuclear (Potential).
52 f: Belongs to the HMG1/HMG2 protein family.
53 f: Contains 1 HMG box domain.
54
55 DT entry is copyright. It is produced through a collaboration
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58 profit institutions as long as its content is in no way
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61 ail to license@isb-sib.ch).
62
63 -----
64 CAB37859.1; -.
65 339556.
66 1HMF.
67 00910; HMG_12_box.
68 : HMG_box; 1.
69 3; HMG; 1.
70 118; HMG_BOX_2; 1.
71 in; DNA-binding.
72 15 114 HMG BOX.
73 21 149 ASP/SLU-RICH (ACIDIC).
74 3 AA; 16659 MW; FE52DF5E6E8E0B3D CRC64;
75
76 1.5%; Score 8; DB 1; Length 149;
77 100.0%; Pred. No. 28;
78 nservative 0; Mismatches 0; Indels 0; Gaps 0;
79
80 DEED 342
81 |||||
82 DEED 142
83
84 STANDARD; PRT; 165 AA.
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S16.
GN RPS16 OR CC3652.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whit
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -|- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AE006023; AAK25614.1; -.
CC PIR; B87702; B87702.
CC DR HSSP; P80379; 1EMW.
CC DR TIGR; CC3652;
CC DR HAMAP; MF_00385; -; 1.
CC DR InterPro; IPR000307; Ribosomal_S16.
CC DR Pfam; PF00886; Ribosomal_S16; 1.
CC DR ProDom; PD003791; Ribosomal_S16; 1.
CC DR TIGRFAMs; TIGR00002; S16; 1-
CC DR PROSITE; PS00732; RIBOSOMAL_S16; 1.
CC KW Ribosomal protein; Complete proteome.
CC SQ SEQUENCE 165 AA; 17605 MW; ED46FC2798C5BE1C CRC64;
65
66 Query Match 1.5%; Score 8; DB 1; Length 165;
67 Best Local Similarity 100.0%; Pred. No. 31;
68 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
69
70 Qy 120 AAAAAAAP 127
71 Db 135 AAAAAAAP 142
72
73 RESULT 81
74 OM19 BRUME
75 ID - OM19 BRUME STANDARD; PRT; 177 AA.
76 AC Q44663; Q44699;
77 DT 28-FEB-2003 (Rel. 41, Created)
78 DT 28-FEB-2003 (Rel. 41, Last sequence update)
79 DT 10-OCT-2003 (Rel. 42, Last annotation update)
80 DE Outer membrane lipoprotein omp19 precursor (Minor outer membrane
81 protein omp19) (19-kDa OMP) (18 kDa immunoreactive antigen).
82 GN OMP19 OR BME10135 OR BR1930.
83 OS Brucella melitensis,
84 OS Brucella suis, and
85 OS Brucella abortus.
86 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
87 OC Brucellaceae; Brucella.
88 OX NCBI_TaxID=29459, 29461, 235;
89 RN [1]
90 RP SEQUENCE FROM N.A.
91 RC SPECIES=B.abortus; STRAIN=544 / Biovar 1;

KW	Complete proteome; Palmitate.	
FT	SIGNAL	1 20 PROBABLE.
FT	CHAIN	21 177 OUTER MEMBRANE LIPOPROTEIN OMP19.
FT	LIPID	21 21 N-palmitoyl cysteine (Probable).
FT	LIPID	21 21 S-diacylglycerol cysteine (Probable).
FT	VARIANT	176 177 SR -> IG (IN STRAIN 2308).
FT	SEQUENCE	177 AA; 17604 MW; 8038DSABD87019E2 CRC64;
QY	Query Match	1.5%; Score 8; DB 1; Length 177;
DB	Best Local Similarity	100.0%; Pred. No. 33;
Matches	8; Conservative	0; Mismatches 0; Indels 0;
QY	133 PPPPPAPV 140	
DB		
DB	34 PPPPPAPV 41	
RESULT 82		
ID	RBMS_CHICK	STANDARD; PRT; 200 AA.
AC	Q9W61L	
DC	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	RNA-binding protein with multiple splicing homolog (RBP-MS) (HEA: RBP-MS)	
DE	RRM Expressed Sequence) (Hermes).	
GN	RRBMS OR HERMES.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasian.	
OC	Gallus.	
OX	NCBI TaxID=9031;	
OX	[1]_	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Heart.	
RX	MEDLINE=99195799; PubMed=10096065;	
RA	Gerber W.V., Yatskevych T.A., Antin P.B., Correia K.M., Conlon I. Krieg P.A.;	
RT	"The RNA-binding protein gene, hermes, is expressed at high level in the developing heart.";	
RT	Mech. Dev. 80:77-86(1999).	
CC	-!- FUNCTION: May bind RNA.	
CC	-!- TISSUE SPECIFICITY: Expressed in developing heart.	
CC	-!- DEVELOPMENTAL STAGE: mRNA already detected at stage 7-8 in the cardiac mesoderm, and become almost undetectable in the curvature of the ventricular region whereas remaining high in developing atrial regions.	
CC	-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch).	
CC	or send an email to license@isb-sib.ch .	
CC	EMBL; AF129933; AAD30273.1; -	
DR	InterPro; IPR000504; RNA_rec_mot.	
DR	Pfam; PF00076; rrm; 1.	
DR	SMART; SM00360; RRM; 1.	
DR	PROSITE; PS50102; RRM; 1.	
DR	PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.	
CC	RNA-binding.	
KW	DOMAIN	22 99 RNA-BINDING (RRM).
FT	DOMAIN	169 176 POLY-ALA.
FT	SEQUENCE	200 AA; 21856 MW; 4093B3C780BBC1DF CRC64;
QY	Query Match	1.5%; Score 8; DB 1; Length 200;
DB	Best Local Similarity	100.0%; Pred. No. 36;
Matches	8; Conservative	0; Mismatches 0; Indels 0;
QY	119 PAAAAAAA 126	

|||
AAA 175

STANDARD; PRT; 205 AA.

rel. 29, Last sequence update)
rel. 43, Last annotation update)
reaction center subunit II, chloroplast precursor
20 kDa subunit (PSI-D).

re (Barley).
Chlorophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
deum.
3;

N.A.
Bonus; TISSUE=Seedling;
96; PubMed=8278501;
Okels J.S.;

sequencing of a full-length cDNA clone encoding the
of photosystem I from barley.";
101:335-336(1993).

1-82; 118-133; 156-195 AND 203-205.

lofs Bonus;
Hoej P.B., Svendsen I., Moeller B.L.;
acid sequence of two nuclear-encoded photosystem I
from barley.";
ys. Acta 933:501-505(1988).

PSAD can form complexes with ferredoxin and ferredoxin-
rase in photosystem I (PS I) reaction center. PSAD may
ferredoxin-docking protein.

R LOCATION: Chloroplast thylakoid membrane, stromal

By light.
Belongs to the psad family.

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AAA18567.1; -.

02247.

03685; Psad.

Psad; 1.

; Photosystem I; Chloroplast; Transit peptide;

ubane.

1 43 CHLOROPLAST.

4 205 PHOTOSYSTEM I REACTION CENTER SUBUNIT II.

80 G -> GG (IN REF. 2).

82 T -> G (IN REF. 2).

8 118 R -> P (IN REF. 2).

1 191 S -> F (IN REF. 2).

5 AA; 21933 MW; 5B6A2CAD81D5E029 CRC64;

1.5%; Score 8; DB 1; Length 205;

irity 100.0%; Pred. No. 37;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

APPA 189

||||

APPA 57

RESULT 84

YNP2 CAEEL STANDARD; PRT; 205 AA.

AC P34535;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical protein T05G5.2 in chromosome III.

GN T05G5.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoid

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA MEDLINE=94150718; PubMed=79063398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,

RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kireten J., Laister N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showknee

RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,

RA Wohldman P.

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of

RT elegans.";

RL Nature 368:32-38(1994).

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z27079; CAA81583.1; -.

DR PIR; S41002; S41002.

DR WormPep; T05G5.2; CE00314.

DR InterPro; IPR001092; HLH_basic.

DR Pfam; PF00010; HLH; 1.

DR SMART; SM00353; HLH; 1.

DR PROSITE; PS00888; HLH; 1.

KW Hypothetical protein; Nuclear protein.

FT DOMAIN 38 89 HELIX-LOOP-HELIX MOTIF (BY SIMILARIT

SQ SEQUENCE 205 AA; 22691 MW; 577E59E04268FA1C CRC64;

Query Match 1.5%; Score 8; DB 1; Length 205;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 8; Conservative 0; Mismatches 0; Indels 0; G;

QY 132 APPPPPP 139

Db 176 APPPPPP 183

RESULT 85

HS27 CANFA

ID HS27 CANFA STANDARD; PRT; 209 AA.

AC P42929;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Heat shock 27 kDa protein (HSP 27).

GN HSPB1 OR HSP27.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC heria; Carnivora; Fissipedia; Canidae; Canis.
CC 15;
CC [ N.A.
CC smooth muscle;
CC 379; PubMed=7665102;
CC Gerthoff W.T., Hickey E., Weber L.A.;
CC sequencing of a cDNA encoding the canine HSP27 protein.
CC 306(1995).
CC INVOLVED IN STRESS RESISTANCE AND ACTIN ORGANIZATION.
CC Y: Belongs to the small heat shock protein (HSP20)
CC
CC -----
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CC
CC -----
CC AAA87172.1; --
CC JC4244.
CC 001436; Crystallin_alpha.
CC 002068; Hsp20.
CC 008978; HSP20_chap.
CC ; HSP20; 1.
CC 031; ACRYSTALIN.
CC 031; HSP20; 1.
CC phosphorylation.
CC 15
CC 15 PHOSPHORYLATION (BY PKC AND PKA)
CC (BY SIMILARITY).
CC 86 PHOSPHORYLATION (BY PKC AND PKA)
CC (BY SIMILARITY).
CC 09 AA; 22939 MW; 7E59F696D8C7F1BD CRC64;
CC
CC 1.5%; Score 8; DB 1; Length 209;
CC arity 100.0%; Pred. No. 38;
CC onservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC AAAAA 126
CC |||||
CC AAAAA 73
CC
CC STANDARD; PRT; 211 AA.
CC
CC (Rel. 41, Created)
CC (Rel. 41, Last sequence update)
CC (Rel. 42, Last annotation update)
CC r group protein 1-like 10 (HMG-1110).
CC
CC (Human).
CC Mazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Theria; Primates; Catarrhini; Hominidae; Homo.
CC 06;
CC
CC A N.A.
CC 7165; PubMed=10591208;
CC int A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
CC ink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
CC Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
CC lakey S.E., Bridgeman A.M., Buck D., Burgess J.,
CC Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
CC Tobley V.E., Cole C.G., Collier R.E., Connor R.,
CC rby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
CC cockree C., Doddsworth S.J., Durbin R.M., Ellington A.G.,
CC Fey J.M., Fleming K., French L., Garner A.A.,
CC z., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
CC all-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
CC ones M.C., Kershaw J., Kimberley A.M., King A.,

```

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RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C
RA Phillips S.H., Plumb R.W., Ramsay H., Ransey Y., Rogers L., Ross
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Stuston J.E., Swann R.M.,
RA Vaudin M., Wallis J.M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming I
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimi:
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan I
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., So:
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing
RA Sheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RA "The DNA sequence of human chromosome 22.";
RT Nature 402:489-495(1999).
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -!- SIMILARITY: Contains 2 HMG box domains.
CC
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CC
CC -----
CC EMBL; Z95115; CAB62951.1; -.
CC HSP; P07156; INHN.
CC Genew; HGNC:4994; HMG1L10.
CC InterPro; IPR000135; Highmobility_12.
CC InterPro; IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 2.
CC PRINTS; PR00886; HIGHMOBILITY12.
CC SMART; SM00398; HMG; 2.
CC PROSITE; PS00353; HMG_BOX_1; 1.
CC PROSITE; PS0118; HMG_BOX_2; 2.
CC Nuclear protein; Chromosomal HMG BOX 1.
CC DNA_BIND 9 79
CC FT DNA_BIND 95 163 HMG_BOX_2.
CC FT DOMAIN 186 211 ASP/GLU-RICH (ACIDIC).
CC SQ SEQUENCE 211 AA; 24218 MW; 2A53BA2AE6DF7CD CRC64;
CC
CC Query Match 1.5%; Score 8; DB 1; Length 211;
CC Best Local Similarity 100.0%; Pred. No. 38;
CC Matches 8; Conservative 0; Mismatches 0; Indels 0;
CC
CC QY 336 EDEDEDD 343
CC Db 203 EDEDEDD 210
CC
CC RESULT 87
CC RSE CORGL STANDARD; PRT; 211 AA.
CC ID - RSE_CORGL

```

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
OX	NCBI_taxID=10116;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=9009348; PubMed=2532363;
RX	Li S., Klein E.S., Russo A.F., Simmons D.M., Rosenfeld M.G.;
RA	"Isolation of cDNA clones encoding small nuclear ribonucleopartic
RT	associated proteins with different tissue specificities.";
RT	Proc. Natl. Acad. Sci. U.S.A. 86:9778-9782(1989).;
RL	!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May ha
CC	functional role in the pre-mRNA splicing or in snRNP structur
CC	!- SUBCELLULAR LOCATION: Nuclear.
CC	!- TISSUE SPECIFICITY: HEART, AND LESS IN BRAIN, PITUITARY, & LI
CC	!- SIMILARITY: BELONGS TO THE snRNP SMB/SMN FAMILY.
CC	-----
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CC	modified and this statement is not removed. Usage by and for c
CC	entities requires a license agreement (See http://www.isb-sib.ch/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M29295; AAA42159.1; -.
DR	PIR; B34503; B34503.
DR	HSP; P14678; 1D3B.
DR	InterPro; IPR001163; snRNP_Sm.
DR	Pfam; PF01423; LSM; 1.
DR	SMART; SM00651; Sm; 1.
DR	Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.
KW	NON_TER 1
FT	DOMAIN 158 211 REPEAT-RICH REGION.
FT	REPEAT 158 164
FT	REPEAT 174 179
FT	REPEAT 199 204
FT	REPEAT 205 211
FT	SEQUENCE 214 AA; 21594 MW; 3FC57DELBF68B603 CRC64;
SQ	
	Query Match 1.5%; Score 8; DB 1; Length 214;
	Best Local Similarity 100.0%; Pred. No. 38;
	Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY	151 AAAAAAATA 158
Dd	135 AAAAAAATA 142

RESULT 89	
HANI_HUMAN	
ID	HANI_HUMAN STANDARD; PRT; 215 AA.
AC	O96004;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Heart- and neural crest derivatives-expressed protein 1
DE	(Extraembryonic tissues, heart, autonomic nervous system and neural crest derivatives-expressed protein 1) (EHAND).
DE	HAND1 OR EHAND.
OS	Homo sapiens (Human).
GN	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Eumariota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	TISSUE=Heart;
RC	MEDLINE=99132638; PubMed=9931445;
RT	Knoefler M., Meinhardt G., Vasicek R., Husslein P., Egarter C.;
RT	"Molecular cloning of the human Hand1 gene/cDNA and its tissue-
RT	restricted expression in cytotrophoblastic cells and heart.";
RL	Gene 224:77-86(1998).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;

8257; PubMed=12477932;
 L.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 J.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Joquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Lton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 W., Touchman J.W., Green E.D., Dickson M.C.,
 C., Grimwood J., Schmutz J., Myers R.M.,
 Y.S.N., Krzyzanski M.I., Skalska U., Smalus D.E.,
 Schein J.E., Jones S.J.M., Matra M.A.;
 and initial analysis of more than 15,000 full-length
 use cDNA sequences.";
 Acad. Sci. U.S.A. 99:16899-16903 (2002).
 : Plays an essential role in early trophoblast
 tiation and in cardiac morphogenesis. In the adult, could
 red for ongoing expression of cardiac-specific genes.
 e DNA sequence 5'-NRTCTG-3' (noncanonical E-box) (By
 ty).
 Efficient DNA binding requires dimerization with another
 tein. Forms homodimers and heterodimers with TCF3 gene
 E12 and E47, HAND2 and HEY1, HEY2 and HEYL (hairly-related
 ction factors) (By similarity).
 PECIFICITY: Heart.
 TY: Contains 1 basic helix-loop-helix (bHLH) domain.
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 mail to license@isb-sib.ch).

 12; AAD19283.1; -;
 56; AAD19280.1; -;
 90; AAD11190.1; -;
 1373; -;
 1807; HAND1.

 00; F:transcription factor activity; TAS.
 07; P:heart development; TAS.
 56; P:transcription from Pol II promoter; TAS.
 2001092; HLH_basic.
 0; HLH; 1.
 53; HLH; 1.
 0888; HLH; 1.
 (protein; transcription regulation; DNA-binding;
 sin.
 9 17 POLY-HIS.
 64 71 POLY-ALA.
 94 106 BASIC DOMAIN
 07 150 HELIX-LOOP-HELIX MOTIF.
 5 AA; 23627 MW; 7ED98EA081A8D6BA CRC64;
 1.5%; Score 8; DB 1; Length 215;
 arity 100.0%; Pred. No. 38;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AATA 158
 |||||
 AATA 71

RSMB_MOUSE STANDARD; PRT; 231 AA.
 P27048;
 01-AUG-1992 (Rel. 23, Created)
 01-AUG-1992 (Rel. 23, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Small nuclear ribonucleoprotein associated protein B (snRNP-B)
 protein B) (Sm-B) (Smb).
 GN SNRPB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=92290275; PubMed=1376292;
 Griffith A., deJonge E., Huang S., Ohosone Y., Craft J.E.;
 "The murine gene encoding the highly conserved Sm B protein cont
 a nonfunctional alternative 3' splice site.";
 Gene 114:193-201 (1992).
 CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May b
 functional role in the pre-mRNA splicing or in snRNP structu
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE SNRNP SMB/SMN FAMILY.

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 the European Bioinformatics Institute. There are no restrictio
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 modified and this statement is not removed. Usage by and for
 entities requires a license agreement (see <http://www.isb-sib.ch>
 or send an email to license@isb-sib.ch).

 EMBL; M58761; AAA40119.1; -;
 DR PIR; I53659; I53659.
 DR HSSP; P14678; ID3B.
 DR MGD; MGI:98342; Snrpb
 DR InterPro; IPR001163; snRNP_Sm.
 DR Pfam; PF01423; LSM; 1.
 DR SMART; SM00651; Sm; 1.
 KW Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.
 FT DOMAIN 175 228 REPEAT-RICH REGION.
 FT REPEAT 175 181
 FT REPEAT 191 196
 FT REPEAT 216 221
 FT REPEAT 222 228
 SQ SEQUENCE 231 AA; 23656 MW; 5CB0BE7E20B93D4A CRC64;

 Query Match 1.5%; Score 8; DB 1; Length 231;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 151 AAAAAATA 158
 |||||
 Db 152 AAAAAATA 159

 RESULT 91
 UCRI_NEUCR STANDARD; PRT; 231 AA.
 ID UCRI_NEUCR STANDARD; PRT; 231 AA.
 AC P07056;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondri
 precursor (EC 1.10.2.2) (Rieske iron-sulfur protein) (RISP).
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=85203899; PubMed=2986972;
 Harnisch U., Weiss H., Sebald W.;

structure of the iron-sulfur subunit of ubiquinol-reductase from Neurospora, determined by cDNA and gene

em. 149:95-99(1985).

Component of the ubiquinol-cytochrome c reductase complex III or cytochrome b-c1 complex), which is a

ry chain that generates an electrochemical potential

o ATP synthesis.

ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2

chrome c.

Binds 1 2Fe-2S iron sulfur cluster per subunit (By

Y).

Fungi bc1 complex contains 10 subunits; 3 respiratory

2 core proteins and 5 low-molecular weight proteins.

AR LOCATION: Mitochondrial inner membrane.

EOUS: The Rieske protein is a high potential 2Fe-2S

Y: Belongs to the Rieske family.

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ail to license@isb-sib.ch).

CRNA26308.1; -.

RDNCUF.

IRIE.

005805; Rieske.

005806; Rieske dom.

006317; Rieske proteo.

004192; UCR_TM_region.

; Rieske; 1.

; UCR_TM; 1.

52; RIESKE.

R01416; Rieske proteo; 1.

199; RIESKE_1; 1.

200; RIESKE_2; 1.

; Electron transport; Respiratory chain; Metal-binding;

[Iron; 2Fe-2S; Oxidoreductase; Inner membrane;

; Transit peptide.

1 32 MITOCHONDRION.

13 231 UBIQUINOL-CYTOCHROME C REDUCTASE IRON-

SULFUR SUBUNIT.

33 61 HYDROPHILIC.

52 86 POTENTIAL.

37 231 HYDROPHILIC.

74 174 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

76 176 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

73 193 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

76 196 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

79 195 BY SIMILARITY.

. AA; 24770 MW; 66B780FE78227351 CRC64;

1.5%; Score 8; DB 1; Length 231;

urity 100.0%; Pred. No. 41;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

PARA 148

|||

PARA 21

|||

STANDARD; PRT; 240 AA.

el. 40, Created)

el. 40, Last sequence update)

el. 42, Last annotation update)

ribonucleoprotein associated protein B' (snRNP-B')

DE (Sm protein B') (Sm-B') (Smb') (snRNP-B').

GN SNRNP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasian

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20027344; PubMed=10556313;

RA Gray T.A., Smithwick M.J., Schaldach M.A., Martone D.L., Graves

RA McCarrey J.R., Nicholls R.D.;

RT "Concerted regulation and molecular evolution of the duplicated

SNRNP/B and SNRNP loci.";

RL Nucleic Acids Res. 27:4577-4584(1999).

CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May h

CC functional role in the pre-mRNA splicing or in snRNP structu

CC similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: BELONGS TO THE SNRNP SMB/SMN FAMILY.

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EMBL; AF134830; AAD54495.1; -.

HSSP; P14678; 1D3B.

InterPro; IPR001163; snRNP_Sm.

Pfam; PF01423; LSM; 1.

SMART; SM00651; Sm; 1.

Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.

DOMAIN 175 236 REPEAT-RICH REGION.

REPEAT 175 181

REPEAT 191 196

REPEAT 216 221

REPEAT 222 228

REPEAT 230 236

SQ SEQUENCE 240 AA; 24588 MW; 2988181A0F54D581 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 240;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158

|||

Db 152 AAAAAATA 159

|||

RESULT 93

RSMB_ERIEU

ID RSMB_ERIEU STANDARD; PRT; 240 AA.

AC Q9TU67; Q9TU64;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Small nuclear ribonucleoprotein associated protein B' (snRNP-B')

DE (Sm protein B') (Sm-B') (Smb') (snRNP-B').

GN SNRNP.

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceae; Erinace

OX NCBI_TaxID=9365;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20027344; PubMed=10556313;

RA Gray T.A., Smithwick M.J., Schaldach M.A., Martone D.L., Graves J.

RA McCarrey J.R., Nicholls R.D.;

RT "Concerted regulation and molecular evolution of the duplicated

SNRNP/B and SNRNP loci.";

RT

[4] SEQUENCE FROM N.A.

RA Gray T.A., Martone D.L., Schaldach M.A., McCarrey J.R., Nicholl:
RA "Concerted regulation and molecular evolution of the duplicated
RT and snRNP loci.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]

RN SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.J.
RA Jones M., Pavlidis G., Almeida J.P., Babbage A.K., Bagguley C.J.
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., John
RA Lehesvaisto M.H., Leversha M.A., Lloyd C., Lloyd G.K., Lawl
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rameay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sim
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.
RA Swann R.D., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., White
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 2
RT Nature 414:865-871(2001).
RN [6]

RN SEQUENCE OF 8-240 FROM N.A.

RX MEDLINE=90308305; PubMed=1694885;
RA Elkon K.B., Hines J.J., Chu J.-L., Parnassa A.;
RT "Epitope mapping of recombinant HeLa Smb and B' peptides obtaine
RT the polymerase chain reaction.";
RN J. Immunol. 145:636-643(1990).
RN [7]

RN SEQUENCE OF 209-240 FROM N.A.

RX MEDLINE=91153665; PubMed=1825643;
RA Chu J.-L., Elkon K.B.;
RT "The small nuclear ribonucleoproteins, Smb and B', are products
RT single gene.";
RN Gene 97:311-312(1991).
RN [8]

RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=99148270; PubMed=10025403;
RA Kambach C., Walke S., Young R., Avis J.M., de la Fortelle E.,
RA Raker V.A., Luhrmann R., Li J., Nagai K.;
RT "Crystal structures of two Sm protein complexes and their implic
RT for the assembly of the spliceosomal snRNPs.";
RN Cell 96:375-387(1999).

CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May h
CC functional role in the pre-mRNA splicing or in snRNP structu
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=SM-B';
CC IsoId=P14678-1; Sequence=Displayed;
CC Name=SM-B;
CC IsoId=P14678-2; Sequence=VSP_005914;
CC -!- DISEASE: Patients with the autoimmune disease systemic lupus
CC erythematosus (SLE) have autoantibodies directed against som
CC the individual snRNP polypeptides. The most common autoantig
CC called Sm. B/b' bear Sm epitopes.
CC -!- SIMILARITY: BELONGS TO THE snRNP SMB/SMN FAMILY.
CC -!- CAUTION: Ref.4 sequence differs from Ref.1.

```

1 prediction.
-----
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-----
CAB57867.1; -
CAB57868.1; -
CAA33902.1; -
5; AAD54488.1; ALT_SEQ.
2; AAD54488.1; JOINED.
3; AAD54488.1; JOINED.
4; AAD54488.1; JOINED.
0; CAB46715.1; -
0; CAB46714.1; -
AAA36578.1; -
AAA36579.1; -
CAA37170.1; -
CAA37171.1; -
S09377.
-DEC-99.
1153; SNRNP.
.
.
2; C:small nuclear ribonucleoprotein complex; TAS.
1; C:spliceosome complex; TAS.
1; P:mRNA splicing; TAS.
001163; snRNP_Sm.
; LSM; 1.
; Sm; 1.
in; Ribonucleoprotein; RNA-binding; Repeat;
s erythematous; Alternative splicing; 3D-structure.
75 236 REPEAT-RICH REGION.
75 181
91 196
16 221
22 228
30 236
30 240
PPQCMRPPRP -> LL (in isoform SM-B).
/FTid=VSP_005914.
3 4
6 10
11 14
16 21
22 23
26 34
36 37
40 51
56 57
51 72
74 76
77 84
) AA; 24610 MW; F2E1D5E11A601170 CRC64;
1.5%; Score 8; DB 1; Length 240;
arity 100.0%; Pred. No. 42;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||||
ATA 159
STANDARD; PRT; 240 AA.
rel. 40, Created)
rel. 40, Last sequence update)

```

```

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small nuclear ribonucleoprotein associated protein B' (snRNP-B')
DE (Sm protein B') (Sm-B') (SMB') (snRNP').
GN SNRNP.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20027344; PubMed=10556313;
RA Gray T.A., Smithwick M.J., Schaldach M.A., Martone D.L., Graves
RA McCarrey J.R., Nicholls R.D.;
RT "Concerted regulation and molecular evolution of the duplicated
RT SNRNP/B and SNRNP loci";
RL Nucleic Acids Res. 27:4577-4584(1999).
CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May ha
CC functional role in the pre-mRNA splicing or in snRNP structu
CC similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE SNRNP SMB/SMN FAMILY.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; AF134827; AAD54482.1; -
DR HSSP; P14678; 1D3B.
DR InterPro; IPR001163; snRNP_Sm.
DR Pfam; PF01423; LSM; 1.
DR SMART; SM00651; Sm; 1.
KW Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.
FT DOMAIN 175 236 REPEAT-RICH REGION.
FT REPEAT 175 181
FT REPEAT 191 196
FT REPEAT 216 221
FT REPEAT 222 228
FT REPEAT 230 236
SQ SEQUENCE 240 AA; 24542 MW; 2498CFABE943C828 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 151 AAAAAATA 158
|||
Db 152 AAAAAATA 159
|||
RESULT 96
YPBE_BACSU STANDARD; PRT; 240 AA.
AC P50731;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein ypbe.
GN YPBE OR BSU23000.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / Marburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA Serron P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region bet
RT the serA and kds loci cloned in a yeast artificial chromosome.";

```

142:2005-2016 (1996).

M N A.

4033; PubMed=9384377;
asawata N., Moszer I., Albertini A.M., Alloni G.,
Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
odani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Eyreton J., Fabret C., Fertari E., Foulger D.,
jita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
laser P., Goffeau A., Golightly E.J., Grand G.,
Gay B.J., Haga K., Hache J., Harwood C.R., Henaut A.,
Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
ramata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Koeter P., Koningsstein G., Krogh S., Kumano M.,
apidus A., Lardinois S., Lauber J., Lazarevic V.,
vine A., Liu H., Masuda S., Mauel C., Medigue C.,
ellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
nl I.M., Portetelle D., Porwollik S., Prescott A.M.,
Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
ilvolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
nlan E., Schleich S., Schroeter R., Scofield F.,
Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
chiyama S., Vandenbol M., Vannier F., Vassarotti A.,
mbutt R., Wedler E., Wedler H., Weitzensegger T.,
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a genome sequence of the Gram-positive bacterium *Bacillus*
19-256(1997).

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:- CAB14216.1; -
H59932.
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002482; LysM.
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17; LysM; 1.
protein; Transmembrane; Complete proteome.
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arity 100.0%; Pred. No. 42;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IASSS 25
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IASSS 167

STANDARD; PRT; 243 AA.

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Rel. 13, Last sequence update)
Rel. 13, Last annotation update)
protein AUX28.

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N.A.

732; PubMed=11234002;
Gleimer K., Parkhill J., James K.D., Thomson N.R.,
Honore N., Garnier T., Churcher C., Harris D.,
Asham D., Brown D., Chillingworth T., Connor R.,
Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Ornsby T., Jagsels K., Lacroix C., Maclean J., Moule S.,
Silver K., Quail M.A., Rajadream M.A., Rutherford K.M.,
Eger K., Simon S., Simmonds M., Skellton J., Squares R.,
Tevens K., Taylor K., Whitehead S., Woodward J.R.,
decay in the leprosy bacillus.";
07-1011(2001).
OTS N-TERMINUS, WHICH CONTAINS THE PROLINE-RICH REPEATS,
IMMUNOREACTIVE.
Y: Y: STRONG, TO M. TUBERCULOSIS PRA HOMOLOG.

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35;
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46 55 1-1.
65 65 1-2.
75 75 1-3.
76 85 1-4 (APPROXIMATE).
11 156 2 X 23 AA APPROXIMATE REPEATS.
11 123 2-1.
14 156 2-2.
1 212 QL-> HV (IN REF. 1).
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pppp 19
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el. 16, Last sequence update)
el. 43, Last annotation update)
NA polymerase III 31 kDa polypeptide (EC 2.7.7.6) (C31).
OR AC22 OR YNLJ51C OR N1769.
cervisiae (Baker's yeast).
igi; Ascomycota; Saccharomycotina; Saccharomycetes;
lles; Saccharomycetaceae; Saccharomycetes.
2;
N.A., AND PARTIAL SEQUENCE.
90; PubMed=2201900;
a M., Beltrame M., Cassar E., Sentenac A., Thuriaux P.;
e of Saccharomycetes cerevisiae encodes a subunit of RNA
III) with an acidic tail.";

protein Rv1995/MT2051/Wb2018.
 2051 OR MTCY39.24C OR MB2018.
 n tuberculosis, and
 n bovis.
 inobacteria; Actinobacteridae; Actinomycetales;
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 773, 1765;
 4 N.A.
 tuberculosis; STRAIN=H37Rv;
 5987; PubMed=9634230;
 rosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Eiglmier K., Gas S., Barry C.E. III, Teklaia F.,
 Asham D., Brown D., Chillingworth T., Connor R.,
 Eskin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 Osborne K., Quail M.A., Rajandream M.A., Rogers J.,
 Seger K., Skelton S., Squares R.,
 Taylor K., Whitehead S., Barrell B.G.;
 the biology of Mycobacterium tuberculosis from the
 me sequence.";
 37-544 (1998).
 4 N.A.
 tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 5494; PubMed=12218036;
 D., Alland D., Eisen J.A., Carpenter L., White O.,
 DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
 Jitterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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 strains.";
 184:5479-5490 (2002).
 4 N.A.
 is; STRAIN=AF2122/97;
 1107; PubMed=12788972;
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 Roy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
 Kin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
 a genome sequence of Mycobacterium bovis";
 Acad. Sci. U.S.A. 100:7877-7882 (2003).
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 CAAA 166

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 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Homeobox protein GSH-1.
 GN GSH1 OR GSH-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
 OX NCBI_TaxID=10090;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss;
 RX MEDLINE=96172995; PubMed=8589431;
 RA Valerius M.T., Li H., Stock J.L., Weinstein M., Kaur S., Singh G
 RA Potter S.S.;
 RA "Gsh-1: a novel murine homeobox gene expressed in the central ne
 RT system.";
 RT Dev. Dyn. 203:337-351 (1995).
 RN [2]
 RP SEQUENCE FROM N.A. AND FUNCTION.
 RX MEDLINE=96181350; PubMed=8631293;
 RA Li H., Zeitler P.S., Valerius M.T., Small K., Potter S.S.;
 RT "Gsh-1, an orphan Hox gene, is required for normal pituitary
 RT development.";
 RL EMBO J. 15:714-724 (1996).
 RN [3]
 RP SEQUENCE OF 146-205 FROM N.A.
 RX MEDLINE=92073356; PubMed=1683707;
 RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Potter S.S.;
 RT "Identification of 10 murine homeobox genes";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710 (1991).
 CC -!- FUNCTION: Probable transcription factor that binds to the DN
 CC the GHRH gene. Plays an important role in pituitary developm
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
 CC -!- SIMILARITY: Contains 1 homeobox domain.
 CC This SWISS-PROT entry is copyright. It is produced through a col
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 CC -----
 CC EMBL; U21224; AAA96814.1; -;
 CC FIR; S63604; S63604.
 CC HSP; P14653; 1B72.
 CC TRANSFAC; T05100; -;
 CC MGD; MGI:95842; Gsh1.
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 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC PRINTS; PR00031; HTHREPRESSR.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; Hox; 1.
 CC PROSITE; PS00027; HOMEBOX 1; 1.
 CC PROSITE; PS00071; HOMEBOX 2; 1.
 CC Transcription regulation; Activator; Homeobox; DNA-binding;
 KW Nuclear protein; Developmental protein.
 FT DNA_BIND 146 205 HOMEBOX.
 FT DOMAIN 110 117 POLY-ALA.
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37; BAA25800.1; -
38; BAA25801.1; -
4; BAA25802.1; -
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AAA78790.1; -
A31400.

017; Hox9 act; 1.
024; HOMEOBOX.
031; HTHREPRESSR.
010; Hox9 act; 1.

1-binding; Developmental protein; Nuclear protein; 1-regulation; Alternative splicing.

06	271	/FTId=VSP_002382. Missing (in isoform HoxA-9T)
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1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 84

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AAAAA 102

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Rel. 26, Created)

protein Hox-A9 (Hox-1G).

tazoa; Chordata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominoidea;
Hominidae; Homo.

Sauvageau G., Largman C.;
C-1996) to the FWP/Corporation

1 N.A.
iharangh

IN-1997) to the EMBL/GenBank/DBJ databases

[4] SEQUENCE FROM N.A.

Strausberg R.L., Feingold E.A., Gro

J. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Piatichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Kahaha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy J.

Willalson D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanche

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N. Krzyżewski M. I Skalska H Smaluc D P

generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." ;

SEQUENCE OF 195-272 FROM N.A., AND CHROMOSOMAL TRANSLOCATION WIT.
JTP98

Corrow J., Sneedman A.M., Stanton V.P., Becher R., Collins T.,
Williams A.J., Dube I., Katz F., Kwong Y.L., Morris C.,

the genes for nucleoporin NUP98 and class I homeoprotein HOXA9." *Nat Genet* 12:159-167 (1996)

SEQUENCE OF 206-271 FROM N.A.
MEDLINE=90098876; PubMed=2574852;

The human HOX gene family.";
Nucleic Acids Res. 17:10385-10402 (1989)

a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis

chromosomal translocation t(7;11)(p15;p15) which involves HO1 and NUP98.

!- DATABASE: NAME=ACIAB Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chroncancer/Genes/HOXU

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MBL; U82759; AAB40867.1; -.
MBL; AF010258; AAD08713.1; -

MBL; BC006537; AAH06537.1; -
MBL; BC010023; AAH10023.1; -

SSP; P02833; 9ANT.
RANSEAC. T01709. -

5; P:development; TAS.
 001356; Homeobox.
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 000047; HTH lambrepres.
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 : Hox9 act; 1.
 24; HOMEBOX.
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 227; HOMEBOX 1; 1.
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 (el. 41, Last annotation update)
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 2;
 N.A.
 76; PubMed=9290207;
 ., Konopka J.B., Sternglanz R.;
 se-specific genes from *Saccharomyces cerevisiae*.";
 1042(1997).
 N.A.
 FY1679;
 75; PubMed=8948101;
 Kordes B., Pujol A., Jauniaux J.-C.;
 analysis of a 40.2 kb fragment of yeast chromosome X
 n reading frames including URA2 (5' end), TRK1, PBS2,
 RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes,
 delta elements and a Ty4 transposon.";
 1474(1996).
 Derepression of silent mating type loci when
 sed.
 : TO S.POMBE C1A1.
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 il to license@isb-sib.ch).

 AAC37512.1; -.

DR EMBL; Z49390; CAA89410.1; -.
 DR PIR; S30766; S30766.
 DR GerOnline; 141727; -.
 DR SGD; S0003651; ASF1.
 DR GO; GO:0005678; Chromatin assembly complex; IDA.
 DR GO; GO:0008630; P:DNA damage response, signal transduction re..
 DR InterPro; IPR006818; Anti-silence.
 DR Pfam; PF04729; Anti-silence; 1.
 FT DOMAIN 170 242 ASP/GLU-RICH (HIGHLY ACIDIC).
 SQ SEQUENCE 279 AA; 31603 MW; 186E76075C0B1644 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 279;
 Best local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 330 EEEEDDED 337
 Db 178 EEEEDDED 185
 RESULT 106
 CEBE RAT
 ID_CEBE RAT STANDARD; PRT; 281 AA.
 AC P56261;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE CCAAT/enhancer binding protein epsilon (C/EBP epsilon) (C/EBP-rel
 DE protein 1).
 GN CEBPE OR CRP1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98256268; PubMed=9593684;
 RA Williams S.C., Du Y., Schwartz R.C., Weiler S.R., Ortiz M.,
 RA Keller J.R., Johnson P.F.;
 RT "C/EBPepsilon is a myeloid-specific activator of cytokine, chemok
 RT and macrophage-colony-stimulating factor receptor genes.";
 RL J. Biol. Chem. 273:13493-13501(1998).
 RN [2]
 RP SEQUENCE OF 31-281 FROM N.A.
 RX MEDLINE=91357471; PubMed=1884998;
 RA Williams S.C., Cantwell C.A., Johnson P.F.;
 RT "A family of C/EBP-related proteins capable of forming covalently
 RT linked leucine zipper dimers in vitro.";
 RL Genes Dev. 5:1553-1567(1991).
 CC -!- FUNCTION: C/EBP ARE DNA-BINDING PROTEINS THAT RECOGNIZE TWO
 CC DIFFERENT MOTIFS: THE CCAAT HOMOLOGY COMMON TO MANY PROMOTERS
 CC THE ENHANCED CORE HOMOLOGY COMMON TO MANY ENHANCERS (BY
 CC SIMILARITY).
 CC -!- SUBUNIT: BINDS DNA AS A DIMER AND CAN FORM STABLE HETERODIMER;
 CC WITH C/EBP DELTA.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the bZIP family. C/EBP subfamily.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF034716; AAC24455.1; -.
 DR InterPro; IPR004827; TF_bZIP.
 DR Pfam; PF00170; bZIP; 1.
 DR SMART; SM00338; BRLZ; 1.
 DR PROSITE; PS50217; bZIP; 1.
 DR PROSITE; PS00036; bZIP_BASIC; Activator; DNA-binding; Nuclear protein.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein.

```
208 228 BASIC MOTIF.
239 267 LEUCINE-ZIPPER.
81 AA; 30589 MW; 68B16455C034E250 CRC64;

1.5%; Score 8; DB 1; Length 281;
larity 100.0%; Pred. No. 48;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAP 145
|||||
AAAAAP 178

STANDARD; PRT; 294 AA.
(Rel. 14, Created)
(Rel. 14, Last sequence update)
(Rel. 39, Last annotation update)
n (NPM) (Nucleolar phosphoprotein B23) (Numatrin)
rotein N038).

s (Chicken).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae;

031;
M N.A.
6792; PubMed=2320420;
Nigg E.A.;
ces of chicken nucleolin/C23 and N038/B23, two major
oteins."
s Res. 18:1286-1286(1990).

F SEQUENCE.
4215; PubMed=2114180;
Krek W.; Nigg E.A.;
nd developmental expression of chicken nucleolin and
nate expression of two abundant non-ribosomal nucleolin
phys. Acta 1049:126-133(1990).
: Associated with nucleolar ribonucleoprotein structures
single-stranded nucleic acids. It may function in the
and/or transport of ribosome.
LAR LOCATION: Nuclear. Generally nucleolar, but is
ated to the nucleoplasm in case of serum starvation or
t with anticancer drugs (By similarity).
PHY: Belongs to the nucleoplasm family.

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mail to license@isb-sib.ch).

-----
; CAA35061.1; --
; DNCHFW.
R004301; Nucleoplasm.
6; Nucleoplasm; 1.
ein; Phosphorylation; RNA-binding.
1 11 MET-RICH.
122 133 ASP/GLU-RICH (ACIDIC).
153 158 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
161 186 ASP/GLU-RICH (HIGHLY ACIDIC).
190 196 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
94 AA; 32632 MW; B1FF98B5F2322DED CRC64;

1.5%; Score 8; DB 1; Length 294;

Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 332 EDDDEDED 339
DB 164 EDDDEDED 171

RESULT 108
PP3D HUMAN
ID PP3D_HUMAN STANDARD; PRT; 299 AA.
AC 095685;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 1, regulatory subunit 3D (Protein phosphatase
DE regulatory subunit 6) (Protein phosphatase 1 binding subunit R6)
GN PP1R3D OR PP1R6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ASSOCIATION WITH GLYCOGEN, AND INTERACTION W
RP PP1CC.
RC TISSUE=Brain;
RX MEDLINE=98074939; PubMed=9414128;
RA Armstrong C.G., Browne G.J., Cohen P., Cohen P.T.W.;
RT "PP1R6, a novel member of the family of glycogen-targeting sub
of protein phosphatase 1.";
RL FEBS Lett. 418:210-214(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.I
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johns
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlc
Lehvesiaiho M.H., Laversha M.A., Lloyd C., Lloyd D.M., Lovell J
Marsh V.D., Martin S.D., McConnachie L.J., McKay K., McMurray A.
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe
Tracy A., Tromans A.C., Vaudin R., Wall M., Wallis J.M.,
Whithead S.L., Whitaker P., Willey D.L., Williams L., Williams
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 2
Nature 414:865-871(2001).
RT
RL
CC -!- FUNCTION: Protein phosphatase 1 regulatory subunit is consid
CC as a glycogen-targeting subunit. PP1 is essential for cell
CC division, and participates in the regulation of glycogen
CC metabolism, muscle contractility and protein synthesis.
CC -!- SUBUNIT: Interacts with PP1CC catalytic subunit of PP1, and
CC associates with glycogen.
CC -!- TISSUE SPECIFICITY: Expressed in all tissue tested. High
CC expression in skeletal muscle and heart.
CC -!- DOMAIN: CBM 21 domain is known to be involved in the localiz
CC to glycogen and is characteristic of some regulatory subunit
CC phosphatase complexes.
CC -!- SIMILARITY: Contains 1 CBM_21 domain.
```

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CAA77081.1; -;
9; CAB92096.1; -;
294; PPI1R3D.
3; P:protein phosphatase type 1 activity; TAS.
05036; CBM_21.
; CBM_21; 1.
/cogen metabolism.
59 278 CBM_21.
01 104 PPI-BINDING MOTIF.
9 AA; 32559 MW; D8848FB1CF55E49B CRC64;
1.5%; Score 8; DB 1; Length 299;
arity 100.0%; Pred. No. 51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
CPAP 133
|||||
CPAP 57
STANDARD; PRT; 303 AA.
rel. 11, Created)
rel. 27, Last sequence update)
rel. 43, Last annotation update)
protein (EC 3.2.2.22) (Opaque-6 protein) (rRNA N-
e).
idiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae;
Panicoideae; Andropogoneae; Zea.
7;
N.A.
87; PubMed=2102870;
azzaroni N., Marsan P.A., Aragay A., Thompson R.,
i Ronzo N., Palau J., Motto M.;
ain from maize endosperm: characterization of genomic
ding two alternative central domains.";
1. 14:1031-1040(1990).
N.A.
xm;
99; PubMed=3419419;
artings H., Brembilla M., Motto M., Soave C.,
lau J., Rhode W., Salamini F.;
ein from maize endosperm, an albumin regulated by the
eic acid (cDNA) and amino acid sequences.";
t. 212:481-487(1988).
A possible regulatory factor for the synthesis of zeins,
group of storage proteins.
Activity: Endohydrolysis of the N-glycosidic bond at one
denosine on the 28S rRNA.
monomer.
R LOCATION: Cytoplasmic.
CIFICITY: Endosperm.
; Belongs to the ribosome-inactivating protein family.
subfamily.
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EMBL; X54212; CAA38124.1; -;
EMBL; X07987; CAA30797.1; -;
PIR; S03172; S03172.
MaizeDB; 30000; -;
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PRO0396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin.
FT DOMAIN 182 188 POLY-ALA.
FT DOMAIN 286 294 POLY-ALA.
FT CONFLICT 269 269 D -> N (IN REF. 2).
SQ SEQUENCE 303 AA; 32428 MW; 24003521CE91790 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 303;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 151 AAAAAATA 158
|||||
Db 286 AAAAAATA 293
RESULT 110
RIP9 MAIZE
ID RIP9 MAIZE STANDARD; PRT; 304 AA.
AC P25892;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ribosome-inactivating protein 9 (EC 3.2.2.22) (rRNA N-glycosidase
DE (B-32 protein).
GN CRIP9.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 282-301.
STRAIN=cv. W64A;
MEDLINE=92338851; PubMed=1633495;
RA Bass H.W., Webster C., Obrian G.R., Roberts J.K.M., Boston R.S.;
RT "A maize ribosome-inactivating protein is controlled by the
transcriptional activator Opaque-2.";
RL Plant Cell 4:225-234(1992).
CC -!- FUNCTION: Possesses features of some constitutive defense age;
CC The coordinate Opaque-2-controlled synthesis of this protein;
CC the major seed storage proteins (zeins) may provide the
CC germinating seedling with both nutritional benefits and prote
CC against pathogen invasion of the surrounding endosperm.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond a
CC specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Accumulates to high levels in seeds.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein fami
CC Type 1 RIP subfamily.
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CC / AAA33454.1; -.
CC 00; -.
CC 2001574; RIP.
CC 1; RIP; 1.
CC 396; SHIGARICIN.
CC 2275; SHIGA-RICIN; 1.
CC 2; Protein synthesis inhibitor; Hydrolase; Toxin;
CC nily.
CC 208 208 BY SIMILARITY.
CC 183 189 POLY-ALA.
CC 287 295 POLY-ALA.
CC 04 AA; 33514 MW; 978789A2DD2BBF3C CRC64;
CC 1.5%; Score 8; DB 1; Length 304;
CC iarity 100.0%; Pred. No. 51;
CC Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC AATA 158
CC |||||
CC AATA 294
CC
CC STANDARD; PRT; 311 AA.
CC (Rel. 32, Created)
CC (Rel. 32, Last sequence update)
CC (Rel. 42, Last annotation update)
CC :ein CDX-2 (Caudal-type homeobox protein 2).
CC ;.
CC (Mouse).
CC :stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC :heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC 0090;
CC 4 N.A.
CC ;.
CC 0086; PubMed=7910823;
CC :xler T., Kazenwadel J.;
CC : the murine homeobox gene cdx-2. Expression in embryonic
CC :estinal epithelium."
CC a. 269:15229-15237(1994).
CC 4 N.A.
CC intestine;
CC 0263; PubMed=7935448;
CC L., Taylor J., Traber P.G.;
CC in protein related to caudal regulates intestine-specific
CC :ption."
CC ol. 14:7340-7351(1994).
CC 04-229 FROM N.A.
CC 0633; PubMed=1671571;
CC :azenwadel J.;
CC re expression in the intestinal epithelium of adult
CC a. 266:3246-3251(1991).
CC (ON OF SER-60.
CC 0654; PubMed=11729123;
CC :oudreau F., Taylor J.K., Moffett J., Suh E.R.,
CC :ion of the serine 60 residue within the Cdx2 activation
CC :es its transactivation capacity."
CC logy 121:1437-1450(2001).
CC : Involved in the transcriptional regulation of multiple
CC :pressed in the intestinal epithelium. Important in broad
CC :functions from early differentiation to maintenance of
CC :stinal epithelial lining of both the small and large
CC :a.
CC :AR LOCATION: Nuclear.

```

```

CC -!- TISSUE SPECIFICITY: Intestine; expressed specifically in gut
CC epithelium where it is not restricted to a particular cell
CC lineage. Abundant expression is seen in the proximal colon w
CC slightly lower levels in distal colon. Expression in the pro
CC colon is not restricted either to a particular cell lineage
CC stage of differentiation while in the distal colon it is mor
CC abundant in the differentiated cells towards the top of the
CC -!- PTM: Phosphorylation of Ser-60 mediates the transactivation
CC capacity.
CC -!- SIMILARITY: Belongs to the Caudal homeobox family.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC
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CC
CC EMBL; U00454; AAA19645.1; -.
CC EMBL; S74520; AAB32251.1; -.
CC PIR; A53808; A53808.
CC HSP; P02835; 1FTZ.
CC TRANSFAC; T02002; -.
CC MGD; MGI:88361; Cdx2.
CC GO; GO:0007389; P:pattern specification; IMP.
CC InterPro; IPR006820; Caudal act.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR000047; HTH_lambrepresr.
CC Pfam; PF04731; Caudal_act; 1.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESSR.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC KW Transcription regulation; Activator; Developmental protein; Home
CC DNA-binding; Nuclear protein; Phosphorylation.
CC FT DNA_BIND 185 244 HOMEBOX.
CC FT DOMAIN 46 53 POLY-ALA.
CC FT DOMAIN 85 92 POLY-ALA.
CC FT DOMAIN 247 257 POLY-GLN.
CC FT MOD_RES 60 60 PHOSPHORYLATION.
CC FT CONFLICT 69 69 Y -> H (IN REF. 2).
CC SQ SEQUENCE 311 AA; 33476 MW; 71FFC4C263462FF3 CRC64;
CC
CC Query Match 1.5%; Score 8; DB 1; Length 311;
CC Best Local Similarity 100.0%; Pred. No. 52;
CC Matches 8; Conservative 0; Mismatches 0; Indels 0;
CC
CC QY 151 AAAAAATA 158
CC DB |||||
CC 46 AAAAAATA 53
CC
CC RESULT 112
CC HEM3_PSEPK
CC ID HEM3_PSEPK STANDARD; PRT; 313 AA.
CC AC Q88RE5;
CC DT 15-MAR-2004 (Rel. 43, Created)
CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC DE Porphobilinogen deaminase (EC 2.5.1.61) (PBG) (Hydroxymethylbila
CC synthase) (HMS) (Pre-uroporphyrinogen synthase).
CC GN HEMC OR PPO186.
CC OS Pseudomonas putida (strain KT2440).
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC OC Pseudomonadaceae; Pseudomonas.
CC OX NCBI_TaxID=160488;
CC RN [1]
CC RP SEQUENCE FROM N.A.

```


262 262 A -> T (IN REF. 1 AND 2).
 17 AA; 34186 MW; 8C85F4CB2B35EACA CRC64;
 1.5%; Score 8; DB 1; Length 317;
 larity 100.0%; Pred. No. 53;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ATAA 20
 |||||
 ATAA 288
 |||||
 STANDARD; PRT; 320 AA.
 (Rel. 34, Created)
 (Rel. 34, Last sequence update)
 (Rel. 42, Last annotation update)
 line (TTP) (TIS11A protein) (TIS11) (Zinc finger protein
 11A.
 ficus (Rat).
 stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 0116;
 X N.A.
 0517; PubMed=1511903;
 shima M., Chung S.Y., Guroff G.;
 a rat TIS11 cDNA, an immediate early gene induced by
 rs and phorbol esters";
 -291(1992).
 : PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
 E INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.
 EXPERIMENTALLY SHOWN TO BE ABLE TO BIND ZINC.
 LAR LOCATION: Nuclear.
 IV: Contains 2 C3H1-type zinc fingers.
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 ; CAA44970.1; -;
 JC1255.
 R000571; Znf CCCH.
 2; Zf-CCCH; 2.
 56; Znf_C3H1; 2.
 sin; Repeat; Metal-binding; Zinc-finger; DNA-binding;
 ion.
 64 68 P-P-P-P-G.
 191 195 P-P-P-P-G.
 212 216 P-P-P-P-G.
 102 121 C3H1-TYPE 1.
 140 159 C3H1-TYPE 2.
 221 221 PHOSPHORYLATION (BY MAPK) (BY
 SIMILARITY).
 20 AA; 33653 MW; CFC597F3C7B5CA76 CRC64;
 1.5%; Score 8; DB 1; Length 320;
 larity 100.0%; Pred. No. 54;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PPAPP 221
 |||||
 PPAPP 307

KHSE_XANCP
 ID KHSE_XANCP STANDARD; PRT; 322 AA.
 AC Q8P9Q0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homoserine kinase (EC 2.7.1.39) (HK).
 GN THRB OR XCC1801.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1].
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.F.
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyana A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with dif
 host specificities";
 RL Nature 417:459-463(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + L-homoserine = ADP + O-phospho-L-
 homoserine
 CC -!- PATHWAY: Threonine biosynthesis from aspartate; fourth step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- SIMILARITY: Belongs to the GHMP kinase family. Homoserine ki
 subfamily.
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL ou
 the European Bioinformatics Institute. There are no restrictio
 use by non-profit institutions as long as its content is i
 modified and this statement is not removed. Usage by and for
 entities requires a license agreement (See <http://www.isb-sib.ch>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE012282; AAM41090.1; -;
 DR HAMAP; MF_00384; -; 1.
 DR InterPro; IPR006204; GHMP_kinase.
 DR InterPro; IPR006203; GHMP_kinase ATP.
 DR InterPro; IPR000870; Homoser_Kin.
 DR Pfam; PF00288; GHMP_kinases_1.
 DR PRINTS; PR00958; HOMSERKINASE.
 DR PROSITE; PS00627; GHMP_KINASES ATP; FALSE NEG.
 KW Threonine biosynthesis; Transferase; Kinase; ATP-binding;
 FT Complete proteome.
 FT NP BIND 106 116 ATP (POTENTIAL).
 SQ SEQUENCE 322 AA; 32924 MW; C3F64B273D3CC70F CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 120 AAAAAAAP 127
 |||||
 DB 286 AAAAAAAP 293
 |||||

RESULT 116
 OLG2_HUMAN

STANDARD; PRT; 323 AA.
 1; rel. 39, Created)
 2; rel. 41, Last sequence update)
 3; rel. 43, Last annotation update)
 4; re transcription factor 2 (Basic helix-loop-helix protein
 5; corein kinase C-binding protein RACK17) (Protein kinase C
 6; in 2).
 7; 31 OR PRKCBP2 OR RACK17.
 8; (Human).
 9; azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 10; eria; Primates; Catarrhini; Hominoidea; Homo.
 11; 06;
 12; N.A.
 13; ampus;
 14; unaga C., Kiyohara Y., Konishi H., Kikkawa U.;
 15; se C-binding protein.";
 16; 3-1996) to the EMBL/GenBank/DBJ databases.
 17; N.A.
 18; 564; PubMed=10737801;
 19; -Sait S.N., Escalon E.A., Carroll A.J., de Jong P.J.,
 20; Aplan P.D.;
 21; (q11.2;q22) chromosomal translocation associated with
 22; lymphoblastic leukemia activates the BHLHB1 gene.";
 23; ad. Sci. U.S.A. 97:3497-3502(2000).
 24; Required for oligodendrocyte and motor neuron
 25; ion in the spinal cord (By similarity).
 26; AR LOCATION: Nuclear (Potential).
 27; Involved in a form of T-cell acute lymphoblastic leukemia
 28; through a chromosomal translocation t(14;21)(q11.2;q22)
 29; olves OLIG2 and T-cell receptor alpha chain (TCRA) genes.
 30; t: Contains 1 basic helix-loop-helix (bHLH) domain.
 31; -----
 32; DT entry is copyright. It is produced through a collaboration
 33; Swiss Institute of Bioinformatics and the EMBL outstation -
 34; Bioinformatics Institute. There are no restrictions on its
 35; profit institutions as long as its content is in no way
 36; this statement is not removed. Usage by and for commercial
 37; res a license agreement (See <http://www.isb-sib.ch/announce/>
 38; ail to license@isb-sib.ch).
 39; -----
 40; AAC72247.1; ALT INIT.
 41;); AAF61215.1; ALT_INIT.
 42;); 98; OLIG2.
 43; -----
 44; 001092; HLH_basic.
 45;); HLH; 1.
 46;); HLH; 1.
 47;); 88; HLH; 1.
 48;); regulation; DNA-binding; Nuclear protein;
 49;); Chromosomal translocation.
 50; 9 120 BASIC DOMAIN.
 51; 1 162 HELIX-LOOP-HELIX MOTIF.
 52; 7 88 POLY-SER.
 53; 6 212 POLY-ALA.
 54; 5 237 POLY-ALA.
 55; 6 270 POLY-ALA.
 56; 3 280 POLY-GLY.
 57; 1 AA; 32384 MW; OEC9223961062509 CRC64;
 58; 1.5%; Score 8; DB 1; Length 323;
 59; 100.0%; Pred. No. 54;
 60; 0; Mismatches 0; Indels 0; Gaps 0;
 61; UAAA 126
 62; |||
 63; UAAA 231

ID AC O9E06; O9JKN4; PRT; 323 AA.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Oligodendrocyte transcription factor 2.
 GN OLIG2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=20544962; PubMed=11091082;
 RA Takebayashi H., Yoshida S., Sugimori M., Kosako H., Kominami R.,
 RA Nakafuku M., Nabeshima Y.;
 RT "Dynamic expression of basic helix-loop-helix Olig family members
 RT implication of Olig2 in neuron and oligodendrocyte differentiatio
 RT identification of a new member, Olig3.";
 RL Mech. Dev. 99:143-148(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20182808; PubMed=10719889;
 RX Zhou Q., Wang S., Anderson D.J.;
 RA "Identification of a novel family of oligodendrocyte lineage-spec
 RA basic helix-loop-helix transcription factors.";
 RL Neuron 25:331-343(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388237; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
 RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez
 RA Blakesley R.W., Touchman J.W., Green E.D., Shvchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Required for oligodendrocyte and motor neuron
 CC specification in the spinal cord.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: Specifically expressed in zones of
 CC neuroepithelium from which oligodendrocyte precursors emerge,
 CC well as in the precursors themselves.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB038697; BAB18907.1; -
 CC EMBL; AF232929; AAF61722.1; -
 CC EMBL; BC051967; AAF51967.1; -
 CC MGD; MGI:1355331; Olig2.
 CC GO; GO:0042055; P:neuroglial lineage restriction; IMP.

3001092; HLH_basic.
 3; HLH; 1.
 388; HLH; 1.
 a regulation; DNA-binding; Nuclear protein.
 109 120 BASIC DOMAIN.
 121 162 HELIX-LOOP-HELIX MOTIF.
 77 88 POLY-SER.
 206 212 POLY-ALA.
 225 237 POLY-ALA.
 266 270 POLY-ALA.
 273 284 POLY-GLY.
 198 198 L -> I (IN REF. 2).
 205 205 P -> PRHGAP (IN REF. 2).
 23 AA; 32406 MW; 598AE76CB512D716 CRC64;
 1.5%; Score 8; DB 1; Length 323;
 larity 100.0%; Pred. No. 54;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAA 126
 |||||
 AAAAA 231
 STANDARD; PRT; 335 AA.
 (Rel. 29, Created)
 (Rel. 36, Last sequence update)
 (Rel. 42, Last annotation update)
 :ein Hox-D13 (Hox-41).
 (41.
 (Human).
 :tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 :heria; Primates; Catarrhini; Hominidae; Homo.
 106;
 1 N.A.
 1671; PubMed=8614804;
 Mundlos S., Upton J., Olsen B.R.;
 th and branching patterns in synpolydactyly caused by
 HOXD13.";
 48-551(1996).
 [N.A.
 K., Kita K., Miwa H., Kamada N., Ohki M.;
 g31;p15) translocation in acute myeloid leukemia fuses
 'rin gene to HOXD13 homeobox gene.";
 (P-1999) to the EMBL/GenBank/DBJ databases.
 68-333 FROM N.A.
 849; PubMed=1675198;
 , Morelli F., Acampora D., Migliaccio E., Simeone A.,
 a homeobox gene homologous to the even-skipped
 gene, is localized at the 5' end of HOX4 locus on
 ";
 3-50(1991).
 LA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-49 INS.
 300; PubMed=8817328;
 Stojlov I., Yilmaz E., Sayli B.S., Sarfarazi M.;
 ctur of HOXD13 gene; a nine polyalanine duplication
 ydactyly in two unrelated families.";
 et. 5:945-952(1996).
 CYS-308 AND LEU-314, AND VARIANT BDD CYS-308.
 987; PubMed=12649808;
 an S.H., Oldridge M., Trembath R.C., Roche P.,
 Giele H., Wilkie A.O.;
 ations in the homeodomain of HOXD13 are associated with

brachydactyly types D and E.";
 Am. J. Hum. Genet. 72:984-997(2003).
 -!- FUNCTION: Sequence-specific transcription factor which is pa
 a developmental regulatory system that provides cells with
 specific positional identities on the anterior-posterior axi
 -!- SUBCELLULAR LOCATION: Nuclear.
 -!- DISEASE: Defects in HOXD13 are the cause of synpolydactyly ([MIM:186000]; also known as syndactyly type II. SPD is a lim malformation that shows a characteristic manifestation in bo hands and feet. This condition is inherited as an autosomal dominant trait with reduced penetrance.
 -!- DISEASE: Defects in HOXD13 are the cause of brachydactyly ty (BDD) [MIM:113200]. BDD is characterized by short and broad terminal phalanges of the thumbs and big toes. Inheritance i autosomal dominant.
 -!- DISEASE: Defects in HOXD13 are the cause of brachydactyly ty (BDE) [MIM:113300]. BDE is characterized by shortening of th fingers mainly in the metacarpals and metatarsals. Inheritan autosomal dominant.
 -!- SIMILARITY: Belongs to the Abd-B homeobox family.
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 EMBL; AF005220; AAC51635.1; -
 EMBL; AF005219; AAC51635.1; JOINED.
 EMBL; AB032481; BAA95352.1; -
 PIR; B39065; B39065.
 HSP; P14653; 1B72.
 TRANSFAC; T03335; -
 Genew; HGNC:5136; HOXD13.
 MIM; 142989; -
 MIM; 113200; -
 MIM; 113300; -
 MIM; 186000; -
 GO; GO:0003677; P:DNA binding; TAS.
 GO; GO:0007275; P:development; TAS.
 GO; GO:0006355; P:regulation of transcription, DNA-dependent; TA
 GO; GO:0001501; P:skeletal development; TAS.
 GO; GO:0006366; P:transcription from Pol II promoter; TAS.
 InterPro; IPR001356; Homeobox.
 Pfam; PF00046; homeobox; 1.
 ProDom; PD000010; Homeobox; 1.
 SMART; SM00389; HOX; 1.
 PROSITE; PS00027; HOMEBOX_1; 1.
 PROSITE; PS50071; HOMEBOX_2; 1.
 Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 Transcription regulation; Disease mutation.
 FT DOMAIN 17 22 POLY-SER.
 FT DOMAIN 24 28 POLY-ALA.
 FT DOMAIN 49 63 POLY-ALA.
 FT DOMAIN 77 84 POLY-SER.
 FT DOMAIN 105 110 POLY-ALA.
 FT DNA_BIND 268 327 HOMEBOX.
 FT VARIANT 49 49 A -> AAAAAAAAAA (in SPD).
 FT /FTID=VAR_003818.
 FT S -> C (in BDE and BDD).
 FT /FTID=VAR_015952.
 FT I -> L (in BDE).
 FT /FTID=VAR_015953.
 SQ SEQUENCE 335 AA; 35210 MW; 0558D7B29F9B6E3E CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 121 AAAAAAPP 128
 |||||

AAPP 112

STANDARD; PRT; 337 AA.

5; Rel. 30, Created)

Rel. 30, Last sequence update)

Rel. 43, Last annotation update)

gamma receptor beta chain precursor (Interferon-gamma

transducer-1) (AF-1) (Interferon-gamma transducer-1).

371.

(Human).

tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

heria; Primates; Catarrhini; Hominidae; Homo.

06;

N.A.

ibroblast;

380; PubMed=8124716;

lly R.J., Kosenko S., Mariano T.M., Cook J.R.,

uel S.L., Schwartz B., Miki T., Pestka S.;

on and sequence of an accessory factor required for

the human interferon gamma receptor.";

02(1994).

N.A.

257; PubMed=12477932;

L., Feingold E.A., Grouse L.H., Derge J.G.,

Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Zeeberg H., Moore T., Max S.I., Wang J., Hsieh F.,

Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Quellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,

Cowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

Adan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Touchman J.W., Green E.D., Dickson M.C.,

Grimwood J., Schmutz J., Myers R.M.,

S.N., Krzywinski M.I., Skalska U., Smalley D.E.,

Schein J.E., Jones S.J.M., Marra M.A.;

nd initial analysis of more than 15,000 full-length

se cDNA sequences.";

cad. Sci. U.S.A. 99:16899-16903 (2002).

-24 FROM N.A.

142; PubMed=8910544;

asperger C., Dembic Z., Pestka S.;

e of the gene for the second chain of the human

gamma receptor.";

. 271:28947-28952(1996).

Part of the receptor for interferon gamma. Required for

anaduction. This accessory factor is an integral part of

gamma signal transduction pathway and is likely to

with GAF, JAK1, and/or JAK2.

AR LOCARION: Type I membrane protein.

Y: Belongs to the type II cytokine family of receptors.

Y: Contains 2 fibronectin type III domains.

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DR EMBL; U05875; AAA16955.1; -.
 DR EMBL; U05877; AAA16956.1; -.
 DR EMBL; BC003624; AAH03624.1; -.
 DR EMBL; U68755; AAC52066.1; -.
 DR PIR; I38500; I38500.
 DR Genew; HGNC:5440; IFNGR2.
 DR MIN; 147569; -.
 DR MIN; 209950; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0003800; F:antiviral response protein activity; TAS.
 DR GO; GO:0004906; F:interferon-gamma receptor activity; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu.
 DR GO; GO:0009619; P:resistance to pathogenic bacteria; TAS.
 DR GO; GO:0009615; P:response to viruses; TAS.
 DR InterPro; IPR000282; Cytok receptor_2.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN_III.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 SIGNAL 1 27
 CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN
 DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 248 268
 DOMAIN 269 337 POTENTIAL.
 CARBOHYD 56 56 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 231 231 N-LINKED (GLCNAC. .) (POTENTIAL).
 VARIANT 64 64 R -> Q.
 SQ SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64; /FTID=VAR_002718.

Query March 1.5%; Score 8; DB 1; Length 337;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; C

Qy 121 AAAAAAPP 128
 Db 17 AAAAAAPP 24

RESULT 120
 LIMA_PSEAE
 ID LIMA_PSEAE STANDARD; PRT; 340 AA.
 AC Q01725; P95420; Q04591;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lipase modulator (lipase helper protein).
 GN LIPIB OR LIPIB OR PA2863.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TE3285;
 RX MEDLINE=92337414; PubMed=1632642;
 RA Chihara-Siomi M., Yoshikawa K., Oshima-Hirayama N., Yamamoto K.,
 RA Sogabe Y., Nakatani T., Nishioka T., Oda J.;
 RT "Purification, molecular cloning, and expression of lipase from
 Pseudomonas aeruginosa".
 RT Arch. Biochem. Biophys. 296:505-513 (1992).
 RL [2]
 RP REVISIONS.
 RC STRAIN=TE3285;
 RA Shibata H.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A.

31156; 7519; PubMed=982856;
Hirano A., Aisaka K.;
ns of Ser for Asn-163, and Pro for Leu-264 are important
ation of lipase from *Pseudomonas aeruginosa*.";
120:915-921(1996).
M N.A.
15692 / PA01;
1478; PubMed=1512563;
Hoesche C., Strunk C., Winkler U.K.;
enetics of the extracellular lipase of *Pseudomonas*
AO1.";
obol. 138:1325-1335(1992).
; AY-1994) to the EMBL/GenBank/DBJ databases.
M N.A.
15692 / PA01;
7337; PubMed=10984043;
Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Coulter S.M., Folger K.R., Kas A., Larbig K., Lim R.M.,
Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
aier M.H., Hancock R.E.W., Lory S., Olson M.V.;
name sequence of *Pseudomonas aeruginosa* PA01, an
c pathogen.";
59-964(2000).
; SEEMS TO BE ACTING IN THE FOLDING OF THE EXTRACELLULAR
URING ITS PASSAGE THROUGH THE PERIPLASM (BY SIMILARITY).
LAR LOCATION: Inner membrane-anchored (By similarity).
TY: Belongs to the lipase chaperone family.
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mail to license@isb-sib.ch).
52; BAA23129.1; -;
; BAA09136.1; -;
; CAA44998.1; ALT INIT.
12; AAG06251.1; ALT_INIT.
S25769.
R004961; Lipase chap.
0; Lipase chap. 1.
ation; Chaperone; Transmembrane; Periplasmic;
ne; Complete proteome.
4 24 POTENTIAL.
210 210 A -> T (IN STRAINS TE3285 AND ATCC
31156).
301 301 T -> A (IN STRAINS TE3285 AND ATCC
31156).
41 42 DR -> VH (IN REF. 6).
40 AA; 37686 MW; 55217FCDF8F8FC251 CRC64;
1.5%; Score 8; DB 1; Length 340;
larity 100.0%; Pred. No. 56;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PAASA 312
|||||
PAASA 49
STANDARD; PRT; 341 AA.

AC QJUKP5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Muscblind-like protein (Triplet-expansion RNA-binding protein)
GN MEN1L OR MEN1 OR EXP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Castagnola P., Monticone M., Borsani G., Bassi M.T., Tonachini I
RT "cDNA cloning of mouse muscblind.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Binds to CUG triplet repeat expansion dsRNA (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 4 C3H1-type zinc fingers.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL ou
CC the European Bioinformatics Institute. There are no restrictio
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF231110; AAF72159.1; -;
CC MGD; MGI:1928482; Mbn1l.
CC GO; GO:0005737; Cytoplasm; ISS.
CC GO; GO:0005634; Cnucleus; ISS.
CC GO; GO:0003725; P:double-stranded RNA binding; ISS.
CC GO; GO:0001701; P:embryonic development (sensu Mammalia); IEP.
CC GO; GO:0030326; P:limb morphogenesis; IEP.
CC GO; GO:0007517; P:muscle development; IEP.
CC GO; GO:0045445; P:myoblast differentiation; IDA.
CC GO; GO:0007399; P:neurogenesis; IEP.
CC InterPro; IPR000571; Znf_CCHC.
CC DR SMART; SM00356; Znf_C3H1; 4.
CC Zinc-finger; Repeat; Nuclear protein; RNA-binding.
FT ZN_FING 14 40 C3H1-TYPE 1.
FT ZN_FING 47 72 C3H1-TYPE 2.
FT ZN_FING 178 205 C3H1-TYPE 3.
FT ZN_FING 215 239 C3H1-TYPE 4.
SQ SEQUENCE 341 AA; 36975 MW; 8E008B5C7EF8AB9 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 341;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 119 PAAAAAAA 126
Db 165 PAAAAAAA 172
|||||
RESULT 122
RLA0 METAC STANDARD; PRT; 347 AA.
AC Q8TI80;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acidic ribosomal protein P0 homolog (L10E).
GN RPLP0 OR MA4276.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;

```

760; PubMed=11932238;
Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
Lor J., Stange-Thomann N., DeArellano K., Johnson R.,
Ewan P., McKernan K., Talamas J., Tirrell A., Ye W.,
Rober R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Unayam L.A., White O., White R.H., de Macario E.C.,
Farrell K.F., Jing H., Macario A.J.L., Paulsen I.,
Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Birren B.,
of Methanosaeta acetivorans reveals extensive metabolic
ical diversity;
2:532-542(2002).
Ribosomal protein P0 is the functional equivalent of
rotein L10.
Y: Belongs to the L10P family of ribosomal proteins.
-----
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B; AAM07620.1; -.
80; -.
001813; Ribosomal 60S.
001790; Ribosomal L10.
; 60S ribosomal; 1.
; Ribosomal L10; 1.
tein; Complete proteome.
7 AA; 37167 MW; 359EBEDB28821F CRC64;
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1.5%; Score 8; DB 1; Length 347;
arity 100.0%; Pred. No. 57;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AASP 127
|||||
AASP 315
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STANDARD; PRT; 353 AA.
rel. 41, Created)
rel. 41, Last sequence update)
rel. 42, Last annotation update)
sin Nkx-2.4 (Homeobox protein NKX2.4) (Homeobox protein
2D.
2D.
(Human).
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
);
N.A.
749; PubMed=11780052;
Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Arides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
clow K.F., Bates K.N., Beard L.M., Beare D.M.,
Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
ill W.D., Butler A.P., Carder C., Carter N.P.,
Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
ley V.E., Collier R.E., Connor R.E., Corby N.R.,
ville G.J., Deadman R., Dhani P.D., Dunn M.,
., Frankland J.A., Fraser A., French L., Garner P.,
Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
riley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

```

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RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johns
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlo
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whithead S.L., Whittaker P., Willey D.L., Williams L., Williams
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 2(
RL Nature 414:865-871(2001).
RN (2)
RP SEQUENCE OF 1-289 FROM N.A.
RX MEDLINE=20279852; PubMed=10818213;
RA Wang C.-C., Brodnicki T., Copeland N.G., Jenkins N.A., Harvey R.I
RT "Conserved linkage of NK-2 homeobox gene pairs Nkx2-2/2-4 and
RT Nkx2-1/2-9 in mammals."
RL Mamm. Genome 11:466-468(2000).
CC -!- FUNCTION: Probable transcription factor.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the NK-2 homeobox family.
CC -!- SIMILARITY: Contains 1 homeobox domain.
-----
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or send an email to license@isb-sib.ch).
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EMBL; AL158013; -. NOT ANNOTATED_CDS.
EMBL; AF202037; AAG35617.1; -.
HSSP; P23441; 1FTT.
Genew; HGNC:7837; NKX2-4.
MIM; 607808;
InterPro; IPR001356; Homeobox.
Pfam; PF00046; Homeobox; 1.
PRINTS; PR00024; HOMEBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEBOX_1; 1.
PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein; Developmental protein.
FT DNA_BIND 189 248 HOMEBOX.
FT DOMAIN 44 47 POLY-ALA.
FT DOMAIN 76 91 POLY-ALA.
FT DOMAIN 181 187 POLY-ALA.
FT DOMAIN 264 272 POLY-PRO.
SQ SEQUENCE 353 AA; 36011 MW; B6780C4E4020BED6 CRC64;
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Query Match 1.5%; Score 8; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 120 AAAAAAAP 127
Db 181 AAAAAAAP 188
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RESULT 124
ID ATH1 HUMAN STANDARD; PRT; 354 AA.
AC Q92858;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Atonal protein homolog 1 (Helix-loop-helix protein hATH-1).

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1. (Human).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Theria; Primates; Catarrhini; Hominidae; Homo.
 606;
 M N.A.
 6280; PubMed=8872459;
 McCall A.E., Berkman S., Eichele G., Bellen H.J.,
 Y conservation of sequence and expression of the bHLH
 al suggests a conserved role in neurogenesis.";
 net. 5:1207-1216(1996).
 : Activates E box-dependent transcription in collaboration
 , but the activity is completely antagonized by the
 regulator of neurogenesis HES1. May play a role in the
 ciation of subsets of neural cells by activating E box-
 t transcription (By similarity).
 Efficient DNA binding requires dimerization with another
 tein.
 LAR LOCATION: Nuclear (Probable).
 IV: Contains 1 basic helix-loop-helix (bHLH) domain.
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 mail to license@isb-sib.ch).
 : AAB41305.1; -
 : 544; -
 : 197; ATOHI.
 0; P:transcription factor activity; TAS.
 7; P:central nervous system development; TAS.
 6; P:transcription from Pol II promoter; TAS.
 001092; HLH_basic.
); HLH; 1.
 3; HLH; 1.
 888; HLH; 1.
 29 38 POLY-PRO
 60 171 BASIC DOMAIN
 72 222 HELIX-LOOP-HELIX MOTIF.
 24 228 POLY-PRO.
 4 AA; 38160 MW; AB12F1E917A00A8D CRC64;
 1.5%; Score 8; DB 1; Length 354;
 arity 100.0%; Pred. No. 58;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 'QPPA 219
 '|||
 'QPPA 39
 STANDARD; PRT; 354 AA.
 0; Q26466; Q99141; Q9TYF5; Q9W3S6;
 Rel. 16, Created)
 Rel. 16, Last sequence update)
 Rel. 42, Last annotation update)
 otein.
 CG33070/CG18350.
 lanogaster (Fruit fly).
 tazo; Arthropoda; Hexapoda; Insecta; Pterygota;
 opterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 27;

RP SEQUENCE FROM N.A. (ISOFORMS MS3 AND CML), FUNCTION, AND DEVELOP
 RP STAGE.
 RC STRAIN=Oregon-R;
 RX MEDLINE=89077532; PubMed=3144435;
 RA Bell L.R., Maine E.M., Schedl P., Cline T.W.;
 RT "Sex-lethal, a Drosophila sex determination switch gene, exhibit
 RT specific RNA splicing and sequence similarity to RNA binding
 RT proteins.";
 RL Cell 55:1037-1046(1988).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS MS3; MS11 AND MS16), FUNCTION, AND
 RP DEVELOPMENTAL STAGE.
 RC TISSUE=Embryo;
 RX MEDLINE=91260708; PubMed=1710769;
 RA Samuels M.E., Schedl P., Cline T.W.;
 RT "The complex set of late transcripts from the Drosophila sex
 RT determination gene sex-lethal encodes multiple related
 RT polypeptides.";
 RL Mol. Cell. Biol. 11:3584-3602(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Berkelley;
 RC MEDLINE=20196006; PubMed=10731132;
 RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandr
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Fabios B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischma
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hosdin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [4]
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
 RA Hradecky P., Huang Y., Kaminker J.S., Bayraktaroglu L., Berman B
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";

3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [N.A. (ISOFORM MS16).
 ey; TISSUE=Embryo;
 Brokstein P., Hong L., Agbayani A., Carlson J.W.,
 avez C., Dorsett V., Drensek D., Farfan D., Friese E.,
 Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
 ungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
 uanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
 B-2003) to the EMBL/GenBank/DBJ databases.
 -26 FROM N.A. (ISOFORM 1), AND FUNCTION.
 272; PubMed=1547493;
 line T.W., Schedl P.;
 sex determination signal of Drosophila acts at the level
 ion.";
 43(1992).
 -41 FROM N.A. (ISOFORM FEMALE-SPECIFIC).
 600; PubMed=8978052;
 ., Sakamoto H., Navarro-Sabate A., Sakashita E.,
 Segarra C., Sanchez L.;
 f the gene Sex-lethal: a comparative analysis of
 lanogaster and Drosophila subobscura.";
 1653-1664(1996).
 ION.
 158; PubMed=1454517;
 Inoue K., Higuchi I., Ono Y., Shimura Y.;
 roso-phila Sex-lethal pre-mRNA splicing by its own female-
 act.";
 Res. 20:5533-5540(1992).
 NMR OF 199-294.
 815; PubMed=7524663;
 ar R., Rio D.C., Wenner D.E.;
 signments and solution structure of the second
 dman of sex-lethal determined by multidimensional
 magnetic resonance.";
 33:13775-13786(1994).
 NMR OF 122-209.
 155; PubMed=9299339;
 Y., Sakamoto H., Kigawa T., Takio K., Shimura Y.,
 stic arrangement of aromatic amino acid residues in the
 ture of the amino-terminal RNA-binding domain of
 c-lethal.";
 272:82-94(1997).
 Sex determination switch protein which controls sexual
 it by sex-specific splicing. Regulates dosage
 on in females by suppressing hyperactivation of X-linked
 pression of the embryo-specific isoform is under the
 primary sex-determining signal, which depends on the
 Chromosomes relative to autosomes (X:A ratio).
 occurs in 2X:2A cells, but not in X:2A cells. The X:A
 is to be signaled by the relative concentration of the X-
 inactivation factors SIs-A and SIs-B. As a result, the
 ific product is expressed early only in female embryos
 ies female-adult specific splicing, in the male where it
 pressed, the default splicing gives rise to a truncated
 nal protein. The female-specific isoform specifies the
 if its own transcript, thereby initiating a positive
 tory feedback loop leading to female development
 he female-specific isoform controls the sex-specific
 of transformer (TRA); acts as a translational repressor
 specific lethal-2 (MSL-2) and prevents male-less (MLE),
 MSL-3 proteins from associating with the female X
 .
 E PRODUCTS:
 nnative splicing; Named isoforms=5;

CC Comment=Additional isoforms seem to exist;
 CC Name=MS3; Synonyms=A, CF1;
 CC IsoId=P19339-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=P19339-2; Sequence=VSP_005881;
 CC Name=CMI;
 CC IsoId=P19339-3; Sequence=VSP_005882, VSP_005884;
 CC Name=MS11;
 CC IsoId=P19339-4; Sequence=VSP_005883, VSP_005885;
 CC Name=MS16;
 CC IsoId=P19339-5; Sequence=VSP_005886;
 CC -!- TISSUE SPECIFICITY: Expressed in somatic tissues, but not in
 CC pole cells, which are the precursors of the germline.
 CC -!- DEVELOPMENTAL STAGE: Isoform 1 is embryo-specific. Isoform C
 CC male-specific. Isoforms MS3, MS11 and MS16 are female specific.
 CC Isoform 1 is expressed for a brief period during the syncyti-
 CC blastoderm stage. Isoform MS11 is expressed in 4-7 hours emb;
 CC -!- DOMAIN: The Gly-Asn rich domain is required for the cooperat-
 CC interaction with RNA and for regulating the splicing activity;
 CC -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
 CC -----
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 CC -----
 CC EMBL; M23635; AAA28885.1; -;
 CC EMBL; M23636; AAA28884.1; -;
 CC EMBL; M59447; AAA28922.1; -;
 CC EMBL; M59448; AAA28921.1; -;
 CC EMBL; AE003439; AAG22410.1; -;
 CC EMBL; AE003439; AAG22411.1; -;
 CC EMBL; BT003583; AAO39587.1; -;
 CC EMBL; S88324; AAB21845.1; -;
 CC EMBL; D84425; BAA20294.1; -;
 CC PIR; A31639; A31639.
 CC PIR; A39725; B31639.
 CC PDB; 1SXU; 30-SEP-94.
 Query Match 1.5%; Score 8; DB 1; Length 354;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 212 PPPQPPA 219
 Db 313 PPPQPPA 320
 RESULT 126
 IF35 HUMAN
 ID IF35_HUMAN STANDARD; PRT; 357 AA.
 AC 000303;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon
 DE (eIF3 p47 subunit) (eIF3F).
 GN EIF385.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98001678; PubMed=9341143;
 RA Asano K., Vornlocher H.-P., Richter-Cook N.J., Merrick W.C.,
 RA Hinnebusch A.G., Hershey J.W.B.;
 RT "Structure of cDNAs encoding human eukaryotic initiation factor 3
 RT subunits. Possible roles in RNA binding and macromolecular assembl

OM N. A.

L. Feingold E.A., Grouse L.H., Derge J.G., Collins F.S., Wagner L., Shennem C.M., Schuler G.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., J.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C., quellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Milten E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., W., Touchman J.W., Green E.D., Dickinson M.C., C., Grimwood J., Schmutz J., Myers R.M., Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J.M., Marra M.A. and initial analysis of more than 15,000 full-length

Acad. Sci. U.S.A. 99:16899-16903 (2002).
 1. BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
 L-TRNAI AND MRNA. ASSOCIATES WITH THE COMPLEX P170-E1F3.
 E1F-3 is composed of at least 12 different subunits.
 E1F-3 contains 1 MPN (TAB/Mcv34) domain.

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90; AAH00490.1; -.
3275; EIF3S5.

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52; C:eukaryotic translation initiation factor 3 . . . ; TAS.
13; F:translation initiation factor activity; TAS.
46; P:regulation of translational initiation; TAS.

2003639; Pept M67_Mov34.
2000555; Peptidase M67.

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3; MOV34; 1.
3422; MOV34 1; 1.
5425; MOV34-2; 1.
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62; JAB MPN; 1.
factor; Protein biosynthesis; Polymorphism.
W -> L (in dbSNP:1044058)
172 172
/FTId=VAR 014452.

67 AA; 37564 MW; 8A70FC6E2BF07737 CRC64;

1.58; Score 8; DB 1; Length 357;

| | | | | | | | |
|--------------|--------|------------|----|--------|---|------|---|
| Conservative | 0 | Mismatches | 0 | Indels | 0 | Gaps | 0 |
| Identity | 100.0% | Pred. No. | 59 | | | | |

AATA 158

WATA 57

STANDARD; PRT; 359 AA.

Rel. 36, Created)

Rel. 36, Created)
Rel. 42, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)
Wnt-9b protein precursor (Wnt-15) (Wnt-14b).
WNT9B OR WNT15 OR WNT14B.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mni
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=21646332; PubMed=11786923;
Kirkoshi H., Katoh M.;
RT "Molecular cloning and characterization of mouse Wnt14b, cluster;
with mouse Wnt3 in mouse chromosome 11.";
RL Int. J. Mol. Med. 9:135-139(2002).
[2]
SEQUENCE FROM N.A.
RT STRAIN=BALB/c;
PC MEDLINE=21646332; PubMed=12573259;
RX Qian J., Jiang Z., Li M., Heaphy P., Liu Y.H., Shackleford G.M.;
RA "Mouse Wnt9b transforming activity, tissue-specific expression,
RT evolution.";
RL Genomics 81:34-46(2003).
[3]
SEQUENCE OF 211-310 FROM N.A.
RX MEDLINE=98110581; PubMed=9441749;
RX Bergstein I., Eisenberg L.M., Bhalarao J., Jenkins N.A.,
RA Copeland N.G., Osborne M.P., Bowcock A.M., Brown A.M.C.;
RA "Isolation of two novel Wnt genes, WNT14 and WNT15, one of which
RT (WNT15) is closely linked to WNT3 on human chromosome 17q21.";
RL Genomics 46:450-458(1997).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors. Probable developmental protein. May
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with
extracellular matrix.
CC -!- SIMILARITY: Belongs to the Wnt family.

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EMBL; AB073819; BAB83866.1; -
EMBL; AF469004; AAL82385.1; -
EMBL; AF031169; AAC39950.1; -
MGD; MGI:1197020; Wnt9b.
InterPro; IPR005817; Wnt.
InterPro; IPR005816; Wnt_grthfactor.
Pfam; PF00110; wnt; 2.
PRINTS; PROJ349; WNTPROTEIN.
SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
Wnt signaling pathway; Developmental protein; Glycoprotein; Signa
SIGNAL 1 23 POTENTIAL.
CHAIN 24 359 WNT-9B PROTEIN.
CARBOHYD 101 101 N-LINKED (GLCNAC..) (POTENTIAL).
CONFLICT 310 310 D -> G (IN REF. 3).
SEQUENCE 359 AA; 38981 MW; C98D7B5F566B70F5 CRC64;

Query Match 1.5%; Score 8; DB 1. Length 359;
Best Local Similarity 100.0%; Pred.No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Query Match 1.5%; Score 8; DB 1; Length 359;
Best Local Similarity 100.0%; Pred.No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; C

STANDARD; PRT; 372 AA.

4;
 Rel. 23, Created)
 Rel. 23, Last sequence update)
 Rel. 40, Last annotation update)
 wth/differentiation factor 1 precursor (GDF-1).

(Human).
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominidae; Homo.
 36;

N.A.
 545; PubMed=2034669;

growth/differentiation factor 1 in the nervous system;
 of a bicistronic structure.";
 J. Biol. Chem. 268:4250-4254 (1991).

N.A.
 McCready P.M., Adamson A.W., Burkhart-Schultz K.,
 Stenseth M., Kyle A., Ramirez M., Stillwagen S.,
 Ignan L., Bruce R., Quan G., Montgomery M., Ow D.,
 Nolan M., Trong S., Olsen A.O., Carrano A.V.;
 (1998) to the EMBL/GenBank/DBJ databases.

May mediate cell differentiation events during embryonic
 development; disulfide-linked (By similarity).

LOCUS: Secreted.
 FUNCTION: Expressed in the brain.
 belongs to the TGF-beta family.

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 or send an email to license@isb-sib.ch).

AAAS58501.1;
 ; AAB94786.1;
 39364.
 1BMP.
 14; GDF1.

; C:extracellular; ISS.
 ; F:cytokine activity; ISS.
 ; F:growth factor activity; ISS.
 ; P:cell differentiation; ISS.
 02400; GF_cysknot.
 02405; Inhibin_alpha.
 01839; TGFb.
 TGF-beta: 1.
 8; GFCYSKNOT.
 9; INHIBINA.
 57; TGFb; 1.
 ; TGFb; 1.
 50; TGF_beta: 1.
 factor; Cytokine; Glycoprotein.

1 29 POTENTIAL.
 0 253 POTENTIAL.
 4 372 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR
 1.
 7 337 BY SIMILARITY.
 6 369 BY SIMILARITY.
 0 371 BY SIMILARITY.
 5 336 INTERCHAIN (BY SIMILARITY).
 5 206 N-LINKED (GLCNAC. .) (POTENTIAL).
 2 158 POLY-ALA.
 9 118 V -> A (IN REF. 2).

SQ SEQUENCE 372 AA; 39502 MW; 10A484AA06304232 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 372;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; C

Qy 120 AAAAAAAP 127
 Db 152 AAAAAAAP 159

RESULT 129

HXA2 HUMAN STANDARD; PRT; 376 AA.
 ID HXA2 HUMAN STANDARD; PRT; 376 AA.
 AC O43364;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Homeobox protein Hox-A2.
 GN HOXA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jones K., Hinds K., Hawkins M., Duckels G.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Sequence-specific transcription factor which is par
 a developmental regulatory system that provides cells with
 specific positional identities on the anterior-posterior axis
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC PROBOSCIPEDIA SUBFAMILY.

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 or send an email to license@isb-sib.ch).

EMBL; AC004079; -; NOT_ANNOTATED_CDS.
 HSSP; P14653; 1B72.
 TRANSFAC; T03317;
 Genew; HGNC:5103; HOXA2.
 MIM; 604685;
 InterPro; IPR001827; Antennapedia.
 InterPro; IPR001356; Homeobox.
 InterPro; IPR000047; HTH_lambdarepressr.
 Pfam; PF00046; homeobox_1

DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 Transcription regulation; Polymorphism.
 FT SITE 94 99 ANTP-TYPE HEXAPEPTIDE.
 FT DNA BIND 143 202 HOMEBOX.
 FT VARIANT 196 196 M -> L (in dbSNP: 941002).
 FT /FTID=VAR_011890.

SQ SEQUENCE 376 AA; 41001 MW; 78EB388FE1EAD72 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 376;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Ga

Qy 151 AAAAAATA 158

|||||
ARATA 119

STANDARD; PRT; 377 AA.

(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
tein Chx10 (Chx-10 homeodomain containing homolog).

s (Chicken).

etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

031;

M N.A.

8593; PubMed=10640715;
, Cepko C.L.;
of Chx10 and Chx10-1 in the developing chicken retina.";

0:293-297(2000).

: Plays a significant role in the specification and
nesis of the sensory retina. May also participate in the
ent of the cells of the inner nuclear layer, particularly
cells (By similarity).

AR LOCATION: Nuclear (By similarity).

PECIFICITY: Retina and spinal cord.

ENTAL STAGE: Expressed throughout the invaginating optic
at stage 12, and uniformly throughout the neural retina
age 14 to stage 18. Expressed in the spinal cord from stage
age 20.

TY: Belongs to the paired homeobox family.

TY: Contains 1 CVC domain.

TY: Contains 1 homeobox domain.

TY: Contains 1 OAR domain.

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71; AAF40313.1; -

1FJL

1142; -

003654; Homeo OAR.

001356; Homeobox.

007104; Paired_homeo.

0; homeobox; 1.

0; OAR; 1.

010; Homeobox; 1.

0; HOX; 1.

027; HOMEBOX_1; 1.

071; HOMEBOX_2; 1.

003; OAR; 1.

1; regulation; Vision; Developmental protein;

in; Homeobox; DNA-binding.

67 226 HOMEBOX.

128 280 CVC.

123 336 OAR.

11 110 PRO-RICH.

36 158 SER/THR-RICH.

152 365 GLU/ASP-RICH (ACIDIC).

77 AA; 40645 MW; 1FCD9EF4664A3C21 CRC64;

1.5%; Score 8; DB 1; Length 377;

arity 100.0%; Pred. No. 61;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 AAAAAPP 129
Db 22 AAAAAPP 29

RESULT 131

SOX1_HUMAN

ID -SOX1_HUMAN STANDARD; PRT; 387 AA.

AC 000570;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE SOX-1 protein.

GN SOX1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98051911; PubMed=9337405;

RA Walas S., Duthie S.M., Mohri F., Lovell-Badge R., Episkopou V.;

RT "Cloning and mapping of the human SOX1: a highly conserved gene

expressed in the developing brain.";

RL Mamm. Genome 8:866-868(1997).

CC -! SUBCELLULAR LOCATION: Nuclear (Probable).

CC -! TISSUE SPECIFICITY: Mainly in the developing central nervous

system.

CC -! SIMILARITY: Contains 1 HMG box domain.

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CC EMBL; Y13436; CAA73847.1; -

DR HSSP; Q05086; LHRV.

DR Genew; HGNC:11189; SOX1.

DR MIM; 602148; -

DR GO; GO:0005634; C:nucleus; NAS.

DR GO; GO:0003700; P:transcription factor activity; NAS.

DR GO; GO:0006325; P:establishment and/or maintenance of chromatin.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NA.

DR InterPro; IPR000910; HMG_box; 1.

DR Pfam; PF00505; HMG_box; 1.

DR SMART; SM00398; HMG; 1.

DR PROSITE; PS00118; HMG_BOX_2; 1.

DR DNA-binding; Nuclear protein.

FT DOMAIN 27 43 POLY-GLY.

FT DNA_BIND 51 119 HMG_BOX.

FT DOMAIN 145 150 POLY-GLY.

FT DOMAIN 197 204 POLY-ALA.

FT DOMAIN 280 287 POLY-ALA.

FT DOMAIN 292 302 POLY-ALA.

FT DOMAIN 353 360 POLY-ALA.

SQ SEQUENCE 387 AA; 38855 MW; 8D43A38002CE3494 CRC64;

Query Match

Best Local Similarity 1.5%; Score 8; DB 1; Length 387;

Matches 8; Conservative 0; Mismatches 0; Indels 0; C

QY 119 PAAAAAAA 126

Db 352 PAAAAAAA 359

|||||

|||||

RESULT 132

MBNL_HUMAN

ID MBNL_HUMAN STANDARD; PRT; 388 AA.

043797;
 rel. 41, Created)
 rel. 41, Last sequence update)
 rel. 42, Last annotation update)
 ke protein (triplet-expansion RNA-binding protein).
 OR EXP OR KIAA0428.
 (Human).
 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Primates; Catarrhini; Hominidae; Homo.
 16;
 N.A. (ISOFORM 1).
 rbieri A.;
 1-1997) to the EMBL/GenBank/DBJ databases.
 N.A. (ISOFORM 2).
 155; PubMed=9455477;
 Nagase T., Nakajima D., Seki N., Ohira M.,
 Tanaka A., Kotani H., Nomura N., Ohara O.;
 the coding sequences of unidentified human genes. VIII.
 ones from brain which code for large proteins in
 7-313(1997).
 N.A. (ISOFORM 3), ALTERNATIVE SPLICING, AND
 ON.
 it4; PubMed=10970838;
 Irbinati C.R., Teng-Umuay P., Stenberg M.G., Byrne B.J.,
 Swanson M.S.;
 of human muscleblind proteins to (CUG) (n) expansions
 th myotonic dystrophy.";
 19-4448(2000).
 AR LOCATION: Nuclear.
 E PRODUCTS:
 ernative splicing; Named isoforms=3;
 ;
 ;
 ; NR56-1; Sequence=Displayed;
 ;
 ; NR56-2; Sequence=VSP_006430;
 ;
 ; NR56-3; Sequence=VSP_006429, VSP_006430;
 uscular dystrophy may be caused by aberrant recruitment
 the DMPC transcript (CUG) (n) expansion.
 ; Contains 4 C3H1-type zinc fingers.
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 il to license@isb-sib.ch).

 CAA74155.1; -;
 ; BAA24858.1; -;
 ; AAF76138.1; -;
 ; 23; MBNL1.
 ; C:cytoplasm; IDA.
 ; C:nucleus; IDA.
 ; F:double-stranded RNA binding; IDA.
 ; P:embryonic development (sensu Mammalia); ISS.
 ; P:limb morphogenesis; ISS.
 ; P:muscle development; ISS.
 ; P:myoblast differentiation; ISS.
 ; P:neurogenesis; ISS.
 ; 00571; Znf.CCCH.
 ; Znf.CCCH; 4.
 ; Znf.C3H1; 4.
 ; Repeat; Nuclear protein; RNA-binding;
 ; licing.

FT ZN_FING 14 40 C3H1-TYPE 1.
 FT ZN_FING 47 72 C3H1-TYPE 2.
 FT ZN_FING 179 206 C3H1-TYPE 3.
 FT ZN_FING 216 240 C3H1-TYPE 4.
 FT VARSPLIC 116 183 Missing (in isoform EXP35).
 FT /FTId=VSP_006429.
 FT VARSPLIC 270 287 Missing (in isoform EXP35 and isoform
 EXP40).
 FT /FTId=VSP_006430.
 SQ SEQUENCE 388 AA; 41817 MW; 118D256A81A86695 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 388;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 119 PAAAAAAA 126
 Db 166 PAAAAAAA 173
 RESULT 133
 SOX1_MOUSE
 ID SOX1_MOUSE STANDARD; PRT; 391 AA.
 AC P53783;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE SOX-1 protein.
 GN SOX1 OR SOX-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=96189340; PubMed=8625802;
 RA Collignon J., Sockanathan S., Hacker A., Cohen-Tannoudji M.,
 RA Norris D., Rastan S., Stevanovic M., Goodfellow P.N.,
 RA Lovell-Badge R.;
 RT "A comparison of the properties of Sox-3 with Sry and two related
 RT genes, Sox-1 and Sox-2.";
 RL Development 122:509-520(1996).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- TISSUE SPECIFICITY: Mainly in the developing central nervous
 CC system. Expressed in developing urogenital ridge.
 CC -!- SIMILARITY: Contains 1 HMG box domain.
 CC
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 CC
 CC EMBL; X94126; CAA63846.1; -;
 CC DR HSSP; Q05066; LHRV.
 CC DR MGD; MGI:98357; Sox1.
 CC DR InterPro; IPR000910; HMG_12_box.
 CC DR Pfam; PF0505; HMG_box; 1.
 CC DR SMART; SM00398; HMG; 1.
 CC DR PROSITE; PS0118; HMG_BOX_2; 1.
 CC KW DNA-binding; Nuclear protein.
 CC FT DOMAIN 30 43 POLY-GLY.
 CC FT DNA_BIND 51 119 HMG_BOX.
 CC FT DOMAIN 145 150 POLY-GLY.
 CC FT DOMAIN 197 204 POLY-ALA.
 CC FT DOMAIN 280 288 POLY-ALA.
 CC FT DOMAIN 296 306 POLY-ALA.
 CC FT DOMAIN 357 364 POLY-ALA.
 CC SEQUENCE 391 AA; 39237 MW; 9F81ED667F947C05 CRC64;
 SQ

1.5%; Score 8; DB 1; Length 391;

Identity 100.0%; Pred. No. 63; 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126

|||||

AAAAA 363

STANDARD; PRT; 392 AA.

(Rel. 28, Created)

(Rel. 40, Last sequence update)

(Rel. 41, Last annotation update)

tein engrailed-1 (Hu-En-1).

(Human).

atazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Primates; Catarrhini; Hominoidea; Homo.

106;

1 N.A.

3339; PubMed=1363401;

W. M.C., Noble-Topham S., Nallainathan D.,

Joyner A.L.;

sequence comparison of the mouse, human, and chicken
genes reveal potential functional domains and regulatory

3:345-358(1992).

288.

W. M.C., Noble-Topham S., Nallainathan D., Provart N.J.,

2000) to the EMBL/GenBank/DBJ databases.

AR LOCATION: Nuclear.

Y: Belongs to the engrailed homeobox family.

Y: Contains 1 homeobox domain.

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AAA53502.2;

AAA53502.2; JOINED.

B48423.

3HDD.

1015; EN1.

1342; EN1.

5; P.embryogenesis and morphogenesis; TAS.

1; P.skeletal development; TAS.

000747; Engrailed.

001356; Homeobox.

000047; HTH lambrapressr.

0100; Homeobox; 1.

026; ENGRAILED.

024; HOMEBOX.

031; HTHREPRESSR.

0100; Homeobox; 1.

09; HOX; 1.

027; HOMEBOX 1; 1.

071; HOMEBOX 2; 1.

033; ENGRAILED; 1.

1-binding; Developmental protein; Nuclear protein.

99 218 POLY-ALA.

124 231 POLY-GLY.

03 362 HOMEBOX.

SQ SEQUENCE 392 AA; 40101 MW; DESE63E7BFC7B51 CRC64;

Query Match

Best Local Similarity 100.0%; Score 8; DB 1; Length 392;

Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAAA 126

|||||

Db 198 PAAAAAAA 205

RESULT 135

HGHI_YEAST

ID HGHI_YEAST STANDARD; PRT; 394 AA.

AC P48362;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE HGHI protein.

GN HGHI OR YGR187C OR G7538.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE OF 111-394 FROM N.A.

RA Sun Z., Liang J., Hampsey M.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c;

RX MEDLINE=97279231; PubMed=9133739;

RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M

RA Nombela C.;

RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right

of Saccharomyces cerevisiae chromosome VII.";

RL Yeast 13:357-363(1997).

CC -!- SIMILARITY: TO S.POMBE SPAC26F1.12C.

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DR EMBL; U27358; AAA77038.1;

DR EMBL; 272972; CAA97213.1;

DR EMBL; X99074; CAA67531.1;

DR PIR; S64505; S64505.

DR Germline; 141499;

DR SGD; S0003419; HGHI.

DR InterPro; IPR008938; ARM.

DR InterPro; IPR007205; DUF383.

DR InterPro; IPR007206; DUF384.

DR Pfam; PF04063; DUF383; 1.

DR Pfam; PF04064; DUF384; 1.

FT DOMAIN 371 389

SQ SEQUENCE 394 AA; 44951 MW; 24D4RFAED5D7A48 CRC64;

Query Match

Best Local Similarity 100.0%; Score 8; DB 1; Length 394;

Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEDDE 336

|||||

Db 379 EEEEDDE 386

RESULT 136

KIM4_HUMAN

ID KIM4_HUMAN STANDARD; PRT; 394 AA.

```

rel. 39, Created)
rel. 39, Last sequence update)
rel. 40, Last annotation update)
I cuticular HA4 (Hair keratin, type I HA4).
1 OR HHA4.
(Human).
taoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
06;
N.A. PubMed=9756910;
582; PubMed=9756910;
Winter H., Wolf C., Heck M., Schweizer J.;
tion of a 190-kilobase pair domain of human type I hair
".
. 273:26683-26691(1998).
30US: THERE ARE TWO TYPES OF HAIR/MICROFIBRILLAR KERATIN,
I AND II (NEUTRAL TO BASIC).
f: Belongs to the intermediate filament family.
-----
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ail to license@isb-sib.ch).
-----
CAA76386.1; -.
152; KRTHA4.
.
1; P:epidermal differentiation; TAS.
301664; IF.
002957; Keratin_I.
; filament; I.
48; TYPE1KERATIN.
226; IF; 1.
Filament; Coiled coil; Keratin.
1 56
57 363 ROD.
54 394 TAIL.
57 91 COIL 1A.
92 102 LINKER 1.
03 203 COIL 1B.
04 219 LINKER 12.
20 363 COIL 2.
35 305 STUTTER.
t AA; 44689 MW; A651BF32918A98BF CRC64;
arity 1.5%; Score 8; DB 1; Length 394;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
CLIQ 78
|||||
CLIQ 89
STANDARD; PRT; 395 AA.
Rel. 32, Created)
rel. 32, Last sequence update)
rel. 41, Last annotation update)
ryotic translation initiation factor 5 (eIF-5).
omyces pombe (Fission yeast).
agi; Ascomycota; Schizosaccharomycetes;
omycetales; Schizosaccharomycetaceae;
omyces.
96;
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehea
RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
RA Weltjens I., Vansteert E., Rieger M., Schaefer M., Mueller-Auer
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhod
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Spakovski G.V., Usery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Catalyzes the hydrolysis of GTP bound to the 40S
CC ribosomal initiation complex (40S.mRNA.Met-tRNA[Met].eIF-2.GTP)
CC the subsequent joining of a 60S ribosomal subunit resulting i
CC release of eIF-2 and the guanine nucleotide. The subsequent
CC joining of a 60S ribosomal subunit results in the formation o
CC functional 80S initiation complex (80S.mRNA.Met-tRNA[Met] (By
CC similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the eIF-2-beta / eIF-5 family.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; Z50142; CAA90492.1; -.
DR PIR; T38553; S59149.
DR GeneDB SPombe; SPAC2F7.05c; -.
DR InterPro; IPR002735; eIF5_eIF2B.
DR InterPro; IPR003307; eIF5C.
DR Pfam; PF01873; eIF5_eIF2B; 1.
DR Pfam; PF02020; W2; 1.
DR ProDom; PD004078; eIF5_eIF2B; 1.
DR SMART; SM00653; eIF2B_5; 1.
DR SMART; SM00515; eIF5C; 1.
DR Hypothetical protein; Initiation factor; Protein biosynthesis;
KW GTP-binding.
FT NP_BIND 28 35 GTP (POTENTIAL).
FT DOMAIN 379 395 ASP/GLU-RICH (HIGHLY ACIDIC).
FT SEQUENCE 395 AA; 44944 MW; 18F49CB3CC8C2D11 CRC64;
SQ
Query Match 1.5%; Score 8; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY 329 EEEEDDE 336
DB 388 EEEEDDE 395

```

STANDARD; PRT; 396 AA.
(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 38, Last annotation update)
Retinal S-antigen) (Rod photoreceptor arrestin).
is (African clawed frog).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
crachia; Anura; Mesobatrachia; Pipidae;
Xenopus.
355;
4 N.A.
a;
a S., Knox B.E.;
EC-1995) to the EMBL/GenBank/DBJ databases.
: Arrestin is one of the major proteins of the rod
rod outer segments; it binds to photoactivated-
ylated rhodopsin, thereby apparently preventing the
in-mediated activation of phosphodiesterase.
NEOUS: Arrestin binds calcium.
TY: Belongs to the arrestin family.
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mail to license@isb-sib.ch).

: AAB88584.1; -;
: 1CF1.
3000698; Arrestin.
3007110; Ig-like.
; arrestin; 1.
; arrestin; 1.
; arrestin; 1.
309; ARRESTIN.
3099; ARRESTIN; 1.
3295; ARRESTINS; 1.
duction; Vision; Calcium-binding.
36 AA; 44623 MW; 3408AG5280CE7C14 CRC64;
1.5%; Score 8; DB 1; Length 396;
larity 100.0%; Pred. No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3EEDD 334
|||||
3EEDD 394
STANDARD; PRT; 396 AA.
(Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 42, Last annotation update)
1 factor SOX-11.
3 (Chicken).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
331;
4 N.A.
; 7693; PubMed=7748786;
Rex M., Cartwright E.J., Pearl G., Healy C.,
Scotting P.J., Sharpe P.T.;
"Embryonic expression of the chicken Sox2, Sox3 and Sox11 genes
suggests an interactive role in neuronal development.";
Mech. Dev. 49:23-36(1995).
-!- FUNCTION: May function as switches in neuronal development.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Low level expression is seen in
undifferentiated proliferating cells of neural epithelium. A
greater expression is seen in the maturing neurons after the
leave the neural epithelium. It is also found in the gut
epithelium and adrenal medulla.
-!- SIMILARITY: Contains 1 HMG box domain.

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or send an email to license@isb-sib.ch).

CC EMBL; U12534; AAB09664.1; -;
DR PIR; I50707; I50707.
DR HSSP; P48436; LSX5.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
DR PROSITE; PS0118; HMG_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DNA_BIND 49 117 HMG_BOX.
FT DOMAIN 162 165 POLY-ALA.
FT DOMAIN 204 212 POLY-GLU.
FT DOMAIN 288 294 POLY-PRO.
FT DOMAIN 332 335 POLY-ARG.
SQ SEQUENCE 396 AA; 43503 MW; 8E4B0A457F8BA833 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 212 PPPQPPA 219
Db 288 PPPQPPA 295
RESULT 140
HXAA MOUSE STANDARD; PRT; 399 AA.
AC P31310;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A10 (Hox-1.8).
GN HOXA10 OR HOXA-10 OR HOX-1.8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RX MEDLINE=95166244; PubMed=7862151;
RA Benson G.V., Nguyen T.-H.E., Maas R.L.;
RT "The expression pattern of the murine Hoxa-10 gene and the sequen
recognition of its homeodomain reveal specific properties of
Abdominal B-like genes";
RT Mol. Cell. Biol. 15:1591-1601(1995).
RL [2]
RP SEQUENCE OF 325-384 FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";

```

:ad. Sci. U.S.A. 88:10706-10710(1991).
{6-370 FROM N.A.
; TISSUE=Spleen;
;57; PubMed=1720547;
eckman J.F., Ruddle F.H.;
homeobox genes in development and evolution.";
:ad. Sci. U.S.A. 88:10711-10715(1991).
SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CENTRAL-REGULATORY SYSTEM THAT PROVIDES CELLS WITH
POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
THE DNA SEQUENCE 5'-AA[AT]TTTATTAC-3'.
AR LOCATION: Nuclear.
FE PRODUCTS:
alternative splicing; Named isoforms=2;
{1310-1; Sequence=Displayed;
{1310-2; Sequence=VSP_002386, VSP_002387;
SPECIFICITY: EXPRESSED IN THE DEVELOPING LIMB BUD WHERE IT
ATED TO THE MESENCHYME ALONG THE PROXIMAL-DISTAL AXIS.
) IN DEVELOPING GUT AND UROGENITAL TRACT. IN ADULT
)TH FORMS FOUND IN KIDNEY BUT ONLY ISOFORM 1 IS EXPRESSED
AL MUSCLE.
ITAL STAGE: EMBRYONIC EXPRESSION INCREASES FROM DAY 9 TO
) THEN DECLINES TO DAY 15.
): Belongs to the Abd-B homeobox family.
-----
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-----
AAA67125.1; -.
AAA63312.1; -.
.49754.
9ANT.
715; -.
.; Hoxa10.
01356; Homeobox.
; homeobox; 1.
;4; HOMEBOX.
;10; Homeobox; 1.
; HOX; 1.
;27; HOMEBOX 1; 1.
;71; HOMEBOX2; 1.
-binding; Developmental protein; Nuclear protein;
regulation; Alternative splicing.
;6 38 GLY-RICH.
;7 90 POLY-GLY.
;3 144 GLN/PRO-RICH.
;5 222 POLY-GLY.
;1 274 POLY-GLY.
;5 384 HOMEBOX.
;1 305 Missing (in isoform 2).
/FTID=VSP_002386.
;6 308 DSL -> MCQ (in isoform 2).
/FTID=VSP_002387.
) AA; 41415 MW; 7529624FC6057042 CRC64;
arity 1.5%; Score 8; DB 1; Length 399;
nservative 0; Pred. No. 64;
Mismatches 0; Indels 0; Gaps 0;
)POP 233
|||||
)POP 124

```

```

HME1 MOUSE
ID HME1 MOUSE STANDARD; PRT; 401 AA.
AC P09065;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein engrailed-1 (Mo-En-1).
GN EN1 OR EN-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93185339; PubMed=1363401;
RA Logan C., Hanks M.C., Noble-Topham S., Nallainathan D.,
RA Provart N.J., Joyner A.L.;
RT "Cloning and sequence comparison of the mouse, human, and chicken
RT engrailed genes reveal potential functional domains and regulator
RT regions.";
RL Dev. Genet. 13:345-358(1992).
RN [2]
RP SEQUENCE OF 278-401 FROM N.A.
RX MEDLINE=88112776; PubMed=2892757;
RA Joyner A.L., Martin G.R.;
RT "En-1 and En-2, two mouse genes with sequence homology to the
RT Drosophila engrailed gene: expression during embryogenesis.";
RL Genes Dev. 1:29-38(1987).
RN [3]
RP SEQUENCE OF 298-401 FROM N.A.
RX MEDLINE=86079501; PubMed=2416459;
RA Joyner A.L., Kornberg T., Coleman K.G., Cox D.R., Martin G.R.;
RT "Expression during embryogenesis of a mouse gene with sequence
RT homology to the Drosophila engrailed gene.";
RL Cell 43:29-37(1985).
RN [4]
RP SEQUENCE OF 321-380 FROM N.A.
RX MEDLINE=91099509; PubMed=1980115;
RA Holland P.W.H., Williams N.A.;
RT "Conservation of engrailed-like homeobox sequences during vertebr
RT evolution.";
RL FEBS Lett. 277:250-252(1990).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the engrailed homeobox family.
CC -!- SIMILARITY: Contains 1 homeobox domain.
-----
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-----
EMBL; L12703; AAA03660.2; -.
DR EMBL; Y00201; CAA68361.1; -.
DR PIR; A48423; A48423.
DR HSP; P02836; 3HDD.
DR TRANSFAC; T02016; -.
DR MGD; MGI:95389; Enl.
DR InterPro; IPR000747; Engrailed.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00026; ENGRAILED.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR PROSITE; PS00033; ENGRAILED; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.

```

52 87 PRO-RICH.
73 87 POLY-PRO.
207 228 POLY-ALA.
312 371 HOMEBOX.
11 AA; 40950 MW; 1F90210950152FAE CRC64;
1.5%; Score 8; DB 1; Length 401;
arity 100.0%; Pred. No. 65;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 126
|||||
AAAA 213

STANDARD; PRT; 405 AA.
35; Q9R221;
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
entiation factor 11 precursor (GDF-11) (Bone
protein 11).
(Mouse).
atazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0990;
A.N.A.
7155; PubMed=10075854;
Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
expressed in developing mouse limb, spinal cord, and tail
ant mesoderm inducer in Xenopus embryos.";
82:222-232(1999).

A.N.A.
3097; PubMed=10391213;
J., Lawler A.M., Lee S.-J.,
of anterior/posterior patterning of the axial skeleton by
centration factor 11.";
22:260-264(1999).

75-405 FROM N.A.
3787; PubMed=10072786;
Toyono T., Akanine A., Joyner A.,
of growth/differentiation factor 11, a new member of the
superfamily during mouse embryogenesis.";
0:185-189(1999).
: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
TICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
AND IN ESTABLISHING THE SKELETAL PATTERN.
Homodimer; disulfide-linked (by similarity).
LAR LOCATION: Secreted (Probable).
PECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD,
Y DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING
NS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT
ULP AND BRAIN
ENTAL STAGE: First strongly expressed in restricted
at 8.5 dpc where it is highest in the tail bud. At 10.5
ressed in the branchial arches, limb bud, tail bud and
r dorsal neural tube. Later, expressed in terminally-
tiated odontoblasts, the nasal epithelium, retina and
regions of the brain.
Ty: Belongs to the TGF-beta family.

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EMBL; AF100906; AAC72853.1;
EMBL; AF100904; AAC72853.1; JOINED.
EMBL; AF100905; AAC72853.1; JOINED.
EMBL; AF028337; AAF21633.1;
EMBL; AF028335; AAF21633.1; JOINED.
EMBL; AF028336; AAF21633.1; JOINED.
EMBL; AF092734; RAD05267.1;
HSSP; PI8075; BMP.
MGD; MG1:1338027; Gdf11.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0001656; P:metanephros development; IDA.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00888; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFb; 1.
PROSITE; PS00250; TGF BETA 1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
SIGNAL 1 20
FT PROPEP 21 236
FT CHAIN 297 405
FT DOMAIN 29 39
FT DOMAIN 208 213
FT DISULFID 311 370
FT DISULFID 339 402
FT DISULFID 343 404
FT DISULFID 369 369
FT CARBOHYD 92 92
FT CONFLICT 75 75
FT CONFLICT 171 171
FT CONFLICT 171 171
SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 119 PAAAAAA 126
Db 28 PAAAAAA 35

RESULT 143
GDFB HUMAN STANDARD; PRT; 407 AA.
AC Q95390; Q9UID1; Q9UID2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 11 precursor (GDF-11) (Bone
morphogenetic protein 11).
DE morphogenetic protein 11).
GN GDF11 OR BMP11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Fetal brain;
RC MEDLINE=99177155; PubMed=10075854;
RX Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.
RA Rosen V.;
RT "A novel BMP expressed in developing mouse limb, spinal cord, an
RT bud is a potent mesoderm inducer in Xenopus embryos.";
RL Dev. Biol. 208:222-232(1999).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=99318097; PubMed=10391213;
RX

Lawler A.M., Lee S.-J.;
 anterior/posterior patterning of the axial skeleton by
 entation factor 11.";
 2:260-264 (1999).
 SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
 ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 ICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
 ND IN ESTABLISHING THE SKELETAL PATTERN.
 Homodimer; disulfide-linked (By similarity).
 AR LOCATION: Secreted (Probable).
 Y: Belongs to the TGF-beta family.
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 7; AAC72852.1; -;
 3; AAF21630.1; -;
 4; AAF21631.1; -;
 BMP.
 216; GDF11.

 5; F: cytokine activity; NAS.
 3; P: mesoderm development; TAS.
 3; P: neurogenesis; TAS.
 1; P: skeletal development; TAS.
 001839; TGFb.
 00111; TGFb.N.
 ; TGF-beta; 1.
 ; TGFb propeptide; 1.
 357; TGFb; 1.
 4; TGFb; 1.
 250; TGF BETA 1; 1.
 ; Cytokine; Glycoprotein; Signal.
 1 24
 25 298 BY SIMILARITY.
 39 407 GROWTH/DIFFERENTIATION FACTOR 11.
 29 41 POLY-ALA.
 10 215 POLY-GLY.
 13 372 BY SIMILARITY.
 41 404 BY SIMILARITY.
 45 406 BY SIMILARITY.
 71 371 INTERCHAIN (BY SIMILARITY).
 94 94 N-LINKED (GLCNAC...) (POTENTIAL).
 7 AA; 45090 MW; E8FF48E3635BA8 CRC64;

 1.5%; Score 8; DB 1; Length 407;
 100.0%; Pred. No. 65;
 0; Mismatches 0; Indels 0; Gaps 0;

 AAAA 126
 ||||
 AAAA 35

 STANDARD; PRT; 407 AA.

 Rel. 28, Created)
 Rel. 28, Last sequence update)
 Rel. 42, Last annotation update)
 zinc finger protein ZK686.4 in chromosome III.

 elegans.
 azoa; Nematoidea; Chromadorea; Rhabditida; Rhabditoidea;
 peloderinae; Caenorhabditis.
 39;

SEQUENCE FROM N.A.
 STRAIN=Bx101 N2;
 MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson
 Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fraser A.,
 Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
 Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.
 Parsons J., Percy C., Rifken L., Ropra A., Saunders D., Showksee
 Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden K.
 Sulston J., Thierrey-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 Waterston R., Watson A., Weinstock L., Wilkinon-Sproat J.,
 Woldman P.;
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of
 elegans".
 Nature 368:32-38 (1994).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: Contains 1 C2H2-type zinc finger.

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 EMBL; L17337; AAA28220.1; -;
 PIR; S44909; S44909.
 WormPep; ZK686.4; CE00458.
 InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR003604; Znf_U1.
 DR SMART; SM00355; Znf_C2H2_1.
 DR SMART; SM00451; Znf_U1; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 KW Hypothetical protein; Zinc-finger; DNA-binding; Metal-binding;
 KW Nuclear protein.
 FT ZN FING 280 304 C2H2-TYPE.
 SQ SEQUENCE 407 AA; 47058 MW; 3DD7BE44966FC771 CRC64;

 Query Match 1.5%; Score 8; DB 1; Length 407;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G

 QY 330 EEDDDDED 337
 Db 378 EEDDDDED 385

 RESULT 145
 BHB3 MOUSE
 ID_BHB3 MOUSE STANDARD; PRT; 410 AA.
 AC Q99PV5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Class B basic helix-loop-helix protein 3 (bHLHB3) (Differentially
 DE expressed in chondrocytes protein 2) (mDEC2).
 GN BHLHB3 OR DEC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21092582; PubMed=11162494;
 RA Fujimoto K., Shen M., Noshiro M., Matsubara K., Shingu S., Honda
 Yoshida E., Suadrita K., Matsuda Y., Kato Y.;
 RT "Molecular cloning and characterization of DEC2, a new member of
 RT helix-loop-helix proteins.";
 RL Biochem. Biophys. Res. Commun. 280:164-171 (2001).
 CC -!- FUNCTION: May be a transcriptional repressor that represses b

activated transcription.
 Homodimerize.
 AR LOCATION: Nuclear (By similarity).
 PEPCIFITY: Expressed in skeletal muscle, brain and lung.
 Y: Contains 1 basic helix-loop-helix (bHLH) domain.
 Y: Contains 1 orange domain.

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90; BAB21503.1; -;
 JG7584.
 9704; Bhlhb3.
 9001092; HLH basic.
 9003650; Orange.
 9; HLH; 1.
 93; HLH; 1.
 91; ORANGE; 1.
 9888; HLH; 1.
 91 regulation; Repressor; DNA-binding; Nuclear protein.
 45 57
 BASIC DOMAIN.
 58 100
 HELIX-LOOP-HELIX MOTIF
 129 175
 ORANGE.
 321 373
 ALA/GLY-RICH
 10 AA; 43946 MW; 40A87281B08E233D CRC64;

1.5%; Score 8; DB 1; Length 410;
 Identity 100.0%; Pred. No. 66;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
 |||||
 AAAAA 341

STANDARD; PRT; 410 AA.
 (Rel. 41, Created)
 (Rel. 41, Last sequence update)
 (Rel. 42, Last annotation update)
 2 helix-loop-helix protein 3 (bHLHB3) (Enhancer-of-split
 related protein 1) (SHARP-1).
 ARF1.
 Gicus (Rat).
 stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Cheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 0116;

N.A.
 re-Dawley; TISSUE=Cerebellum;
 3761; PubMed=9532582;
 Doert J., Gass P., Schwab M.H., Nave K.-A.;
 nalian enhancer-of-split- and hairy-related proteins
 neuronal stimulation.";
 euroscl. 10:460-475(1997).
 May be a transcriptional
 d activated transcription.

Homodimerize.
 LAR LOCATION: Nuclear (By similarity).
 PEPCIFITY: Highly expressed in subregions of the brain,
 ly expressed in skeletal muscle, heart. Weakly expressed
 TY: Contains 1 basic helix-loop-helix (bHLH) domain.
 TY: Contains 1 orange domain.
 This is a conceptual translation; a frameshift was
 ed in position 249 to extend the similarity with mouse

ortholog.

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 CC modified and this statement is not removed. Usage by and for
 CC entities requires a license agreement (See <http://www.isb-sib.ch>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AF009329; AAB63586.1; ALT_FRAME.
 CC InterPro; IPR001092; HLH basic.
 CC InterPro; IPR003650; Orange.
 CC Pfam; PF00010; HLH; 1.
 CC SMART; SM00353; HLH; 1.
 CC SMART; SM00511; ORANGE; 1.
 CC PROSITE; PS50888; HLH; 1.
 CC Transcription regulation; Repressor; DNA-binding; Nuclear protei-
 KW DNA_BIND 45 57
 FT DOMAIN 58 100
 FT DOMAIN 129 175
 FT DOMAIN 321 344
 FT ALA/GLY-RICH.
 SQ SEQUENCE 410 AA; 43917 MW; 829705CA3A013127 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 410;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAAA 126
 |||||
 Db 334 PAAAAAAA 341

RESULT 147
 HMH2 DROME
 ID HMH2 DROME STANDARD; PRT; 410 AA.
 AC F10035;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Homeobox protein H2.0.
 GN H2.0.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88329003; PubMed=2901348;
 RA Barad M., Jack T., Chadwick R., McGinnis W.;
 RT "A novel, tissue-specific, Drosophila homeobox gene.";
 RL EMBO J. 7:2151-2161(1988).
 CC -!- FUNCTION: May have an important role in the morphogenesis of
 CC single tissue type.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: Exhibits a tissue specific pattern of
 CC expression. It accumulates in cells of the visceral musculat
 CC and its anlagen.
 CC -!- SIMILARITY: Belongs to the H2.0 homeobox family.
 CC -!- SIMILARITY: Contains 1 homeobox domain.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; Y00843; CAA68766.1; -;
 CC PIR; S00994; WJFFH2.
 CC HSP; P06601; 1FJUL.

0001170; H2.O.
 001356; Homeobox.
 000047; HTH lambdarepressor.
 ; homeobox; 1.
 24; HOMEBOX.
 31; HTHREPRESSOR.
 010; Homeobox; 1.
 9; HOX; 1.
 027; HOMEBOX 1; 1.
 071; HOMEBOX 2; 1.
 -binding; Developmental protein; Nuclear protein.
 80 204 HHS/GLN-RICH (OPA-REPEAT).
 87 346 HOMEBOX.
 0 AA; 44950 MW; D81E71395A12D5BD CRC64;
 arity 1.5%; Score 8; DB 1; Length 410;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAA 126
 |||||
 AAAA 259
 STANDARD; PRT; 412 AA.
 Rel. 35; Created)
 Rel. 35; Last sequence update)
 Rel. 42; Last annotation update)
 binding nuclear protein (EC 5.2.1.8) (Peptidyl-prolyl
 merase) (PPIase) (Rotamase).
 ugiherda (Fall armyworm).
 tazoza; Arthropoda; Hexapoda; Insecta; Pterygota;
 opterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 shipyriinae; Spodoptera.
 08;
 N.A.
 110; PubMed=7527037;
 Fernandes-Alnemri T., Pomeroy K., Robertson N.M.,
 boia G.C., Litwack G.;
 vel Sf9 insect cell nuclear immunophilin that forms a
 e complex.";
 . 269:30828-30834(1994).
 PPIases accelerate the folding of proteins. It catalyzes
 rans isomerization of proline imidic peptide bonds in
 ides. Binds double-stranded DNA in vitro.
 ACTIVITY: Peptidylproline (omega=180) = peptidylproline
 .
 ULATION: Inhibited by both FK506 and rapamycin.
 AR LOCATION: Nuclear.
 phosphorylated by a nuclear kinase in the presence of Mg(2+)
 f: Belongs to the FKBP-type PPIase family.
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 ail to license@isb-sib.ch).

 AAA58962.1; -.
 455320.
 1FKJ.
 001179; FKBP_PPIase.
 ; FKBP; 1.
 153; FKBP_PPIASE 1; FALSE_NEG.
 154; FKBP_PPIASE 2; 1.
 DR PROSITE; PS50059; FKBP_PPIASE 3; 1.
 KW Isomerase; Rotamase; Nuclear Protein; DNA-binding; Phosphorylati
 FT DOMAIN 91 112 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 120 145 LYS-RICH (BASIC).
 FT DOMAIN 152 216 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 219 302 LYS-RICH (BASIC).
 FT DOMAIN 324 412 PPIASE, FKBP-TYPE.
 SQ SEQUENCE 412 AA; 45810 MW; F2A69159AEF4FE22 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 412;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 331 EEDDDDE 338
 DB 194 EEDDDDE 201
 RESULT 149
 CRTC MOUSE
 ID CRTC MOUSE STANDARD; PRT; 416 AA.
 AC P14211,
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 CX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A. AND SEQUENCE OF 18-48 AND 129-161.
 RP STRAIN=BALB/C; TISSUE=Liver;
 RX MEDLINE=9005955; PubMed=2583110;
 RA Smith M.J., Koch G.L.E.;
 RT "Multiple zones in the sequence of calreticulin (CRP55, calreguli
 RT HACBP), a major calcium binding ER/SR protein.";
 RL EMBO J. 8:3581-3586(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9301303; PubMed=1398135;
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
 RT "Determination of the sequence of an expressible cDNA clone encod
 RT ERP60/calregulin by the use of a novel nested set method.";
 RL Gene 120:217-225(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N-3; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 18-38.
 RC TISSUE=Fibroblast;

907; PubMed=7523108;
 . Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 and sequencing of familial and novel murine proteins
 active two-dimensional gel electrophoresis.";
 sis 15:735-745(1994).
 : This protein binds calcium. There are both high and
 nity calcium-binding sites.
 Monomer (By similarity).
 AR LOCATION: Endoplasmic reticulum lumen.
 TY: Belongs to the calreticulin family.

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 / CAA33053.1; -.
 53; AAA37569.1; -.
 S06763.
 ; P14211; MOUSE.
 52; Calr.
 09; F:calcium ion binding; IDA.
 R009033; Calret_calmex_P.
 R001580; Calreticulin.
 R008985; ConA like lec_gl.
 R000886; ER_target_S.
 2; calreticulin; 1.
 J02356; Calreticulin; 1.
 526; CALRETICULIN.
 1866; Calreticulin; 1.
 J014; ER TARGET; 1.
 J003; CALRETICULIN_1; 1.
 J004; CALRETICULIN_2; 1.
 J005; CALRETICULIN_REPEAT; 3.
 reticulum; Calcium-binding; Repeat; Signal.
 1 17
 18 416 CALRETICULIN.
 18 197 N-DOMAIN.
 198 308 P-DOMAIN.
 309 416 C-DOMAIN.
 191 255 4 X APPROXIMATE REPEATS.
 191 202 1-1.
 210 221 1-2.
 227 238 1-3.
 244 255 1-4.
 259 297 3 X APPROXIMATE REPEATS.
 259 269 2-1.
 273 283 2-2.
 287 297 2-3.
 351 407 ASP/GLU/LYS-RICH.
 137 163 BY SIMILARITY.
 413 416 PREVENT SECRETION FROM ER.
 16 AA; 47994 MW; 24C03B00913408D8 CRC64;
 1.5%; Score 8; DB 1; Length 416;
 Larity 100.0%; Pred. No. 67;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 EDED 342
 |||||
 EDED 399

 STANDARD; PRT; 416 AA.
 52;
 (Rel. 10, Created)
 (Rel. 16, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (CAL
 GN Calcium-binding protein 3) (CABP3).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370496; PubMed=2395661;
 RA Murthy K.K., Hanville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product a
 the Onchocerca volvulus antigen Ral-1";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported
 the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function i
 Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN=LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin
 autoimmune antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high an
 affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC -!- CAUTION: Was originally (Ref.2) thought to be D-beta-
 hydroxybutyrate dehydrogenase.

 CC

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BA11345.1; -
CAA37446.1; -
CAA31987.1; ALT_SEQ.
CAA55890.1; -
JH0819.
-FEB-02.
-OCT-02.
-OCT-02.
009033; Calret_calmex P.
001580; Calreticul.
008985; ConA like lec_gl.
000886; ER target_S.
; calreticul. 1.
02356; Calreticul. 1.
26; CALRETICULIN.
366; Calreticul. 1.
014; ER TARGET; 1.
303; CALRETICULIN 1; 1.
304; CALRETICULIN 2; 1.
305; CALRETICULIN REPEAT; 3.
; Calcium-binding; Repeat; Signal; 3D-structure.
1 17
-8 416 CALRETICULIN.
-8 197 N-DOMAIN.
08 308 P-DOMAIN.
09 416 C-DOMAIN.
11 255 4 X APPROXIMATE REPEATS.
11 202 1-1.
0 221 1-2.
17 238 1-3.
4 255 1-4.
9 297 3 X APPROXIMATE REPEATS.
9 269 2-1.
3 283 2-2.
17 297 2-3.
1 407 ASP/GLU/LYS-RICH.
7 163 BY SIMILARITY.
3 416 PREVENT SECTATION FROM ER.
AA; 47995 MW; 2E6713CED31A2970 CRC64;
1.5%; Score 8; DB 1; Length 416;
rity 100.0%; Pred.No.67;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
BED 342
|||
BED 399

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arch 30, 2004, 15:01:08